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FOR THE RECORD

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Population Genetic Data on the STR Loci D2S1338, D19S433 and SE33 in Hungary

POPULATION: Hungarian population. Allele frequency and profile database for the STR loci D2S1338, D19S433 and SE33 (ACTBP2) were obtained from a population sample of 224 unrelated individuals living in the Budapest area of Central Hungary. One sample showed a three-allele pattern at the SE33 locus.

KEYWORDS: forensic science, Hungarian population, D2S1338, D19S433, SE33, short tandem repeat, three-allele pattern, DNA typing, population genetics, Budapest, Central Hungary

Blood samples of 225 unrelated individuals living in Central Hungary were collected irrespective of ethnic background in a blood bank of Budapest (1). The genomic DNA of the samples was isolated from whole blood using proteinase K digestion, organic extraction and Microcon-100 (Millipore) ultrafiltration. PCR amplification was carried out on 1–2 ng template DNA in 25 μL reaction volume following manufacturers' instructions (AmpFℓSTR Identifiler PCR amplification kit, Applied Biosystems; PowerPlex® ES System, Promega). The PCR products were analyzed on ABI3100 Genetic Analyzer. For fragment sizing and genotyping GeneScan Analysis v3.1.2 and Genotyper v2.5.2 softwares were used. Analysis of the Hardy-Weinberg equilibrium was performed by the exact test (2), as well as the observed and expected heterozygosity values were calculated using the Arlequin ver.2001 software (http://lgb.unige.ch/arlequin) (3). Allelic designation and nomenclature of the genotypes during the analyses was done according to previous recommendations (4,5). Until now no published data were available for the loci D2S1338 and D19S433 in the Hungarian population. Genotyping the population sample at the locus SE33 one sample possessed three alleles (14,16,17) showing a well-balanced three-allele pattern. This and three other samples that have carried 16.3 or 18.3 alleles at locus SE33 have been re-extracted and re-analyzed. The repeated analyses showed the same allele pattern. The sample harbouring the three-allele pattern was removed from the database, therefore the original sample size decreased from 225 to 224. The forensically informative population genetic data are demonstrated in Table 1.

Access to the data: Available upon request via electronic mail from corresponding author, Balazs Egyed, at balazs.egyed@mail.orfk.b-m.hu

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TABLE 1—*Allele frequencies and forensically informative statistical values for the analyzed STR loci in the Hungarian population (N = 224).*

Allele	D2S1338	D19S433	SE33
11		0.0089	0.0022
12		0.1116	0.0022
13		0.2344	0.0067
13.2		0.0089	0.0045
14		0.3304	0.0491
14.2		0.0179	0.0045
15		0.1607	0.0446
15.2		0.0513	0.0022
16	0.0469	0.0335	0.0580
16.2		0.0246	
16.3			0.0045
17	0.2121	0.0067	0.0714
17.2		0.0045	
18	0.0781		0.0781
18.2		0.0067	
18.3			0.0022
19	0.0893		0.0893
19.2			0.0045
20	0.1518		0.0469
20.2			0.0045
21	0.0402		0.0335
21.2			0.0067
22	0.0179		0.0022
22.2			0.0201
23	0.1161		
23.2			0.0357
24	0.1094		
24.2			0.0223
25	0.1138		
25.2			0.0469
26	0.0223		
26.2			0.0513
27	0.0022		
27.2			0.0826
28.2			0.0603
29.2			0.0603
30.2			0.0513
31.2			0.0134
32.2			0.0201
33			0.0067
33.2			0.0022
34			0.0022
34.2			0.0067
P_{exact}	0.7144	0.3286	0.3153
H_{obs}	0.8475	0.8206	0.9107
H_{exp}	0.8779	0.7962	0.9480
PD	0.9701	0.9179	0.9908
PE	0.7489	0.6053	0.8888
PIC	0.8624	0.7655	0.9423

P_{exact} = Hardy-Weinberg equilibrium, probability of exact test based on 10000 total permutations; H_{obs} = observed heterozigosity; H_{exp} = expected heterozigosity; PD = power of discrimination; PE = power of exclusion; and PIC = polymorphism information content.