

Announcement of population data

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

Damir Marjanovic<sup>a,\*</sup>, Narcisa Bakal<sup>a</sup>, Naris Pojskic<sup>a</sup>,  
Lejla Kapur<sup>a</sup>, Katja Drobnic<sup>b</sup>, Dragan Primorac<sup>c</sup>,  
Kasim Bajrovic<sup>a</sup>, Rifat Hadziselmovic<sup>a</sup>

<sup>a</sup> *Institute for Genetic Engineering and Biotechnology (INGEB), Kemalbegova 10, 71.000 Sarajevo, Bosnia and Herzegovina*

<sup>b</sup> *Forensic Laboratory and Research Center, Ministry of the Interior, Stefanova 2, 1501 Ljubljana, Slovenia*

<sup>c</sup> *Laboratory for Clinical and Forensic Genetics, University Hospital Split, Spinciceva 1, 21000 Split, Croatia*

Received 7 December 2004; received in revised form 30 December 2004; accepted 12 January 2005

Available online 26 February 2005

## 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.

© 2005 Elsevier Ireland Ltd. All rights reserved.

**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<sup>®</sup> 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 data<sup>1</sup> [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 data<sup>1</sup> [10–22] as well

\* Corresponding author. Tel.: +387 33 220926; fax: +387 33 442891.

E-mail addresses: [damirm@ingeb.ba](mailto:damirm@ingeb.ba), [marjanovd@hotmail.com](mailto:marjanovd@hotmail.com) (D. Marjanovic).

<sup>1</sup> 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].

## References

- [1] M. Nei, Molecular Evolutionary Genetics, Columbia University Press, New York, USA, 1987.
- [2] K. Liu, S. Muse, PowerMarker: new genetic data analysis software, Version 3.0., 2004, free program distributed by the authors over the internet from <http://www.powermarker.net>.

- [3] A. Tereba, Tools for analysis of population statistics, *Profiles DNA* 3 (1999) 14–16.
- [4] S. Schneider, D. Roessli, L. Excoffier, *Arlequin Version 2000: A Software for Population Genetics Data Analysis*, Genetics and Biometry Laboratory, University of Geneva, Switzerland, 2000.
- [5] M. Schanfield, N.M. Ganriel, S. Andelinovic, R.L. Reynolds, C. Ladd, H.C. Lee, D. Primorac, Allele frequencies for the 13 CODIS STR loci in a sample of Southern Croatians, *J. Forensic Sci.* 47.3 (2002) 669–670.
- [6] I. Zupanic, J. Balazic, R. Komel, Analysis of nine short tandem repeat (STR) loci in the Slovenian population, *Int. J. Legal Med.* 111 (1998) 248–250.
- [7] I. Zupanic Pajnic, H. Sterlinko, J. Balazic, R. Komel, Parentage testing with 14 STR loci and population data for 5 STRs in the Slovenian population, *Int. J. Legal Med.* 114 (2001) 178–180.
- [8] K. Drobnic, B. Budowle, The analysis of three short tandem repeat (STR) loci in the Slovene population by multiplex PCR, *J. Forensic Sci.* 45.4 (2000) 893–895.
- [9] K. Drobnic, A. Regent, B. Budowle, STR data for the AmpFISTR SGM plus from Slovenia, *Forensic Sci. Int.* 115 (2001) 107–109.
- [10] E. Ambach, W. Parson, H. Niederstätter, B. Budowle, Multiplex PCR and automated fluorescence detection of four tetrameric STRs in a Western Austrian population, *Adv. Forensic Haemogenet.* 6 (1996) 483–485.
- [11] D.W.M. Schwartz, E.M. Dauber, B. Glock, W.R. Mayr, AMPFLP-typing of the D21S11 microsatellite polymorphism: allele frequencies and sequencing data in the Austrian population, *Adv. Forensic Haemogenet.* 6 (1996) 622–625.
- [12] E. Ambach, W. Parson, H. Niederstätter, B. Budowle, Austrian Caucasian population data for the quadruplex plus amelogenin: refined mutation rate for HumvWFA31/A, *J. Forensic Sci.* 42 (1997) 1136–1139.
- [13] U. Ricci, M. Klintschar, F. Neuhuber, M.L. Giovannucci Uzielli, Study on the STR TPOX in an Italian and an Austrian population using two different primer pairs and three different electrophoretic methods, *Int. J. Legal Med.* 111 (1998) 212–214.
- [14] M. Klintschar, U. Ricci, N. Al Hammadi, B. Reichenpfader, A. Ebner, M.L. Giovannucci Uzielli, Genetic variation at the STR loci D12S391 and CSF1PO in four populations from Austria, Italy, Egypt and Yemen, *Forensic Sci. Int.* 97 (1998) 37–45.
- [15] F. Neuhuber, M. Klintschar, M. Radacher, A collaborative genetic study on the STR system FGA in two Austrian population samples, *Forensic Sci. Int.* 91 (1998) 1–6.
- [16] E.M. Dauber, B. Glock, D.W.M. Schwartz, W.R. Mayr, Sequencing and population data of a short tandem repeat locus in the human alpha fibrinogen gene (HUMFGA) in an Austrian population sample, *Prog. Forensic Genet.* 7 (1998) 264–266.
- [17] M. Klintschar, A. Ebner, B. Reichenpfader, Population genetic studies on nine tetrameric short tandem repeat loci using fluorescence dye-labeled primers and capillary electrophoresis in the Austrian population, *Electrophoresis* 20 (1999) 1740–1742.
- [18] E.M. Dauber, G. Dorner, S. Stadlbacher, B. Glock, D.W.M. Schwartz, W.R. Mayr, Denaturing versus non-denaturing electrophoresis for D21S11 and additional sequence and population data, *Prog. Forensic Genet.* 8 (2000) 148–150.
- [19] C.H. Brenner, Summary of polymorphic STR allele frequencies and Y chromosome haplotype frequencies, *Prog. Forensic Genet.* 8 (2000) 109–125.
- [20] J. Ross, W. Parson, I. Furac, M. Kubat, M. Holland, Multiplex PCR amplification of eight STR loci in Austrian and Croatian Caucasian populations, *Int. J. Legal Med.* 115 (2001) 57–60.
- [21] M. Steinlechner, B. Berger, R. Scheithauer, W. Parson, Population genetics of ten STR loci (AmpF/STR SGM plus) in Austria, *Int. J. Legal Med.* 114 (2001) 288–290.
- [22] C. Nussbaumer, S. Hanslik, M. Fichtinger, G. Bauer, STR data for the AmpFISTR SGM plus from a regional population of Austria, *Forensic Sci. Int.* 122 (2001) 181–183.
- [23] D. Marjanovic, L. Kapur, K. Drobnic, B. Budowle, R. Hadziselimovic, Comparative study of genetic variation at fifteen STR loci in three isolated populations of Bosnian mountain area, *Hum. Biol.* 76.1 (2004) 15–31.
- [24] D. Marjanovic, N. Bakal, N. Pojskic, L. Kapur, K. Drobnic, D. Primorac, K. Bajrovic, R. Hadziselimovic, Population data for the twelve Y-chromosome short tandem repeat loci from the sample of multinational population in Bosnia and Herzegovina, *J. Forensic Sci.* 50.1 (2005) 223–225.
- [25] D. Marjanovic, S. Fomarino, S. Montagna, R. Hadziselimovic, S. Vidovic, N. Pojskic, V. Battaglia, A. Achilli, A. Torroni, D. Primorac, S. Santachiara-Benerecetti, O. Semino, The distribution of Y-chromosome haplogroups in the three main ethnic groups of Bosnia and Herzegovina, in: Sixth Balkan Meeting on Human Genetics, Thessaloniki, Greece, 2004, *Book of Abstracts*, 37 pp.
- [26] P. Lincoln, A. Carracedo, Publication of population data of human polymorphisms, *Forensic Sci. Int.* 110 (2000) 3–5.