FOR THE RECORD

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

Genetic Data of 4 X-Chromosomal Short Tandem Repeats in a North of Portugal Population

POPULATION: One hundred unrelated females and 100 unrelated males, autochthonous, healthy, from the North of Portugal.

KEYWORDS: forensic science, DNA typing, X-chromosome, Portugal, population genetics, DXS8378, HPRTB, DXS7423, DXS7132

Extraction

DNA was extracted from blood samples or buccal swabs using the Chelex $^{(R)}$ method (1).

PCR

The coamplification of DXS8378, HPRTB, DXS7423, DXS7132, and amelogenin was performed with the commercial kit Mentype[®] Argus X-UL PCR Amplification kit (Biotype[®] AG, Germany). PCR was prepared according to the Mentype[®] Argus X-UL Manual (2) and carried out in a thermocycler GeneAmp[®] PCR System 9700 (Applied Biosystems, Foster City, CA).

Typing

The amplified products were detected and separated by capillary electrophoresis in an ABI PRISM[®] 310 Genetic Analyzer (Applied Biosystems). Fragment sizes were determined automatically using the Genescan[®] Analysis Software version 3.7 and allele designations were determined automatically, with the Genotyper[®] Software version 3.7 (Applied Biosystems), by comparison with ladder included in the kit. The X-chromosomal DNA-profiling applying Mentype[®] Argus X-UL corresponds to the guidelines of the ISFH (3).

Results and Analysis

For each locus, allele frequencies were calculated separately for males and females, by the direct counting method (Table 1). The Hardy–Weinberg equilibrium was tested using the exact test, involving the GENEPOP version 3.4 software package (4). The potential usefulness of the considered loci was assessed by calculating some statistical parameters of forensic interest (Table 1).

 TABLE 1—Allele frequencies and statistical parameters of forensic interest of the 4 X-chromosomal STRs in a North of Portugual population (100 females, 100 males).

	DXS8378		HPRTB		DXS7423		DXS7132	
Allele	Female	Male	Female	Male	Female	Male	Female	Male
9	0.015	0.020	0.010	0.010	_	_	_	_
10	0.335	0.370	_	_	_	_	_	
11	0.295	0.270	0.175	0.150		_	0.010	0.010
12	0.335	0.260	0.285	0.360		_	0.085	0.140
13	0.015	0.060	0.290	0.230	0.065	0.060	0.315	0.260
14	0.005	0.020	0.180	0.220	0.365	0.330	0.340	0.360
15		_	0.055	0.030	0.315	0.360	0.175	0.180
16		_	0.005	_	0.220	0.180	0.075	0.030
17	_	_	_	_	0.035	0.060	_	0.020
18		_	_	_	_	0.010	_	
р	0.5945	_	0.5255	_	0.8720	_	0.1061	
\hat{P}_{d}	0.8390	0.8667	0.9082	0.8901	0.8627	0.8699	0.8868	0.8932
P_{e}^{-}	0.4103	0.4688	0.5481	0.5133	0.4620	0.4808	0.5113	0.5240
PĨC	0.6235	0.6674	0.7306	0.7033	0.6617	0.6741	0.6991	0.7094
MEC	0.5081	0.5467	0.5962	0.5704	0.5569	0.5712	0.5838	0.5865

MEC, mean exclusion chance; p, Hardy–Weinberg equilibrium exact test; P_d , power of discrimination; P_e , power of exclusion; PIC, polymorphic information content; STR, short tandem repeat.

The results among the females demonstrate that all loci were in Hardy–Weinberg equilibrium (Table 1). The forensic parameters indicated that these four loci are useful, mainly in the investigation of kinship analysis and affiliation complex cases.

The complete data set is available upon request at laurakaine@ hotmail.com

References

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

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Additional information and reprint requests: Laura Mendes Cainé, M.S. Delegação do Porto do Instituto Nacional de Medicina Legal Jardim Carrilho Videira 4050-167 Porto Portugal E-mail: laurakaine@hotmail.com