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FOR THE RECORD

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Allele Frequency Distribution of Three STR Loci (D5S818, Penta D, and Penta E) in Turkish Population

POPULATION: 143 unrelated individuals from Turkey

KEYWORDS: forensic science, DNA typing, population genetics, short tandem repeats, polymerase chain reaction, D5S818, Penta D, Penta E, Turkey

The samples were collected from unrelated individuals randomly selected from criminal cases. The DNA was extracted from bloodstains, and single hairs by Chelex 100 method (1).

The extracted DNA was quantitated according to the quantification procedure (2). Slot-blot hybridization was done using the Quantiblot® Human DNA Quantitation Kit (Perkin Elmer, Norwalk, CT).

PCR amplification was performed according to the manufacturer's instructions, using the GenePrint® PowerPlex™ 16 System (Promega Corporation, Madison, WI). In PCR, 0.5–1 ng of template DNA were used. The samples were amplified using GeneAmp PCR System 9700 (PE Biosystems, Foster City, CA). The amplified products were detected with the ABI PRISM®310 Genetic Analyzer using the separation medium Performance Optimmized Polymer (POP) 4™ (PE Biosystems, Foster City, CA).

The results were analyzed using Gene Scan analysis software v.3.1.2 and genotypes were determined by comparison to allelic ladder using Genotyper DNA fragment analysis software v.2.5 (PE Biosystems, Foster City, CA) with the PowerTyper™ 16 Macro (Promega Corporation, Madison, WI).

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Allele designations were determined by comparison of the sample fragments with those of allelic ladders provided with kit. The frequency of each allele for each locus was calculated from the numbers of each genotype in the sample set. Exact test was performed by using the computer program GDA (3) for the Hardy-Weinberg expectations. Population statistics data were analyzed by PowerStats (4).

The dataset can be accessed at http://hadicakir.medyatext.gen.tr.

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TABLE 1—*Observed alleles frequencies for three STR loci in a sample population (*n *= 143) from Turkey.*

Allele	D5S818	Penta D	Penta E
5	…	…	0.056
6	…	0.003	…
7	0.003	0.010	0.112
8	0.014	0.007	0.010
9	0.084	0.185	0.007
10	0.077	0.140	0.073
11	0.304	0.241	0.122
12	0.283	0.112	0.182
13	0.217	0.161	0.108
14	0.010	0.105	0.049
15	0.003	0.035	0.063
16	0.003	…	0.087
17	…	…	0.049
18	…	…	0.042
19	…	…	0.014
20	…	…	0.003
21	…	…	0.010
22	…	…	0.010
Ho	0.734	0.839	0.860
He	0.770	0.839	0.904
P*	0.269	0.926	0.099
P**	0.126	0.934	0.056
PD	0.900	0.949	0.975
PEP	0.483	0.674	0.715
MP	0.100	0.051	0.025
TPI	1.88	3.11	3.58
PIC	0.73	0.82	0.89

Ho: (observed heterozygosity), He: (expected heterozygosity), P*: (Heterozygosity, $\chi^2|_{df}$ based on unbiased estimate with 3200 shufflings), P**: (exact test; based on 3200 shufflings), PD: (power of discrimination), PEP: (excluding probability of paternity), MP: (matching probability), TPI: (typical paternity index), PIC: (polymorphism information content).