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SHORT COMMUNICATION

Z. Jakovski · K. Nikolova · I. Furac · M. Masic · B. Janeska · M. Kubat

Allele frequencies for 15 STR loci in a population from the Republic of Macedonia

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Abstract Allele frequencies of 15 STR loci (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, and FGA) were determined in a sample of 163 unrelated individuals from the Republic of Macedonia. AmpFISTR Identifiler Kit (Applied Biosystems) was used for PCR amplification. For all 15 loci, the combined matching chance is 6.6×10^{18} and the power of exclusion is 99.999954%.

Keywords Short tandem repeats (STR) · Macedonian population data · AmpFISTR identifiler

Introduction

This population study was carried out to establish a Macedonian population forensic database. Population data were obtained for the 15 STR loci included in the AmpFISTR Identifiler kit (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, and FGA). Similar population databases were found for most countries in the area [1–5]. Similarity comparisons with Kosovo Albanians [2] and Serbian [4] population were done.

Z. Jakovski (✉) · K. Nikolova · B. Janeska
Institute for Forensic Medicine and Criminology,
School of Medicine,
University St. Ciril and Methodius,
Skopje, Republic of Macedonia
e-mail: zlatedr@yahoo.com
Tel.: +389-2-3177044
Fax: +389-2-3178831

I. Furac · M. Masic · M. Kubat
Institute for Forensic Medicine and Criminology,
School of Medicine,
Salata 11,
10 000 Zagreb, Republic of Croatia
e-mail: ivanaf@mef.hr
Tel.: +385-1-4590235
Fax: +385-1-4590235

Materials and methods

In this study, 163 unrelated healthy individuals from the Republic of Macedonia were tested. Whole blood samples were collected on FTA classic cards (Whatman) and stored at room temperature. DNA was extracted from bloodstains with Chelex-100 reagent [6].

Multiplex PCR amplification was performed using 1–3 ng of genomic DNA according to the manufacturer's protocol. Amplification was carried out in a 9600 Thermal Cycler (Applied Biosystems).

For electrophoresis, 1 μl of the PCR product was combined with 12 μl of formamide and 0.5 μl of GeneScan 500 LIZ size standard. Detection of PCR products and genotyping were carried out on the ABI PRISM 310 Genetic Analyser (Applied Biosystems) using the ABI PRISM collection software and Genotyper 3.7 analysis software (Applied Biosystems).

Statistical analyses for this population study and similarity comparisons with Serbian and Kosovo populations were done using DNA View Charles Brenner software.

Results and discussion

The observed allele frequencies and statistical parameters that could be useful for forensic testing in the Macedonian population are summarized in Table 1.

Table 2 lists interpopulation comparisons between Macedonians and two other populations from the Balkan–Kosovo Albanians and Serbians. Locus-by-locus DNA View shows statistically significant differences between populations from Macedonia and Kosovo with respect to one loci, CSF1PO, and between Macedonia and Serbia with respect to one locus, D7S820.

In summary, based on presented allelic frequencies and statistical parameters for forensic testing for the AmpFISTR Identifiler detection system, the combination of these 15 STR loci presents a powerful strategy for individual identification and parentage analyses in the Macedonian population.

Table 1 Allele frequencies and statistical parameters of 15 STR loci in the Macedonian population

Allele	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
6	–	–	–	–	0.025	0.528	–	–	–	–	–	–	–	–	–
7	–	–	0.037	–	0.006	0.331	–	–	–	–	–	–	–	0.006	–
8	0.018	–	0.417	0,006	–	0.264	0.319	0.037	–	–	–	1.049	–	0.006	–
9	0.024	–	0.269	0.031	0.006	0.301	0.129	0.215	–	–	–	0.215	0.006	0.067	–
9.3	–	–	–	–	–	0.485	–	–	–	–	–	–	–	–	–
10	0.086	–	0.454	0.558	–	0.024	0.098	0.116	–	–	–	0.104	0.012	0.166	–
10.3	–	–	–	–	–	0.006	–	–	–	–	–	–	–	–	–
11	0.129	–	0.466	0.601	–	0.006	0.663	0.644	–	0.006	0.025	0.528	0.049	0.570	–
11.1	–	–	0.006	–	–	0.006	–	–	–	–	–	–	–	–	–
12	0.233	–	0.307	0.675	–	–	0.613	0.564	–	0.129	0.012	0.079	0.245	0.761	–
12.2	–	–	–	–	–	–	–	0.006	–	–	–	–	–	–	–
13	0.705	–	0.024	0.067	–	–	0.135	0.356	–	0.441	0.012	–	0.319	0.405	–
13.2	–	–	–	–	–	–	–	–	–	0.031	–	–	0.006	–	–
13.3	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
14	0.521	–	0.012	0.024	0.178	0.006	0.055	0.067	–	0.730	0.178	–	0.313	0.018	–
14.2	–	–	–	–	–	–	–	–	–	0.073	–	–	–	–	–
15	0.245	–	0.006	0.018	0.521	–	–	0.006	–	0.288	0.239	–	0.251	–	–
15.2	–	–	–	–	–	–	–	–	–	0.092	–	–	–	–	–
16	0.043	–	–	0.012	0.539	–	–	–	0.184	0.147	0.435	–	0.294	–	–
16.2	–	–	–	–	–	–	–	–	–	0.030	–	–	–	–	–
17	0.006	–	–	0.006	0.429	–	–	–	0.442	–	0.540	–	0.190	–	–
17.2	–	–	–	–	–	–	–	–	–	0.012	–	–	–	–	–
18	–	–	–	0.006	0.282	–	–	–	0.153	0.006	0.417	–	0.172	–	0.031
18.2	–	–	–	–	–	–	–	–	–	0.006	–	–	–	–	–
19	–	–	–	–	0.018	–	–	–	0.190	–	0.134	–	0.080	–	0.159
20	–	–	–	–	–	–	–	–	0.251	0.006	0.018	–	0.031	–	0.227
21	–	–	–	–	–	–	–	–	0.552	–	–	–	0.024	–	0.374
21.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.012
22	–	–	–	–	–	–	–	–	0.031	–	–	–	0.012	–	0.380
22.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.012
23	–	–	–	–	–	–	–	–	0.282	–	–	–	0.006	–	0.307
23.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.006
24	–	–	–	–	–	–	–	–	0.165	–	–	–	–	–	0.251
24.2	–	0.006	–	–	–	–	–	–	–	–	–	–	–	–	–
25	–	0.006	–	–	–	–	–	–	0.208	–	–	–	–	–	0.159
25.5	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.006
26	–	–	–	–	–	–	–	–	0.037	–	–	–	–	–	0.074
26.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
27	–	0.061	–	–	–	–	–	–	0.012	–	–	–	–	–	0.006

Allele	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
28	–	0.276	–	–	–	–	–	–	–	–	–	–	–	–	–
29	–	0.472	–	–	–	–	–	–	–	–	–	–	–	–	–
29.2	–	0.018	–	–	–	–	–	–	–	–	–	–	–	–	–
30	–	0.374	–	–	–	–	–	–	–	–	–	–	–	–	–
30.2	–	0.086	–	–	–	–	–	–	–	–	–	–	–	–	–
31	–	0.129	–	–	–	–	–	–	–	–	–	–	–	–	–
31.2	–	0.227	–	–	–	–	–	–	–	–	–	–	–	–	–
32	–	0.031	–	–	–	–	–	–	–	–	–	–	–	–	–
32.2	–	0.177	–	–	–	–	–	–	–	–	–	–	–	–	–
33.2	–	0.202	–	–	–	–	–	–	–	–	–	–	–	–	–
34.2	–	0.006	–	–	–	–	–	–	–	–	–	–	–	–	–
PE (%)	50	71	62	50	58	58	50	50	76	57	62	30	76	50	73
H (%)	23	14	19	28	21	21	24	23	12	22	19	40	12	28	13
PD (%)	92.0	96.5	94.0	87.0	92.0	92.0	91.0	91.0	97.4	93.0	94,0	82.0	97.5	88.0	96.9
S (%)	21	13	21	31	18	18	28	23	15	23	23	38	13	23	13
P	0.25840	0.58280	0.49740	0.06460	0.72440	0.55290	0.25180	0.32610	0.64660	0.98245	0.33825	0.22575	0.28508	0.73831	0.16640

For all 15 loci, the combined matching chance=6.6×10^{18}, PE=99.999954%, PI=69.7×10^{6}, and mPI=150000
PE Power of exclusion, *H* expected homozygosity rate, *PD* power of discrimination, *S* observed homozygosity rate, *P* Hardy–Weinberg exact test

Table 2 Interpopulation comparisons (p value) between Macedonians and two Balkan populations

Locus	Macedonia vs Kosovo	Macedonia vs Serbia
D3S1358	0.19	0.82
vWA	0.26	0.73
FGA	0.54	0.89
TH01	0.20	0.14
TPOX	0.12	0.08
CSF1PO	0.006[a]	0.35
D5S818	0.98	0.75
D13S317	0.09	0.39
D7S820	0.18	0.002[a]

Interpopulation comparisons between Macedonians and two other populations from the Balkan–Kosovo Albanians and Serbians. Locus by locus DNA View shows statistically significant differences between populations from Macedonia and Kosovo with respect to one loci, CSF1PO, and between Macedonia and Serbia with respect to one locus, D7S820
[a]Statistically significant

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