

FOR THE RECORD

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Population Data of the COfiler STR Loci in Koreans

POPULATION: Koreans

KEYWORDS: forensic science, COfiler STRs, allele frequency, Koreans

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 μ L 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.

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TABLE 1—Allele frequencies and forensic efficiency of the COfiler STR loci in Koreans.

Allele	D3S1358	D16S539	TH01	TH0X	CSF1PO	D7S820
6			0.167			
7			0.218		0.003	0.002
8		0.002	0.030	0.500	0.002	0.153
9		0.257	0.518	0.117	0.035	0.053
9.3			0.048			
10		0.142	0.018	0.032	0.250	0.188
11		0.255		0.305	0.225	0.338
12	0.003	0.225		0.043	0.403	0.223
13	0.003	0.112		0.003	0.072	0.037
14	0.033	0.008			0.010	0.005
15	0.405					
16	0.292					
17	0.210					
18	0.050					
19	0.003					
<i>P</i>	0.366	0.064	0.123	0.545	0.165	0.976
Obs-H	0.713	0.800	0.650	0.653	0.760	0.787
Exp-H	0.704	0.787	0.653	0.642	0.719	0.774
PIC	0.651	0.752	0.607	0.583	0.671	0.738
PD	0.865	0.921	0.837	0.811	0.864	0.915
MEC	0.452	0.576	0.415	0.386	0.477	0.562

P: Fisher's exact test for Hardy-Weinberg equilibrium; Obs-H: observed heterozygosity; Exp-H: expected heterozygosity; PIC: polymorphism information content; PD: power of discrimination; MEC: mean exclusion chance.

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

Acknowledgments

This work was supported by a grant from the Korea Science and Engineering Foundation through the Biometrics Engineering Research Center at Yonsei University.

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