Announcement of population data

Allele frequencies for 15 short tandem repeat loci in a representative sample of Bosnians and Herzegovinians

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Abstract

Allele frequencies for the 15 STR loci (D3S1358, TH01, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, vWA, D8S1179, TPOX, FGA) included in the PowerPlex 16 kit were obtained from a multiethnic sample of 100 unrelated individuals born in Bosnia and Herzegovina.

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Keywords: Short tandem repeats; Representative sample; B&H population data; PowerPlex 16 kit

Population: Unrelated healthy individuals born in the Bosnia and Herzegovina, from three main ethnical groups (Bosniacs: 44%; Serbs: 31%; Croats: 17%) and others (8%).

Extraction: QIagen extraction from buccal swabs and blood spots.

PCR: Approximately 2 ng targeted DNA following manufacturer’s protocol (PowerPlex 16 kit, Promega Corp., Madison, WI).

Results: Explained in Table 1.

Analysis of data: Deviation from Hardy–Weinberg equilibrium, observed and expected heterozygosity [1] were calculated within Powermarker [2], power of discrimination and power of exclusion within Microsoft® Excel workbook template—PowerStats [3], exact test of population differentiation within Arlequin version 2000 [4].

Access to the data: http://www.ingeb.ba/edat/str/strbase.html.

Other remarks: We have compared B&H data with data obtained from geographically closer (neighboring) European populations, as well as with PPI examined Caucasian populations (data kindly provided by Rita Weispfenning—Promega company). Bonferroni’s correction was used before each comparative analysis. In comparison of B&H and southern Croatian data [5] no significant difference was found at any individual locus. The same statistical parameters were obtained in comparison with pooled Slovenian data¹ [6–9]. Significant differences (P < 0.05 with Bonferroni’s correction) were found at FGA locus in comparative analysis of B&H and pooled Austrian data¹ [10–22] as well.

¹ Pooled data for each loci are available on http://www.uni-duesseldorf.de/WWW/Medfek/Serology.

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## TABLE 1—Allele frequency distribution and gene diversity for the PowerPlex® Y System STR loci in B&H population sample.

<table>
<thead>
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<th>Locus</th>
<th>Allele</th>
<th>Num</th>
<th>%</th>
<th>Locus</th>
<th>Allele</th>
<th>Num</th>
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## TABLE 2—PowerPlex® Y haplotypes that have detected more than once in B&H population sample and observed haplotype diversity.

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<tr>
<th>PowerPlex® Y Haplotypes</th>
<th>Number</th>
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<td>10-13-12-30-10-14-13-11-13-24-16-18</td>
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<td>10-13-11-29-11-14-16-11-13-25-11-14</td>
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<tr>
<td>10-14-14-31-10-14-13-11-13-24-16-18</td>
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<tr>
<td>11-13-13-12-10-15-14-13-24-14-15</td>
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</tbody>
</table>

Haplotype diversity (H) = 0.9941 ± 0.0027

## TABLE 3—Major allele frequency and gene diversity for the PowerPlex® Y locus examined sample of B&H population.

<table>
<thead>
<tr>
<th>Locus</th>
<th>Major Allele Frequency</th>
<th>Gene Dive</th>
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<tbody>
<tr>
<td>DYS391</td>
<td>0.5400</td>
<td>0.5089</td>
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<td>DYS3891</td>
<td>0.7900</td>
<td>0.3525</td>
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<td>DYS439</td>
<td>0.5000</td>
<td>0.7293</td>
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<td>DYS3891</td>
<td>0.4100</td>
<td>0.7169</td>
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<td>DYS438</td>
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<td>DYS392</td>
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<td>DYS393</td>
<td>0.8200</td>
<td>0.3105</td>
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<td>DYS390</td>
<td>0.6100</td>
<td>0.5565</td>
</tr>
<tr>
<td>DYS385</td>
<td>0.3300</td>
<td>0.8496</td>
</tr>
</tbody>
</table>

Average H = 0.9941 ± 0.0027

Additional information and reprint requests:
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