



Allele frequency distribution of 13 STRs in an Italian and immigrant population sample

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Abstract

In the present study, we analysed allelic and genotypic distribution of 13 STR in the population of Brescia (North Italy) and in the immigrant population (North Africans and East Europeans) to create a database. DNA was extracted from 120 samples; STR amplification was carried out according to the AmpF/STR Profiler Plus and SGM kit protocols. Amplified products were analysed using an ABI Prism 310 Genetic Analyzer. The distributions were also compared with those from other Italian populations.

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1. Introduction

Recently, foreigners, especially Asians, North Africans and East Europeans, have been immigrating to Italy and they are sometimes involved in criminal action or in paternity testing to rejoin their families.

Consequently, it is necessary for a forensic lab to create an adequate database to calculate the probabilities in personal identification, bloodstain analysis and paternity testing.

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Table 1
Allele frequencies distribution

Allele	Italy	Est Europe	Africa
<i>D3S1358</i>			
13	0.0143		
14	0.0572		0.0625
15	0.2143	0.2858	0.1875
16	0.2573	0.3571	0.25
17	0.2143	0.1428	0.4375
18	0.2143	0.1428	0.0625
19	0.0283	0.0715	
<i>Vwa</i>			
14	0.048	0.1428	0.1111
15	0.1732	0.1428	0.1667
16	0.25	0.5	0.2222
17	0.2404	0.1428	0.0556
18	0.2211	0.0716	0.3333
19	0.048		0.1111
20	0.0193		
<i>FGA</i>			
19	0.0294	0.0714	
20	0.0883	0.1429	0.0625
21	0.2206	0.0714	0.0625
22	0.2207	0.1429	0.1875
23	0.147	0.2143	0.125
24	0.1323	0.2857	0.25
25	0.1029	0.0714	0.1875
26			0.0625
27	0.0441		
28			
29	0.0147		
30			0.0625
<i>D8S1179</i>			
8	0.0167	0.1428	
9			
10	0.1833	0.0715	0.125
11	0.0667	0.1428	0.0625
12	0.1333	0.0715	0.1875
13	0.3	0.3572	0.375
14	0.2166	0.2142	0.0625
15	0.0667		0.125
16			0.0625
17	0.0167		
<i>D18S51</i>			
10	0.0441	0.0714	
11	0.0148		
12	0.1617	0.0714	0.0625
13	0.1324		0.0625
13*2	0.0148		

Table 1 (continued)

Allele	Italy	Est Europe	Africa
<i>D18S51</i>			
14	0.147	0.0714	0.1875
14*2	0.0295		
15	0.147	0.1429	0.1225
16	0.0882	0.2857	0.255
17	0.0441	0.1429	0.0625
18	0.1029	0.1429	0.0625
19	0.0735		0.1225
20			0.0625
21		0.0714	
<i>D5S818</i>			
7	0.0152		
9	0.0152		0.1875
10	0.0607	0.1428	0.0625
11	0.3181	0.3571	0.1875
12	0.3484	0.2143	0.4375
13	0.2121	0.2143	0.125
14	0.0303	0.0715	
<i>D13S317</i>			
8	0.2084	0.1875	0.1875
9	0.0139		
10	0.0416		
11	0.2361	0.5625	0.0625
12	0.3472	0.25	0.5625
13	0.0972		0.1875
14	0.0556		
<i>D7S820</i>			
7	0.0556		0.1111
8	0.125	0.0625	0.2222
9	0.125	0.25	
10	0.2638	0.1875	0.4444
11	0.2083	0.375	0.0556
12	0.125	0.0625	0.1667
13	0.0695	0.0625	
14	0.0278		
<i>D21S11</i>			
27	0.03		
28	0.076	0.1667	0.1875
29	0.288	0.0834	0.125
30	0.303	0.25	0.1875
30*2		0.0834	0.0625
31	0.03		0.1875
31*2	0.075		0.1875
32	0.045		
32*2	0.107	0.3331	

(continued on next page)

Table 1 (continued)

Allele	Italy	Est Europe	Africa
<i>D21S11</i>			
33*2	0.046	0.0834	
34*2			0.0625
<i>D19S433</i>			
12	0.0455		
13	0.1818		
14	0.409		
14*2	0.0455		
15	0.1818		
16	0.0455		
16*2	0.1909		
<i>TH01</i>			
5	0.0167		
6	0.1167		0.1667
7	0.1499		0.5
8	0.25		
9	0.2333		0.3333
9*3	0.1167		
10	0.1		
11	0.0167		
<i>D2S1338</i>			
17	0.25		
18	0.0625		
19	0.25		
20	0.25		
23	0.0625		
24	0.125		
<i>D16S539</i>			
5	0.1429		
8	0.0715		
9	0.2144		
10	0.1071		
11	0.2144		
12	0.1429		
13	0.071		
14	0.0358		

The aim of this study is to analyse allelic and genotypic distributions of 13 STRs loci (D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, D2S1338, D19S433, TH01) in a sample of native and immigrant populations living in Brescia (Northern Italy) to establish a DNA database, which allow us to analyse more accurately some of the cases requested by the Court.

2. Materials and methods

Blood samples were collected from a sample of 120 unrelated individuals: 72 from Italy (Brescia area) and the others from North Africa (Morocco, Tunisia and Egypt) and East Europe (Albania, ex-Yugoslavia and CSI).

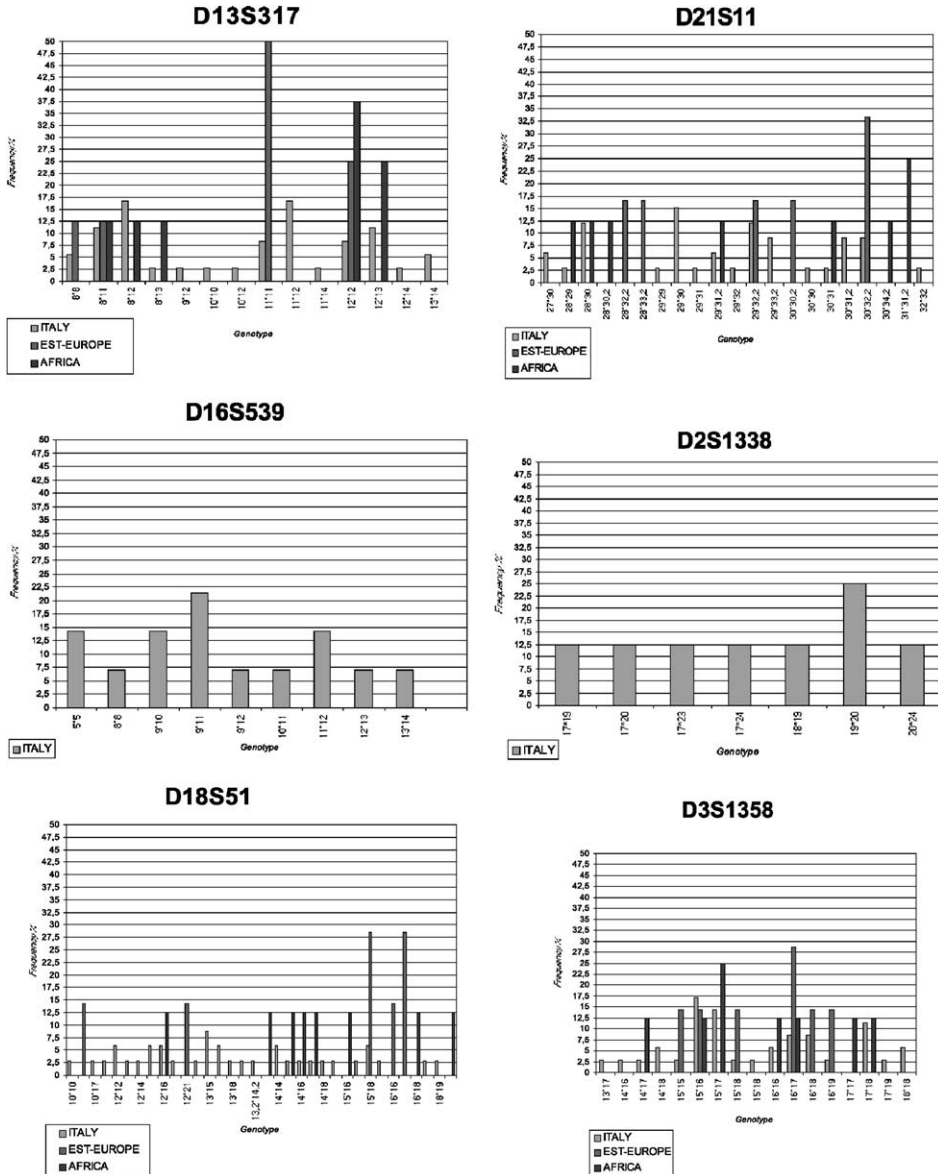


Fig. 1. Genotype distribution of 13STR.

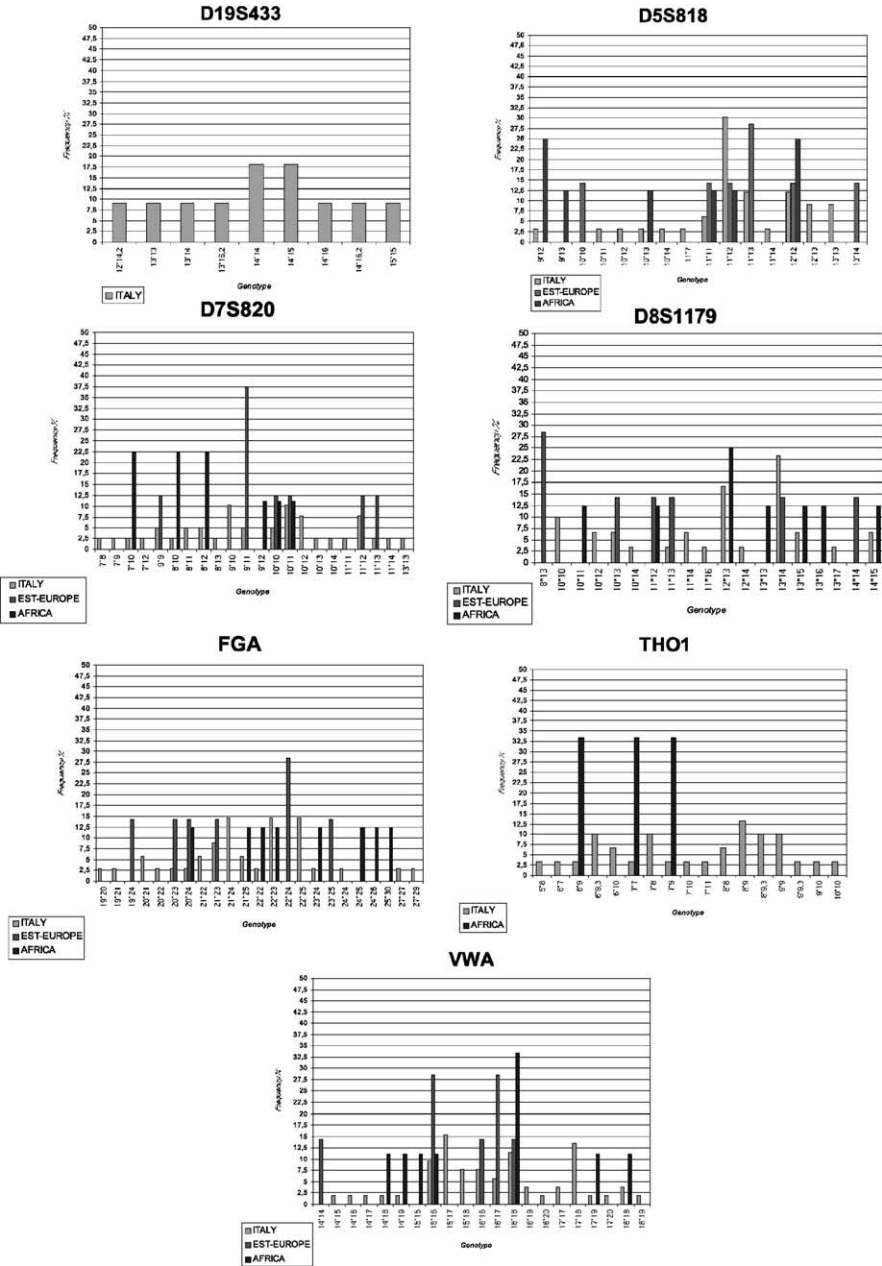


Fig. 1 (continued).

DNA was obtained from EDTA-treated blood samples by proteinase K-pCIA extraction.

Amplification of 13 loci was carried out simultaneously using the AmpFI STR Profiler Plus and SGM amplification kits by Perkin-Elmer. DNA samples were amplified according to the manufactures' instructions.

Amplified fragments were separated by capillaries electrophoresis using the ABI Prism 310 DNA Genetic Analyzer. Allele size determination and genotyping were performed using ABI Prism GeneScan Analysis 3.1.2 by comparison of amplified fragments with internal size standards and allelic ladders.

3. Results and discussion

The distributions of allelic frequencies in the three different population samples analysed for the 13 loci are summarised in [Table 1](#) while the observed genotypes are shown in [Fig. 1](#).

The Italian population data were observed to be in Hardy Wienberg equilibrium (statistical analysis not shown) while for the other populations, the sample was too small to be taken into consideration. For Italy, comparison between both populations [[1–4](#)] showed no significant differences, but we propose to continue compiling a more complete and wider database to have a better and more precise valuation of these results.

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