

**16 Y-CHROMOSOMAL STR HAPLOTYPES IN JAPANESE AND DNA SEQUENCE ANALYSIS OF VARIANT ALLELES**

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A total of 1193 Japanese males were typed for the following 16 Y chromosomal short tandem repeat (Y-STR) loci: DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385, DYS393, DYS391, DYS439, DYS635, DYS392 Y GATA H4, DYS437, DYS438 and DYS 448 using an AmpFISTR® Yfiler™ PCR amplification kit. A total of 1039 haplotypes for the 16 Y-STR loci were detected and, of these, 965 haplotypes were unique. The most frequent haplotype was found in 23 Japanese males. Mean pairwise difference was calculated to be 9.92 loci. Haplotype diversity was calculated to be 0.9992. The 16 Y-STR haplotyping appears to have a good potential for differentiating between Japanese male individuals.

There was one haplotype (one individual) with no allele detected at DYS437. The DNA sample from this individual was also analyzed using the PowerPlex® Y system and no allele was detected. There were 10 haplotypes (10 individuals) with no allele detected at DYS448. There were 2 haplotypes (2 individuals) with more than two alleles detected at DYS385. At the DYS458, a variant allele migrating as an allele 14.1 was observed in two individuals. Sequence analysis revealed an A insertion downstream the repeat region in both individuals at the same nucleotide position. At the DYS385, a variant allele migrating as an allele 9.2 was observed in three individuals. Sequence analysis found [AAGG]6[GAAA] 5 [AA] [GAAA] 4 in the repeat region in the three individuals. At the DYS392, a variant allele migrating as an allele 20 was observed in one individual. Sequence analysis confirmed 20 repeats of TAT.