

FOR THE RECORD

David Abrantes,¹ M.S.; Gabriela Lima,¹ M.S.; Laura Cainé,¹ M.S.; Lurdes Pontes,¹ M.S.; and Fátima Pinheiro,¹ Ph.D.

Allele Frequencies of 15 Loci Using AmpF ℓ STR Identifiler Kit in a Northern Portuguese Population

POPULATION: 250 unrelated and healthy individuals from Portugal

KEYWORDS: forensic science, DNA typing, Portugal, population genetics, short tandem repeat, D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, FGA

Extraction: Blood stains were collected and air dried. DNA was extracted using the Chelex® resin (1).

PCR: The co-amplification of D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818 and FGA loci was performed using the AmpF ℓ STR® Identifiler™ PCR Amplification Kit (Applied Biosystems). About 1–2 ng of template DNA was used. Reactions for multiplex PCR were prepared according to the kit manufacturer's instructions (2) and carried out using a thermocycler GeneAmp® PCR System 9600 (Perkin Elmer).

Typing: The amplified products were detected and separated by capillary electrophoresis using an ABI PRISM® 3100 Genetic Analyzer (Applied Biosystems). The results were analyzed with the Genescan® Analysis Software v. 3.7 and allele designations were determined automatically using the Genotyper® Software v. 3.7 (Applied Biosystems) typed by comparison with an allelic ladder.

Analysis and Results: Allele frequencies were calculated by the direct counting method (Table 1) and the Hardy-Weinberg equilibrium was tested using the exact test, involving the GENEPOL version 3.1a software package (3). Independence among loci was estimated by means of genotype disequilibrium testing for each locus pair using Fisher's method using the same package. The potential usefulness of the considered loci was assessed by calculating

some statistical parameters of forensic interest (Table 2). The results demonstrate that all loci were in Hardy-Weinberg equilibrium (Table 2). The independence of loci was also verified with the exception of the pair D18S51-TH01 (data not shown). The forensic parameters indicated that these 15 loci are highly discriminating in the Portuguese population for both paternity testing and routine forensic casework.

The complete dataset is available upon request to any interest party from the corresponding author at biologia@dpinml.mj.pt.

References

- Walsh PS, Metzger DA, Higuchi R. CHELEX® 100 as a medium for simple extraction of DNA for PCR-based typing from forensic material. *BioTechniques* 1991;10:506–13.
- Applied Biosystem, AmpF ℓ STR® Identifiler PCR Amplification Kit User's Manual, 2001.
- Raymond M, Rousset F. GENEPOL (version 1.2): population genetics software for exact tests and ecumenicism. *J Hered* 1995;86:248–9.

[PubMed]

Additional information and reprint requests:

Maria de Fátima Pinheiro, Ph.D.
Delegação do Porto do Instituto Nacional de Medicina Legal
Jardim Carrilho Videira
4050-167 Porto
Portugal
Phone: (351) 22 207 38 50
Fax: (351) 22 332 59 31
E-mail: biologia@dpinml.mj.pt

¹ Service of Forensic Genetics, National Institute of Legal Medicine, Porto Delegation, Portugal.

TABLE 1—Allele frequencies of the 15 loci in a Northern Portuguese population (n=250).

TABLE 2—*Statistical parameters of forensic interest.*

	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
p	0.8917	0.4756	0.8902	0.8428	0.8827	0.9186	0.3023	0.2031	0.8476	0.4562	0.9999	0.7031	0.6346	0.3546	0.3393
H _{obs}	0.8320	0.8600	0.8280	0.7200	0.7840	0.8080	0.8000	0.7720	0.8760	0.7480	0.8040	0.6320	0.8320	0.6960	0.8760
H _{exp}	0.8140	0.8484	0.8143	0.7194	0.7851	0.8018	0.7745	0.7706	0.8587	0.7821	0.8164	0.6440	0.8797	0.6980	0.8674
PD	0.9372	0.9575	0.9374	0.8646	0.9176	0.9292	0.9097	0.9069	0.9629	0.9154	0.9388	0.7914	0.9728	0.8452	0.9672
PE	0.6329	0.6960	0.6255	0.4625	0.5740	0.5992	0.5722	0.5561	0.7192	0.5841	0.6316	0.3928	0.7522	0.4405	0.7286
PIC	0.7876	0.8290	0.7856	0.6645	0.7495	0.7692	0.7415	0.7334	0.8425	0.7501	0.7889	0.5891	0.8653	0.6414	0.8508

p: Hardy-Weinberg equilibrium exact test; H_{obs}: observed heterozygosity; H_{exp}: expected heterozygosity; PD: power of discrimination; PE: probability of exclusion; PIC: polymorphic information content.