

NEWLY DEVELOPED MULTIPLEX SNPS TYPING SYSTEM BASED ON INVADER ASSAY

Hiroaki Nakahara¹, Tetsushi Kitayama¹, Kazumasa Sekiguchi¹, Naoya Hosono², Mitsuaki Kubo², Yusuke Nakamura²

¹*National Research Institute of Police Science, Japan*

²*Center for Genomic Medicine, RIKEN, Japan*

We have developed a new multiplex, single nucleotide polymorphism (SNP) typing system based on the Invader assay for forensic identification.

In our experiment, twenty-one SNP loci were amplified in one reaction by multiplex PCR. PCR products were analyzed using newly designed Analyzing Chip and instrument (Toppan printing). Direct sequencing analysis of DNA samples was carried out in order to confirm the typing results. And new SNP typing criterion value available for multiplex SNPs typing by Invader assay was defined and applied for our experiment. The sensitivity of this system was examined using small amount of template DNA and artificially degraded DNA samples.

More than one thousand of SNPs typing results were proved to be correct by direct sequencing analysis. The comparison between this SNP typing method and usual short tandem repeat (STR) typing method was performed. The detection sensitivity was higher than that of multiplex STR typing and all SNP loci could be detected and typed correctly from 0.16 ng of template DNA. All of SNPs could be detected correctly from degraded samples from which typing of STR markers was impossible. In conclusion, the multiplex SNPs typing using new system is advantage in forensic identification and will be especially useful for typing of degraded DNA samples.