FOR THE RECORD

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Population Data of the COfiler STR Loci in Koreans

POPULATION: Koreans

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Buccal swab samples were obtained from 300 unrelated healthy individuals living in Seoul, Korea. Genomic DNA was extracted using QIAamp DNA Mini Kit (QIAGEN) according to the manufacturer’s protocols. PCR amplification was performed by using the AmpF/STR® COfiler™ PCR Amplification Kit (Applied Biosystems) on a GeneAmp PCR system 9600 (Perkin Elmer) according to the technical manual (1) with exception of 13 μl volume reactions.

The PCR products were loaded into an ABI Prism 310 Genetic Analyzer (Applied Biosystems) and the allele-size data of both the allelic ladders and unknown samples were generated by the GeneScan 3.1 (Applied Biosystems) software. Alleles were automatically designated using Genotyper 2.5 (Applied Biosystems) Kazam macro by comparison with the kit allelic ladders.

The allele frequency of each locus was calculated from the observed number of each genotype. To evaluate linkage equilibrium and Hardy-Weinberg equilibrium (HWE), the Fisher’s exact test based on 100,000 shuffling using GDA (Genetic Data Analysis) program (http://lewis.eeb.uconn.edu/lewishome/software.html) was performed. The observed heterozygosity (Obs-H) and the expected heterozygosity (Exp-H) (2), the polymorphism information content (PIC) (3), the power of discrimination (PD) (4) and the mean exclusion chance (MEC) (5) were also calculated (Table 1).

No deviation of linkage equilibrium was found among loci ($p > 0.05$). Also, we did not find significant deviation from Hardy-Weinberg equilibrium in each marker ($p > 0.05$). In the previous work, we reported allele frequencies of the Profiler Plus STR loci in a Korean population (6). Therefore, these resultant data for all 13 CODIS core STR loci will be very useful for human identification and paternity analysis in Koreans.

The complete data are available to any interested researcher upon request from the corresponding author.

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References


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