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FOR THE RECORD

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Population Data at Two Short Tandem Repeat Loci D2S1338 and D19S433 in the Sample of Multinational Bosnia and Herzegovina Residents

POPULATION: We have analyzed the distribution of allele frequencies at two short tandem repeats loci (D2S1338 and D19S433) in a multinational sample of Bosnia and Herzegovina (B&H) residents. A total of 110 unrelated male and female individuals (Caucasians) from different regions of B&H were sampled for the analysis. We ensured that the sample reflected approximate proportional participation of the three main ethnic groups in the population of B&H (Bosniacs-Muslim [45%], Serbs [34%], Croats [21%]).

KEYWORDS: forensic science, DNA typing, short tandem repeats, D2S1338, D19S433, population data, Bosnia, Herzegovina

Some of the 110 tested subjects were involved in legal proceedings concerning paternity or other type of forensic testing, while the others were voluntary donors. Buccal swabs and blood samples (blood stains) were used as sources of DNA. The specimens were air-dried on the spot, placed in 1.5 mL tubes, and immediately transported to the Laboratory for Forensic Genetics at the Institute for Genetic Engineering and Biotechnology, Sarajevo, Bosnia and Herzegovina (B&H). Until DNA extraction, the samples were stored at -80°C. The Qiagen Dnaeasy™ Tissue Kit was used for DNA extraction (1). An AmpFlSTR® Identifiler® (ABI, Foster City, CA) was used to amplify simultaneously 15 short tandem repeat (STR) loci including D2S1338 and D19S433. Similar amounts of DNA were used in all PCR reactions. PCR amplification was carried out in a PE Gene Amp PCR System Thermal Cycler (ABI) according to the previously described reaction conditions (2). The total reaction volume was 12.5 μL. The amplified fragments were analyzed on an ABI PRISM 3100 instrument (ABI). GeneScan® 3.7.1 and Genotyper® 3.7 were applied in numerical allele designations. Deviation from Hardy–Weinberg equilibrium (3), observed, and expected heterozygosity (4) were calculated using Powermarker software (5), power of discrimination, and power of exclusion using Microsoft® Excel workbook template—POWERSTATS (6) and exact test of population differentiation (7) using Arlequin ver. 3.01 (8). All results are shown in Table 1. The entire data are available at http://www.ingeb.ba/edat/str/strbase.html

TABLE 1—*Bosnian and Herzegovinian allele frequencies for D2S1338 and D19S433 (N = 110).*

Allele	D2S1338	D19S433
10	—	—
11	—	0.014
12	—	0.159
13	—	0.223
14	—	0.277
14.2	—	0.050
15	—	0.136
15.2	—	0.045
16	0.045	0.045
16.2	—	0.041
17	0.227	0.009
18	0.068	—
19	0.105	—
20	0.173	—
21	0.032	—
22	0.014	—
23	0.091	—
24	0.114	—
25	0.109	—
26	0.023	—
27	—	—
28	—	—
26	—	—
27	—	—
H(ob)	0.8545	0.8182
H(ex)	0.8621	0.8173
P	0.7943	0.1153
PD	0.964	0.935
PE	0.704	0.633

H(ob), observed heterozygosity; H(ex), expected heterozygosity; P, deviation from Hardy–Weinberg equilibrium; PD, power of discrimination; PE, power of exclusion.

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In our previous population studies of B&H human population, we applied 15 STR loci included in the *PowerPlex 16® System* (9), 12 Y-chromosomal STRs loci incorporated in the *PowerPlex® Y System* (10), as well as 28 Y-chromosome NRY bi-allelic markers (11). Now, we have compared our data for these two loci with data obtained from geographically closer (neighboring) European populations. No statistically significant deviation ($p > 0.05$) from Hardy–Weinberg equilibrium was found for either of the observed loci. We compared B&H allele frequencies with the data from Slovenia (12), Serbia (Kosovo Albanians) (13), Serbia (Vojvodina) (14), and Macedonia (15). These exact tests of population differentiation show statistically significant differences (the significance level after Bonferroni's correction was $p = 0.01$) in allele frequencies at the D2S1338 locus between B&H and Serbia (Kosovo Albanians) samples. The same type of difference was noticed at the D19S433 locus between our's and the Serbia (Kosovo Albanians) and Macedonia samples.

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