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FOR THE RECORD

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Allele Frequencies for Six STR Loci (D5S818, D7S820, D8S1179, D13S317, D16S539, FGA) in a Population Sample of North Italy

POPULATION: North Italy ($n = 170$)

KEYWORDS: forensic science, DNA typing, population genetics, D5S818, D7S820, D8S1179, D13S317, D16S539, FGA, North Italy

Whole blood samples were collected from 170 unrelated healthy individuals living in the North Italy. Genomic DNA was extracted using GenomicPrep Blood DNA Isolation Kit (Amersham-Pharmacia-Biotech, Milano, Italy) and its concentration was determined spectrophotometrically. Two to five ng of target DNA was amplified in singleplex for FGA and D8S1179, while duplex amplification was adopting for D13S317/D16S539 and D5S818/D7S820. PCR amplification conditions were the same for all six loci and the program of amplification were carried out in a GeneAmp® PCR System 9700 Thermal Cycler (PE-Biosystems, Foster City, CA). The amplified products were separated and detected using the A.L.F. express DNA sequencer (Pharmacia-Biotech, Uppsula, Sweden). Allele designation was established following the recommendations of the DNA commission of the ISFH (1). Statistical analysis was performed as previously reported (2) by a computer program made from the authors using Excel spread sheets.

Allele and genotype frequencies were determined and Hardy-Weinberg equilibrium (HEW) was tested by a Chi-square test (χ^2). A significant departure from HWE was found for D5S818 ($P = 0.01$) due to an excess of heterozygotes and deficiency of homozygotes, but when Bonferroni correction (3) was applied to the six loci analyzed, that observation was not significant. For each locus was calculated the following forensic parameter: Observed and Expected Heterozygosity (Hobs, Hexp), allelic diversity (h) and correlative standard error (s.e.), Polymorphic Information Content (PIC), Power of Discrimination (PD), Power of Exclusion (PE), Matching probability and Typical Paternity Index. It was furthermore calculated the Combined Power of Discrimination and the Combined Power of Exclusion for the six STR loci analyzed.

TABLE 1—*Allele frequencies in a North Italy population sample (n = 170).*

Allele	D5S818	D7S820	D13S317	D16S539	D8S1179	FGA
7	…	0.008	…	…	…	…
8	0.004	0.150	0.089	0.029	0.013	
9	0.034	0.116	0.069	0.121	0.008	
10	0.073	0.195	0.064	0.072	0.104	
11	0.301	0.279	0.321	0.310	0.034	
12	0.396	0.187	0.311	0.266	0.139	
13	0.189	0.045	0 084	0.189	0.339	
14		0.020	0.049	0.009	0.195	
15			0.010		0.150	
16					0.040	
17						
18						0.007
19						0.105
20						0.124
20.2						0.003
21						0.161
22						0.165
22.2						0.007
23						0.187
24						0.150
25						0.026
26						0.048
27						0.011
Hobs	0.681	0.783	0.792	0.805	0.843	0.849
Hexp	0.749	0.841	0.774	0.781	0.764	0.895
PIC	0.668	0.797	0.750	0.755	0.776	0.855
PD	0.861	0.935	0.921	0.910	0.926	0.956
PE	0.400	0.568	0.584	0.610	0.682	0.694

Hobs: observed heterozygosity; Hexp: expected heterozygosity; PIC: polimorphic information content; PD: power of discrimination; PE: probability of exclusion.

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The complete data set is available to any interested researcher upon request to the corresponding author, Prof. Domenico De Leo.

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