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POPULATION GENETICS OF EIGHT X-CHROMOSOMAL STRS IN A JAPANESE POPULATION

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X-chromosomal STRs (X-STRs) have been recognized as important tools in forensic analysis, particularly in complex cases of kinship testing. In this report, we investigated 8 X-STRs in 516 unrelated Japanese (309 males and 207 females) and built a X-SNPs Japanese database for identification. Genomic DNA was extracted from blood sample or buccal swab using automatic DNA extraction system QuickGene-800 (FUJIFILM). X-STRs multiplex amplification was performed by the MentypeR Argus X-8 PCR Amplification Kit (Biotype AG) which contains eight X-STRs, that is DXS7132, DXS7423, DXS8378, DXS10074, DXS10101, DXS10134, DXS10135 and HPRTB, as well as Amelogenin for sex determination. Electrophoresis and allele typing were carried on ABI PRISM 310 Genetic Analyzer and GeneMapper ID ver.3.7 software (Applied Biosystems). Allele frequencies and polymorphism information content (PIC) were calculated from the combined data of males and females, whereas power of discrimination (PD) was figured out for each data. The DXS10135 locus proved to be highly polymorphic (PIC:0.914), DXS7423 showed the lowest value (0.441). The value of PD for male indicated the value ranging from 0.505(DXS7423) to 0.920(DXS10135), while PD for female ranged from 0.705(DXS7423) to 0.987(DXS10135). Furthermore, no significant deviation from Hardy-Weinberg Equilibrium was detected. We concluded that these eight X-STR markers offer high effectiveness for forensic application