SHORT COMMUNICATION

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A Spanish population study of the STR loci HumLPL, D5S818, D7S820 and D13S317

Abstract Allele and genotype frequencies for four tetrameric short tandem repeat loci were determined in a Spanish population sample ($N = 193$-225) using PCR. All loci met Hardy-Weinberg expectations and the results demonstrated the assumption of independence of the loci analysed. The allele frequency data can be used in identity testing to estimate the frequency of a multiple PCR-based DNA profile in the Spanish population.

Key words PCR · STR · HUMLPL · D5S818 · D7S820 · D13S317 · Population database · Spain · Hardy-Weinberg equilibrium

Introduction

This study presents allele and genotype frequency data in a Spanish population sample for the four STR loci HUMLPL [1], D5S818 [2], D13S317 [2] and D7S820 [3].

Materials and methods

DNA was extracted by the standard phenol/chloroform extraction procedure from 193–225 individuals residing in North Spain (communities of Galicia $n = 15$, Asturias $n = 2$, Cantabria $n = 3$, Pais Vasco $n = 15$, La Rioja $n = 3$, Aragón $n = 2$ and Cataluña $n = 3$), in Central Spain (communities of Madrid $n = 77$, Castilla La Mancha $n = 26$, Castilla-León $n = 30$ and Extremadura $n = 1$) and in Eastern Spain (communities of Valencia $n = 44$ and Murcia $n = 4$).

PCR amplification was performed according to the manufacturer's recommendations using the Perkin Elmer AmpFlSTR Yellow PCR Amplification Kit (D5S818, D7S820 and D13S317) and the Gene Print STR system of Promega Corporation (HUMLPL).

For D5S818, D7S820 and D13S317 typing was performed on an ABI 377 sequencer according to the recommendations of the

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AmpFlSTR Profiler user's manual (Perkin Elmer), using the Genescan 2.1 analysis software and the Genotyper 2.0 analysis software. For the HUMLPL locus the PCR products were typed as described previously [4]. Allele designations were made according to recommendations of the DNA Commission of the International Society for Forensic Haemogenetics [5].

The statistical evaluations including the possible divergence from Hardy-Weinberg expectations and other parameters of forensic importance were performed using the HWE-Analysis, version 3.3. (Christoph Puers, Institute of Legal Medicine, University of Münster). The possible associations between loci were tested using the computer program GDA (Genetic Data Analysis: software for the analysis of discrete genetic data. PO Lewis, D Zaykin).

Results and discussion

The genotype frequency distributions showed no deviations from HWE expectations based on the χ^2-test, the logarithmic likelihood ratio (G) test and the exact test [6] (Tables 1 and 2). The test based on the number of distinct genotypes observed in the sample population showed that the observed numbers of distinct heterozygote and homozygote genotypes [7] are in accordance with their respective HWE predictions (data not shown). The heterozygosity rates and other parameters of forensic impor-

Table 1 Observed allele frequencies for the STR loci in a Spanish population

	HUMLPL	D5S818	D7S820	D13S317
Allele	($n = 193$)	($n = 225$)	($n = 225$)	($n = 225$)
7		0.0022	0.0267	
8	0.0026		0.1667	0.1578
9	0.0337	0.0311	0.1267	0.0533
10	0.3731	0.0733	0.2822	0.0667
11	0.3135	0.3600	0.1867	0.2911
12	0.2254	0.3556	0.1689	0.2733
13	0.0492	0.1689	0.0378	0.1200
14	0.0026	0.0089	0.0044	0.0378
Minimum frequency	0.0140	0.0127	0.0135	0.0136

n = sample size

Table 2 HWE tests on STR loci

	HUMLPL	D5S818	D7S820	D13S317
χ^2 test	0.7300	0.6050	0.1860	0.3985
G test	0.6105	0.4945	0.4310	0.4030
Exact test	0.5435	0.5470	0.4415	0.4255

Number of random shuffles performed: 2000

Table 3 Statistical parameters of forensic importance

	HUMLPL	D5S818	D7S820	D13S317
H_{obs}	0.6839	0.7556	0.8178	0.8222
H_{exp} [a]	0.7100	0.7106	0.8128	0.7943
MEC	0.4537	0.4617	0.6259	0.5981
PIC	0.6546	0.6580	0.7847	0.7631
D	0.8659	0.8579	0.9338	0.9269

[a] Expected heterozygosity is an unbiased estimate
H obs. Observed heterozygosity [9]
H exp Expected heterozygosity [9]
MEC Mean exclusion chance [10]
PIC Polymorphism information content [11]
DP Discrimination power [12]

Table 4 Two loci inter-class correlation test for STR loci in a Spanish population sample

	LPL	D5S818	D7S820	D13S317
LPL	–			
D5S818	0.8320	–		
D7S820	0.3390	0.5895	–	
D13S317	0.6640	0.5920	0.3900	–

tance (Table 3) are similar to those found in other Caucasians populations [8] (U.S. Caucasian databases 1997 population genetics. AmpFl STR Profiler Amplification Kit. User's Manual. Cap. 13. PE Applied Biosystems). An interclass correlation test analysis demonstrated that there is no evidence for correlation between the alleles at any of the pairs of loci (Table 4).

In conclusion, a Spanish population database has been established for the HUMLPL, D5S818, D7S820 and D13S317 loci. The combined power of exclusion is estimated as 95.441% and the combined power of discrimination is 99.991%. The allele frequency data can be used for deriving estimates of multiple locus profile frequencies for identity and paternity testing purposes using the product rule.

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