

Genetic analysis of the short tandem repeat loci FGA, D7S820, D1S355, D9S304, D12S1090, D3S1744 and D18S849 in an Antioquia (Colombia) population sample

J.J. Builes^{a,b,*}, M.L.J. Bravo^a, J.D. Garcia^b, M.A. Moreno^{a,b}

^a*Paternity Testing, Laboratorio de Genética Forense y Huellas Digitales del DNA, GENES Ltda., Carrera 48 No. 10-45 Cons. 612, Medellín, Antioquia 1252, Colombia*

^b*Instituto de Biología, Universidad de Antioquia, Medellín, Colombia*

Abstract. In this study, the validation of seven short tandem repeated (STR) systems is presented in a sample of the population from Antioquia, central region of Colombia. The DNA for the analyses of PCR was obtained from 261–450 unrelated individuals (selected using some cases of paternity from the Human Genetics Laboratory, University of Antioquia, and Laboratorio de Genética Forense y Huellas Digitales del DNA, GENES). PCR amplification was performed according to the manufacturer's instructions, using the STR Multiplex I (FGA, D7S820, D1S355 and D9S304) and STR Multiplex II (D12S1090, D3S1744 and D18S849) kits (Lifecodes, Stanford, CT). The seven loci met the Hardy–Weinberg expectations, and they possess a combined power discrimination higher than 0.999999999 and a combined power exclusion similar to 0.9996, showing them to be a group of excellent markers as complement in paternity testing in the identification of individuals and in forensic applications in general. © 2003 Elsevier B.V. All rights reserved.

Keywords: Antioquia; Colombia; Population; DNA; STR

1. Introduction

Short tandem repeats (STR) are polymorphic markers widely distributed throughout the human genome [1], and they can be PCR amplified, but only some of them have been studied for use in forensic genetic and paternity testing. The general criteria for selecting STRs include characteristics such as high heterozygosity, low stutter, few and low extra-peaks, robustness, easy multiplexing and a low mutation rate [2].

The aim of this study was to report allele frequency distributions for the FGA, D7S820, D1S355, D9S304, D12S1090, D3S1744 and D18S849 loci in a sample of the population from Antioquia, a central region of Colombia [3–5], as well as statistical evaluations,

* Corresponding author. Paternity Testing, Laboratorio de Genética Forense y Huellas Digitales del DNA, GENES Ltda. Carrera 48 No. 10-45 Cons. 612, Medellín, Antioquia 1252, Colombia. Tel.: +57-4-2684875; fax: +57-4-3185270.

E-mail address: genforense@epm.net.co (J.J. Builes).

Table 1
Allele frequencies and statistical parameters

Allele	FGA	D7S820	D1S355	D9S304	D12S1090	D3S1744	D18S849
4				0.04441			
5				0.00987	0.00114		
6		0.00299		0.01316			
7		0.01045	0.01724	0.01151			0.00118
8		0.13284	0.07471	0.30757		0.00117	0.00118
9		0.11045	0.08238	0.11349	0.06023		0.00353
10		0.31045	0.05556	0.07566	0.01591	0.00233	0.00118
11		0.28209	0.09387	0.09211	0.05568	0.00233	0.00471
12		0.12687	0.20498	0.22039	0.04659	0.00233	0.00471
13		0.02388	0.26437	0.07895	0.03750	0.00117	0.00471
14	0.00299		0.13027	0.02796	0.03977	0.00117	0.03882
15			0.06897	0.00164	0.01818	0.07925	0.16706
16	0.00149		0.00766	0.00164	0.00227	0.08741	0.45412
17	0.00149			0.00164	0.00455	0.14336	0.23176
18	0.02090				0.01250	0.37646	0.07882
19	0.07313				0.03864	0.14802	0.00824
20	0.09403				0.07955	0.11305	
21	0.15672				0.06477	0.03613	
22	0.10448				0.12614	0.00350	
23	0.12687				0.08977		
24	0.16269				0.05341		
25	0.13433				0.06818	0.00233	
26	0.08806				0.08068		
27	0.02388				0.06705		
28	0.00448				0.01250		
29	0.00488				0.00795		
30					0.00909		
31					0.00682		
32					0.00114		
Minimum	0.0097	0.0088	0.0116	0.0099	0.0080	0.0067	0.0064
<i>n</i>	670	670	522	608	880	896	900
<i>Parameters</i>							
Ho	0.886567	0.785075	0.823755	0.809211	0.938636	0.781250	0.724444
He	0.882230	0.778582	0.843360	0.821696	0.933566	0.787458	0.708671
HWE-H	0.6224	0.7294	0.7336	0.7254	0.2943	0.9968	0.2928
Exact test	0.5252	0.5956	0.3252	0.0635	0.3970	0.0747	0.0968
PD	0.9717	0.9141	0.9578	0.9464	0.9893	0.9261	0.8690
PE	0.7681	0.5716	0.6438	0.6162	0.8748	0.5647	0.4671
MP	0.0283	0.0859	0.0422	0.0536	0.0107	0.0739	0.1310
PIC	0.8689	0.7442	0.8238	0.7997	0.9285	0.7627	0.6669
TPI	4.44079	2.3264	2.8370	2.6207	8.1481	2.2857	1.8145

n: Allele number, Ho: heterozygosity observed, He: heterozygosity expected, HWE-H: Hardy–Weinberg test, PD: power of discrimination, PE: power of exclusion, MP: matching probability, PIC: polymorphism information content, TPI: Typical Paternity Index.

including the possible divergence from Hardy–Weinberg expectations and other forensic parameters of interest.

2. Material and methods

Samples were obtained from 261 to 450 unrelated Caucasian individuals from Antioquia with a similar proportion of male and females. Genomic DNA was extracted by a salt precipitation extraction procedure [6]. PCR amplification was performed according to the manufacturer's directions, using the STR Multiplex I (FGA, D7S820, D1S355 and D9S304) and STR Multiplex II (D12S1090, D3S1744 and D18S849) kits (Lifecodes, Stanford, CT).

The frequency of each allele for each locus tested was calculated from the number of observed genotypes in the sample using GENEPOP software Ver. 3.2a [7]. The exact test for the Hardy–Weinberg equilibrium and linkage disequilibrium between loci was carried out by using the GENEPOP Ver. 3.2a [7] and the GDA Ver. 1.0 software. The forensic parameters were performed using the POWERSTAS software Ver. 12 (Promega) and GDA software Ver. 1.0 [8].

3. Results and discussion

Antioquia population data for the seven STRs are shown in Table 1. No deviations from the Hardy–Weinberg equilibrium were observed for all markers in the studied population. On the other hand, Antioquia population showed a similar allele distribution with other Caucasian European populations. This confirms the findings of past research about high Caucasian component of the Antioquia population [3,5,6].

The seven loci met the Hardy–Weinberg expectations. The combined power discrimination was > 0.999999999 and the combined power exclusion was similar to 0.9996.

In conclusion, a database of Caucasian population from Antioquia has been established for the analyzed systems. The results show that all seven loci are very useful for personal identification and paternity testing in the Antioquia population.

Acknowledgements

This work was supported by GENES Ltda. Juan José Builes has a PhD fellowship (0058/2001) from COLCIENCIAS.

References

- [1] J.S. Beckman, J.L. Weber, *Genomics* 12 (1992) 627–631.
- [2] M.V. Lareu, S. Barral, A. Salas, M. Rodríguez, C. Pestoni, A. Carracedo, in: G.F. Senasabaugh, P.J. Lincoln, B. Olaisen (Eds.), *Progress in Forensic Genetics*, vol. 7, Elsevier, Amsterdam, 2000, pp. 198–200.
- [3] M.L. Bravo, C.Y. Valenzuela, O.M. Arcos-Burgos, *Gene Geogr.* 10 (1996) 11–17.
- [4] L.G. Carvajal-Carmona, I.D. Soto, N. Pineda, D. Ortiz-Barrientos, C. Duque, J. Ospina-Duque, M. MacCarthy, P. Montoya, V.M. Alvarez, G. Bedoya, A. Ruiz-Linares, *Am. J. Hum. Genet.* 67 (2000) 1287–1295.
- [5] J.J. Parsons, Berkeley: University of California Press, 1949.
- [6] S.A. Miller, D.D. Dykes, H.F. Polesky, *Nucleic Acids Res.* 16 (1988) 1215.
- [7] M. Raymond, F. Rousset, *J. Heredity* 86 (1995) 248–249.
- [8] P.O. Lewis, D. Zaykin, 2001. Free program distributed by the authors over the Internet from <http://lewis.ceb.uconn.edu/lewishome/software.html>.