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SHORT COMMUNICATION

P. Nievas · B. Martinez-Jarreta · E. Abecia
M. V. Lareu

Fluorescence-based amplification of the STR loci D18S535, D1S1656 and D12S391 in a population sample from Aragon (North Spain)

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Abstract Population data were generated for the STR loci D18S535, D1S1656 and D12S391 in a population sample of unrelated healthy individuals born and living in Aragon (North Spain). The three loci were amplified using a fluorescence-based PCR method and were typed automatically. No deviation from Hardy-Weinberg expectations were observed. The three loci proved to be highly discriminating and valuable polymorphisms for forensic analyses.

Key words Short tandem repeats · D18S535 · D1S1656 · D12S391 · Population genetics · Spain

Introduction

Recently new STR loci have been identified and proposed for application to routine forensic casework [1–4].The aim of this work was to investigate the usefulness of the STR loci D18S535, D1S1656 and D12S391 and set up databases for these polymorphisms in a relevant Spanish population sample residing in Aragon.

Material and methods

Genomic DNA was extracted by the standard phenol/chloroform extraction procedure. D18S535, D1S1656 and D12S391 singleplex amplifications were performed as described previously by Lareu et al. [1, 3, 4]. Separation was carried out on 6% (w/v acrylamide/bisacrylamide) polyacrylamide denaturing high-perfomance DNA sequencing gels (Ready Mix Gel ALF grade, Pharmacia). Sequenced allelic ladders were provided by A. Carracedo (Institute of Legal Medicine, Santiago de Compostela, Galicia, Spain) and used for each system as recommended by the DNA Commission of the International Society of Forensic Haemogenetics [5, 6]. Statistical evaluations were performed as described elsewhere [7].

P. Nievas · B. Martínez-Jarreta (✉) · E. Abecia
Department of Legal Medicine, Faculty of Medicine,
University of Zaragoza, C/Domingo Miral s/n,
E-50009 Zaragoza, Spain
e-mail: mjarreta@posta.unizar.es
Fax +34-75-76166

M. V. Lareu
Institute of Legal Medicine, Faculty of Medicine,
E-15705 Santiago de Compostela, Galicia, Spain

Table 1 Observed allele frequency distribution for the STR loci: D18S535, D1S1656 and D12S391 in a population sample from Aragon

Alleles	D18S535 $n = 104$	D1S1656 $n = 104$	D12S391 $n = 100$
9	0.053		
10	0.005		
11	0.024	0.058	
12	0.216	0.144	
13	0.288	0.053	
14	0.260	0.087	
15	0.135	0.159	0.035
15.3	–	0.063	–
16	0.014	0.087	0.030
17		0.149	0.125
17.3		0.120	–
18		–	0.170
18.3		0.072	–
19			0.105
19.3		0.010	–
20			0.130
21			0.090
22			0.155
23			0.095
24			0.040
25			0.020
26			0.005
HWE tests		*p* values	
χ^2	$P = 0.981$	$P = 0.854$	$P = 0.951$
Likelihood ratio test	$P = 0.976$	$P = 0.773$	$P = 0.782$
Exact test	$P = 0.986$	$P = 0.879$	$P = 0.789$

Results and discussion

The genotype and allele frequencies for the three STR systems in the analysed population are shown in Table 1. The distribution of the genotypes at all three loci were found to be in Hardy-Weinberg equilibrium (Table 1) and an interclass correlation test analysis demonstrated that there was no evidence for correlation between the alleles for any of the pair-wise comparisons of loci (D1S1656/D12S391: 0.992; D1S1656/D18S535: 0.983; D12S391/D18S535: 0.991).

A comparison of the allele frequencies in the population under study with other European populations studied to date [2, 8, 9] revealed no significant differences except at the D12S391 locus with Catalonians ($P < 0.0001$) [9] and with non-Caucasian populations such as Chinese ($P < 0.0001$) [8].

Some statistics of medico-legal interest were also calculated and revealed that these systems have a high forensic efficiency and can be very useful tools for personal identification (power of discrimination: 0.915 for D18S535, 0.968 for D1S1656 and 0.966 for D12S391).

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