



Population data on D16S539, D2S1338 and D19S433 loci in a population sample from Brescia (Italy)

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Abstract. To establish databases for D16S539, D2S1338 and D19S433 loci for an Italian population sample from Brescia (Northern Italy), 77 unrelated persons were typed. DNA samples were amplified in a multiplex reaction with subsequent automatic detection using capillary electrophoresis. The obtained data are very useful in our practice and they give a contribution to the definition of Italian population short tandem repeat (STR) allelic and genotypic frequencies for the three analysed. © 2003 Elsevier B.V. All rights reserved.

Keywords: STRs loci; Population data; Italy

1. Introduction

Short tandem repeat (STR) markers are widely used in forensics as well as in paternity testing [1]. However, before a new system can be introduced into forensic casework, a database for the relevant population must be established for statistical evaluation of the evidence. Indeed, it is well known that different ethnic group have different allelic frequencies and therefore different kind of genotypes [2–5]. In Italy, there are already data regarding a lot of STRs loci, but no data about D16S539, D2S1338 and D19S433 loci. To have allelic frequencies data regarding the population living in Brescia province (Northern Italy) and so have our own database for these three loci, it has been studied a sample of people from Brescia (Italy).

2. Materials and methods

It was considered 77 unrelated individuals from Brescia province. For each case, DNA was obtained from whole blood or oral swabs. Genomic DNA was extracted using Chelex®-100 method [6]. Amplification was carried out applying AmpFISTR SGM plus PCR Amplification Kit (PE-AB) in a Perkin Elmer 2400 thermal cycler, according to

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manufacturer's recommendations. Products were loaded on the ABI Prism 310 Genetic Analyser and analysed with the GeneScan analysis software V.3.2.1.

3. Results and discussion

This work gives a relatively detailed picture of allelic and genotypic frequencies in people from Brescia province regarding three STRs loci widely used in forensics (Tables 1, 2).

The preliminary results in the distribution of allelic and genotypic frequencies are similar to that regarding Caucasian population. Among the three loci considered, D2S1338 presents the most relevant polymorphic information contents (0.8276), power of exclusion (0.8253) and power of distribution (0.9571). In no samples were found mutations that were not described in literature yet. These data are very useful in our practice and they give a contribution in the definition of Italian population STRs allelic and genotypic frequencies for the three analysed loci.

Table 1
Genotypes

D19S433		D16S539		D2S1338	
12–13	0.026667	8–11	0.012987013	16–17	0.013333
12–14	0.066667	8–12	0.012987013	16–19	0.013333
12–15	0.026667	9–9	0.012987013	16–20	0.013333
12–15.2	0.013333	9–11	0.12987013	17–17	0.053333
12–16	0.013333	9–12	0.12987013	17–18	0.04
13–13	0.133333	9–13	0.051948052	17–19	0.053333
13–14	0.186667	10–11	0.038961039	17–20	0.08
13–14.2	0.013333	10–12	0.051948052	17–21	0.026667
13–15	0.066667	10–13	0.025974026	17–22	0.04
13–15.2	0.026667	11–11	0.038961039	17–23	0.053333
13–16	0.08	11–12	0.168831169	17–24	0.053333
13–16.2	0.013333	11–13	0.103896104	17–25	0.04
13.2–14	0.013333	12–12	0.051948052	17–26	0.013333
13.2–16	0.013333	12–13	0.090909091	17–27	0.013333
14–14	0.133333	12–14	0.012987013	18–20	0.053333
14–14.2	0.013333	13–13	0.064935065	18–22	0.013333
14–15	0.053333			18–23	0.013333
14–15.2	0.026667			19–20	0.04
14.2–14.2	0.026667			19–23	0.026667
14.2–16	0.013333			19–24	0.026667
15–15.2	0.013333			20–21	0.026667
15–16	0.013333			20–23	0.04
16–16	0.013333			20–24	0.053333
				20–25	0.04
				21–23	0.013333
				22–24	0.04
				22–25	0.013333
				23–23	0.013333
				23–25	0.053333
				25–25	0.026667

Table 2
Allelic frequencies and statistical evaluation

Allele	D16S539	D2S1338	D196433
8	0.012987	–	–
9	0.168831	–	–
10	0.058442	–	–
11	0.266234	–	–
12	0.285714	–	0.08
13	0.201299	–	0.346667
13.2	–	–	0.013333
14	0.006494	–	0.32
14.2	–	–	0.026667
15	–	–	0.086667
15.2	–	–	0.04
16	–	0.02	0.08
16.2	–	–	0.006667
17	–	0.266667	–
18	–	0.06	–
19	–	0.08	–
20	–	0.173333	–
21	–	0.033333	–
22	–	0.053333	–
23	–	0.113333	–
24	–	0.086667	–
25	–	0.1	–
26	–	0.006667	–
27	–	0.006667	–
<i>n</i>	77	75	75
Observed <i>H</i>	0.831169	0.92	0.733334
Expected <i>H</i>	0.770661	0.854044	0.754656
PIC	0.732337	0.827679	0.719416
<i>E</i>	0.61343	0.82531	0.545997
<i>D</i>	0.902007	0.957156	0.905956

H—rate of heterozygosity, PIC—polymorphic information contents, *E*—power of exclusion, *D*—power of discrimination.

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