

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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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 with PP16 examined Caucasian populations (data kindly provided by Rita Weispfening—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

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

Table 1
B&H allele frequencies for 15 autosomal loci ($N = 100$)

Allele	D3S1358	THO1	D21S11	D18S51	PENTE	D5S818	D13S317	D7S820	D16S539	CSF1P0	PENT.D	vWA	D8S1179	TPOX	FGA
5	–	0.005	–	–	0.045	–	–	–	–	–	–	–	–	–	–
6	–	0.225	–	–	–	–	–	–	–	–	–	–	–	0.005	–
7	–	0.110	–	–	0.190	–	–	–	–	–	0.010	–	–	–	–
8	–	0.115	–	–	–	–	0.115	0.155	0.035	–	0.005	–	0.005	0.570	–
9	–	0.195	–	0.005	0.020	0.025	0.075	0.200	0.095	0.050	0.245	–	0.030	0.085	–
9.3	–	0.330	–	–	–	–	–	–	–	–	–	–	–	–	–
10	–	0.020	–	0.010	0.165	0.070	0.055	0.290	0.050	0.250	0.105	–	0.070	0.060	–
11	–	–	–	0.020	0.120	0.375	0.360	0.185	0.340	0.245	0.195	0.005	0.090	0.260	–
12	–	–	–	0.080	0.125	0.340	0.270	0.125	0.280	0.345	0.205	–	0.165	0.020	–
13	–	–	–	0.110	0.155	0.175	0.075	0.030	0.180	0.100	0.15	0.015	0.345	–	–
14	0.090	–	–	0.215	0.055	0.015	0.045	0.015	0.020	0.005	0.06	0.095	0.210	–	–
15	0.280	–	–	0.175	0.035	–	0.005	–	–	0.005	0.015	0.120	0.080	–	–
16	0.265	–	–	0.150	0.035	–	–	–	–	–	–	0.205	0.005	–	0.005
17	0.190	–	–	0.100	0.030	–	–	–	–	–	0.010	0.275	–	–	0.005
18	0.155	–	–	0.050	0.020	–	–	–	–	–	–	0.195	–	–	0.005
19	0.020	–	–	0.050	–	–	–	–	–	–	–	0.065	–	–	0.095
20	–	–	–	0.020	–	–	–	–	–	–	–	0.025	–	–	0.145
20.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.010
21	–	–	–	0.010	–	–	–	–	–	–	–	–	–	–	0.155
22	–	–	–	0.005	–	–	–	–	–	–	–	–	–	–	0.190
22.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.005
23	–	–	–	–	0.005	–	–	–	–	–	–	–	–	–	0.155
23.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.010
24	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.085
25	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.090
26	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.025
27	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.015
28	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.005
26	–	–	0.005	–	–	–	–	–	–	–	–	–	–	–	–
27	–	–	0.025	–	–	–	–	–	–	–	–	–	–	–	–
28	–	–	0.165	–	–	–	–	–	–	–	–	–	–	–	–
29	–	–	0.265	–	–	–	–	–	–	–	–	–	–	–	–
30	–	–	0.210	–	–	–	–	–	–	–	–	–	–	–	–
30.2	–	–	0.065	–	–	–	–	–	–	–	–	–	–	–	–
31	–	–	0.035	–	–	–	–	–	–	–	–	–	–	–	–
31.2	–	–	0.085	–	–	–	–	–	–	–	–	–	–	–	–
32	–	–	0.020	–	–	–	–	–	–	–	–	–	–	–	–
32.2	–	–	0.085	–	–	–	–	–	–	–	–	–	–	–	–
33.2	–	–	0.040	–	–	–	–	–	–	–	–	–	–	–	–
H(ob)	0.8100	0.7600	0.8600	0.8900	0.8600	0.6900	0.7500	0.7600	0.7900	0.8100	0.8300	0.8200	0.7600	0.5800	0.8900
H(ex)	0.7790	0.7727	0.8318	0.8619	0.8689	0.7038	0.7640	0.7967	0.7568	0.7425	0.8183	0.8118	0.7852	0.5932	0.8650
P	0.2038	0.5389	0.9733	0.3282	0.1160	0.6057	0.2007	0.2348	0.8642	0.0435	0.0823	0.8111	0.0435	0.9771	0.7984
PD	0.906	0.915	0.948	0.956	0.962	0.866	0.918	0.927	0.902	0.875	0.930	0.937	0.923	0.794	0.962
PE	0.618	0.527	0.715	0.775	0.725	0.413	0.510	0.527	0.581	0.618	0.775	0.637	0.527	0.268	0.775

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

at Penta E locus in comparison with PP16 examined Caucasian populations. Joint result of this study are going to be used as guidelines in additional investigation of genetic relationship between recent B&H and neighboring human populations, originated in our previous studies [23–25]. This paper follows the guidelines for publication of population data requested by journal [26].

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