FOR THE RECORD

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Genetic Data of Five STR Loci in a Population Sample of Santa Catarina, Brazil

POPULATION: 185 unrelated, autochthonous healthy individuals from Santa Catarina, Brazil

KEYWORDS: forensic science, DNA typing, Santa Catarina, Brazil, population genetics, short tandem repeats, D2S1338, D19S433, Penta E, Penta D, SE33 (ACTBP2)

DNA was extracted from blood stains using the Chelex® method (1) and purified, if necessary, using the organic phenol-chloroform-isoamylalcohol method modified.

The locus SE33 (ACTBP2) and two the pentameric STRs Penta E and Penta D were amplified using respectively the kits PowerPlex® ES Monoplex System SE33 and PowerPlex® 16 System (Promega). The loci D2S1338 and D19S433 were co-amplified using the AmpFℓSTR® Identifiler™ PCR Amplification Kit (Applied Biosystems). Reactions for multiplex PCR were prepared according to manufacturer's instructions (2–4) and carried out using a thermocycler GeneAmp® PCR System 9700 (Applied Biosystems).

The amplified products were detected and separated by capillary electrophoresis using an ABI PRISM® 310 Genetic Analyzer (Applied Biosystems). Fragment sizes were determined automatically using 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.

Allele frequencies were calculated by the direct counting method (Table 1) and the Hardy-Weinberg equilibrium was tested using the exact test, involving the GENEPOP version 3.1a software package (5). Independence among loci was estimated by means of genotype disequilibrium testing for each locus pair (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 show that all loci were in Hardy-Weinberg equilibrium. The independence of loci was also verified in all pairs (data not shown). The forensic parameters indicated that these five loci are highly discriminating in the Southern Brazilian population for both paternity testing and routine forensic casework, being the less discriminating system the D19S433. The acumulated PEX is 0.999124956.

In routine forensic casework, it is important to establish a population database for further reliable statistical analysis. The genetic analysis of these 5 STRs performed, it is a complementary study of other previously published for this same population (6).

The complete dataset is available upon request at biologia@dpinml.mj.pt.

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TABLE 1—*Allele frequencies of the 5 loci in a population from Santa Catarina (n = 185).*

Allele	D2S1338	D19S433	Penta E	Penta D	SE33 (ACTBP2)
2.2	⋯	⋯	⋯	0.0135	⋯
5	⋯	⋯	0.0595	0.0027	⋯
7	⋯	⋯	0.1757	0.0108	⋯
8	⋯	⋯	0.0135	0.0270	⋯
9	⋯	⋯	⋯	0.1784	⋯
10	⋯	0.0027	0.0838	0.1405	⋯
11	⋯	0.0108	0.0892	0.1486	⋯
12	⋯	0.0946	0.2162	0.1703	0.0027
12.2	⋯	0.0054	⋯	⋯	⋯
13	0.0054	0.2838	0.1108	0.1784	0.0270
13.2	⋯	0.0162	⋯	⋯	⋯
14	⋯	0.2811	0.0595	0.1000	0.0351
14.2	⋯	0.0324	⋯	⋯	⋯
15	⋯	0.1784	0.0378	0.0162	0.0703
15.2	0.0027	0.0297	⋯	⋯	0.0027
16	0.0432	0.0405	0.0649	0.0108	0.0676
16.2	⋯	0.0108	⋯	⋯	⋯
17	0.2919	0.0054	0.0351	0.0027	0.0676
17.2	⋯	0.0027	⋯	⋯	⋯
18	0.1081	⋯	0.0216	⋯	0.0973
19	0.1243	⋯	0.0162	⋯	0.0703
20	0.0865	⋯	0.0027	⋯	0.0540
20.2	⋯	⋯	⋯	⋯	0.0270
21	0.0270	⋯	0.0054	⋯	0.0189
22	0.0486	⋯	0.0054	⋯	0.0081
22.2	⋯	⋯	⋯	⋯	0.0108
23	0.1027	⋯	⋯	⋯	0.0027
23.2	⋯	⋯	⋯	⋯	0.0135
24	0.0676	0.0027	0.0027	⋯	⋯
24.2	⋯	⋯	⋯	⋯	0.0486
25	0.0649	0.0027	⋯	⋯	⋯
25.2	⋯	⋯	⋯	⋯	0.0297
26	0.0243	⋯	⋯	⋯	⋯
26.2	⋯	⋯	⋯	⋯	0.0460
27	0.0027	⋯	⋯	⋯	⋯
27.2	⋯	⋯	⋯	⋯	0.0486
28.2	⋯	⋯	⋯	⋯	0.0838
29	⋯	⋯	⋯	⋯	0.0027
29.2	⋯	⋯	⋯	⋯	0.0540
30.2	⋯	⋯	⋯	⋯	0.0514
31.2	⋯	⋯	⋯	⋯	0.0297
32.2	⋯	⋯	⋯	⋯	0.0162
33	⋯	⋯	⋯	⋯	0.0027
34.2	⋯	⋯	⋯	⋯	0.0027
36	⋯	⋯	⋯	⋯	0.0027
37	⋯	⋯	⋯	⋯	0.0054

TABLE 2—*Statistical parameters of forensic interest.*

	D2S1338	D19S433	Penta E	Penta D	SE33 (ACTBP2)
p	0.0101	0.1000	0.4425	0.1001	0.0200
H_{obs}	0.7622	0.7784	0.8811	0.8324	0.9081
H_{exp}	0.8576	0.7977	0.8826	0.8564	0.9462
PD	0.9623	0.9264	0.9740	0.9617	0.9944
PE	0.7216	0.6072	0.7624	0.7050	0.8858
PIC	0.8421	0.7675	0.8693	0.8366	0.9407

* p: Hardy-Weinberg equilibrium exact test (for standard error <0.01); H_{obs}: observed heterozygosity; H_{exp}: expected heterozygosity; PD: power of discrimination; PE: probability of exclusion; PIC: polymorphic information content.

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