

FORENSIC PARAMETERS AND ALLELE FREQUENCY DISTRIBUTIONS OF 33 STR IN A JAPANESE POPULATION

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Recently, more STR loci have been required to confirm positive human identification by many domestic and international forensic agencies. We investigated the genetic parameters and allele frequencies for 396 unrelated Japanese DNA samples using 33 autosomal short tandem repeat (STR) loci which are available in several commercial STR multiplex kits.

The analyzed 33 STR were listed; TPOX, D5S818, D13S317, D7S820, CSF1PO, D16S539, TH01, D3S1358, D8S1179, D18S51, D21S11, FGA, vWA, D12S391, D1S1656, D10S1248, D22S1045, D2S441, SE33, D2S1338, D19S433, D6S1043, D2S1360, D3S1744, D4S2366, D5S2500, D6S474, D7S1517, D8S1132, D10S2325, D21S2055, Penta D and Penta E. In addition, the amelogenin and DYS391 loci were examined at the same time for gender analysis and reconfirmation. We typed these STR loci according to manufacturer's protocols with PowerPlex Fusion (Promega), PowerPlex ESX17 (Promega), Investigator HDplex (QIAGEN) and AmpFISTR Sinofiler (Life Technologies). The electrophoresis was performed with ABI 3500 Genetic Analyzer (Life Technologies) and the STR alleles were determined by the GeneMapper ID-X software (Life Technologies). The statistical data was calculated by the Alrequin 3.5 software and the PowerStats v12 (Promega).

The SE33 locus proved to be highly polymorphic (PIC:0.934), 0.566 showed the lowest value (D2S1360). The value of PD for male indicated the value ranging from 0.808 (D2S1360) to 0.988 (SE33). The total matching probability indicated 4.63×10^{-40} . Furthermore, no significant deviation from Hardy-Weinberg Equilibrium was detected excluding D22S1045 after Bonferroni correction. Finally, we established the Japanese 33 STR database for forensic application such as human identification or paternity test.