For the Record

Allele Frequency Distributions for D1S1656, D8S1132, D10S2325, D18S51, and D21S11 Loci in a North Italy Population

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Population: North Italy (n = 110).

Keywords: forensic science, DNA typing, population genetics, D1S1656, D8S1132, D10S2325, D18S51, D21S11, Italy

Whole blood samples were obtained from 110 unrelated North Italians. Genomic DNA was extracted using a commercial kit: GenomicPrep Blood DNA Isolation Kit (Pharmacia-Biotech, Upp-

sala, Sweden) and its concentration was determined spectrophotometrically. PCR amplifications were carried out in a GeneAmp® PCR System 9700 Thermal Cycler (PE-Biosystems, Foster City, CA) using 1 to 5 ng of genomic DNA (50 μL reaction volume) and adopting the optimum conditions for each locus. The amplified products were detected using the A.L.F. express DNA sequencer (Pharmacia-Biotech, Uppsula, Sweden). Alleles were classified according to the recommendations of the ISFH (1). Statistical analysis was performed as previously reported (2). The complete data set is available to any interested researcher upon request from the corresponding author.

References

- DNA recommendations. Report concerning further recommendations of the DNA commission of the ISFH regarding PCR-based polymorphisms in STR (short tandem repeat) systems. Int J Legal Med 1994; 107:159–60.
- Turrina S, De Leo D, Marigo M. Northeast Italy population data using multiplex PCR (HUMCD4, HUMTH01, HUMTPOX and HUMCSF1P0) loci. J Forensic Sci 2000;45(6):1288–90.

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Allele	D1S1656	D8S1132	D10S2325	D18S51	D21S11
7			0.195		
8			0.055		
9			0.065		
10	0.005		0.150	0.005	
11	0.095		0.155	0.025	
12	0.105		0.165	0.155	
13	0.060		0.115	0.165	
14	0.090		0.060	0.125	
14.3	0.005				
15	0.180	0.005	0.030	0.110	
15.3	0.045	0.00-	0.010	0.440	
16	0.135	0.005	0.010	0.140	
16.3	0.055	0.120		0.005	
17	0.040	0.120		0.085	
17.3	0.085	0.200		0.120	
18	0.040	0.200		0.120	
18.3 19	0.050 0.005	0.165		0.050	
19.3	0.005	0.163		0.030	
20	0.003	0.140		0.015	
21		0.140		0.015	
22		0.135		0.003	
23		0.035			
24		0.040			
25		0.010			
26		0.010			
27					0.025
28					0.135
29					0.230
30					0.185
30.2					0.045
31					0.065
31.2					0.095
32					0.015
32.2					0.150
33.2					0.045
34.2					0.005
35					0.005
PIC	0.898	0.852	0.861	0.872	0.848
PD	0.971	0.952	0.958	0.972	0.962
PE	0.816	0.734	0.582	0.675	0.734

Based on χ^2 test, the five loci meet HWE expectations (p>0.05). PIC: polymorphic information content. PD: power of discrimination. PE: probability of exclusion.