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"FAST" SNPS ANALYSIS FOR HUMAN IDENTIFICATION

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Single nucleotide polymorphisms (SNPs) have some characteristics that make them very appropriate for forensic studies and applications. They are abundant and genetically stable. However, because of the low discrimination power in each single locus, it is necessary to analyze as many loci as possible for human identification. We investigated 120 autosomal SNPs in 100 unrelated Japanese and built a SNPs Japanese database for identification. In addition, the rapid analysis system was established by the modified TaqMan FAST Assay. Genomic DNA was extracted from buccal swab using automatic DNA extraction system QuickGene-800 (FUJIFILM). One hundred twenty informative autosomal SNPs markers were selected from JSNP database (http://snp.ims.u-tokyo.ac.jp/index_ja.html) and TaqMan SNP Genotyping Assays database (AppliedBiosystem). SNPs typing were performed by the TaqMan SNP Genotyping Assays using the 9800 Fast Thermal Cycler (AppliedBiosystems) and the ABI PRISM 7700 or 7500 FAST Real-Time PCR System (AppliedBiosystems). The mean value of matching probability of 120 SNPs was 0.383, and total ones of this system was 9.81 x E–51. Furthermore, no significant deviation from Hardy-Weinberg Equilibrium was detected. In this study, it took an hour or less to detect alleles including DNA extraction procedures using the latest high-throughput technologies. A 96 well palate shows only 24 SNPs at one time. The best matching probability of 24 SNPs was 6.06 x E–11, and it was a similar value of AmpFlSTR Plofiler (AppliedBiosystems). A 384 well plate can analyze 96 SNPs, matching probability 3.00 x E–41. A SNPs examination is expected to replace STRs as a prompt test of DNA profiling.