

ALLELE FREQUENCY DISTRIBUTIONS AT PENTANUCLEOTIDE STRS INCLUDED IN A NEWLY COMMERCIALY RELEASED TRIPLEX TYPING SYSTEM IN A JAPANESE POPULATION

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Since, in general, the peak height ratios of stutter bands to the main bands at pentanucleotide STR loci are lower than those at tetranucleotide ones, it is said that the former are more useful than the latter for genotyping from forensic mixed specimens. Recently, a novel triplex primer sets for pentanucleotide STRs, Penta BEC Multiplex Primers, has been released from Promega. In the present study, we analyzed 300 unrelated healthy Japanese (Nagoya area) using this triplex primer sets for Penta B, Penta E and Penta C loci with a Genetic Analyzer 310, and calculated the allele frequencies at each loci. The genotyping was performed semi-automatically with a macro in a Genotyper 2.5 temporarily constructed from the fragment sizes of each allele at those loci. Two irregular alleles (18.4 and 19.4) were observed at Penta E, of which sequences were confirmed by sequencing and were the same as those reported previously in a Japanese population. Tests for Hardy-Weinberg equilibrium (HWE) were carried out using homozygosity test, likelihood ratio test and exact test. No significant deviations ($P < 0.05$) from HWE were observed at those loci with all three tests. The observed heterozygosity, PD and MEC values were 0.80, 0.93 and 0.61 at Penta B, 0.92, 0.98 and 0.84 at Penta E, and 0.73, 0.90 and 0.48 at Penta C, respectively. We also calculated the peak height ratios of stutter bands to the main bands at those pentanucleotide loci. Those ratios were less than a few %, which were lower than those at tetranucleotide ones. Therefore, it was suggested that genotyping for pentanucleotide STRs would be more useful to interpret genotypes from forensic mixed specimens than that for tetranucleotide ones.