

FOR THE RECORD

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Genetic Data of Four X-Chromosomal STRs in a Population Sample of Santa Catarina, Brazil

POPULATION: A total of 184 healthy unrelated individuals (70 females and 114 males), autochthonous from Santa Catarina, Brazil.

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

Extraction

DNA was extracted from blood samples using the Chelex[®] method (1) and purified, if necessary, using a modified organic phenol–chloroform–isoamylalcohol method.

PCR

DNA was amplified with the commercial kit Mentype[®] Argus X-UL PCR amplification kit (Biotype[®] AG, Germany), which allows coamplification of the four loci: DXS8378, HPRTB, DXS7423, DXS7132, and amelogenin. 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. Allele designation of the analyzed samples was performed automatically, with the Genotyper[®] Software version 3.7, in combination with the Mentype Argus X-UL Template File, and by comparison with the ladder included in the kit. The X-chromosomal DNA-profiling applying Mentype[®] Argus X-UL corresponds to the guidelines of the ISFG (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

TABLE 1—Allele frequencies and statistical parameters of forensic interest of the four X-chromosomal STRs in a population sample of Santa Catarina, Brazil.

Allele	DXS8378		HPRTB		DXS7423		DXS7132	
	Female	Male	Female	Male	Female	Male	Female	Male
8	—	—	0.014	0.009	—	—	—	—
9	0.007	0.009	—	—	—	—	—	—
10	0.382	0.277	0.014	0.009	—	—	—	—
11	0.298	0.366	0.083	0.116	—	—	0.021	0.009
12	0.285	0.321	0.389	0.321	—	—	0.076	0.080
13	0.021	0.027	0.278	0.348	0.062	0.107	0.271	0.321
14	0.007	—	0.180	0.161	0.306	0.348	0.306	0.313
15	—	—	0.028	0.018	0.417	0.366	0.243	0.205
16	—	—	0.014	0.018	0.194	0.125	0.062	0.045
17	—	—	—	—	0.021	0.054	0.021	0.027
18	—	—	—	—	—	—	—	—
<i>p</i>	0.887	—	0.993	—	0.957	—	0.653	—
PD	0.836	0.834	0.879	0.881	0.843	0.863	0.905	0.891
PE	0.406	0.435	0.501	0.502	0.434	0.473	0.544	0.520
PIC	0.619	0.618	0.688	0.692	0.636	0.666	0.725	0.706
MEC	0.514	0.555	0.577	0.581	0.549	0.567	0.598	0.587

n = 184 (70 females, 114 males).

p, Hardy–Weinberg equilibrium exact test; PD, power of discrimination; PE, expected probability of exclusion; PIC, polymorphic information content; MEC, mean exclusion chance.

calculating some statistical parameters of forensic interest (Table 1). 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 dataset is available upon request at biologia@dpinml.mj.pt.

References

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