Allele frequency distribution of cofiler STRs in a Canary Islands population (Spain)

I. Frías [a],*, A. Hernández [a], O. García [b], J.M. Pérez [a],
J.J. Sánchez [c], J.A. Cuellas [a]

[a]*Instituto Nacional de Toxicología. Campus de Ciencias de La Salud La Laguna, 38320 Islas Canarias, Spain*
[b]*Area de Laboratorio de la Ertzainza, Sección de Biología, Bilbao, Spain*
[c]*Departamento de Fisiología. Universidad de La Laguna, Islas Canarias, Spain*

Abstract

Genotype and allele frequencies of the STRs included in Cofiler Kit were determined in a sample of the Canary Islands population. The results obtained do not deviate from HWE.
© 2003 Elsevier Science B.V. All rights reserved.

Keywords: STR; Cofiler; Canary Islands population

1. Introduction

The forensic application of polymorphic markers requires a representative data base of the reference population for correct use of the analysis results. The AmpliF*l*STR Cofiler STR multiplex system coamplifies the following six loci, and the homologous gene amelogenin:

D3S1358: (3 p) TCTA $(TCTG)_{1-3}$
D16S317: (16 q24-qter) $(AGAT)_n$
CSF1PO: (5 q33.3–34) $(AGAT)_n$
TPOX: (2 p23-2 per) $(AGAT)_n$
TH01: (11 p15.5) $(AATG)_n$
D7S820: (7 q11.21–22)$(GATA)_n$

---

* Corresponding author.

We present a study of allele and genotype frequencies for these loci included in the Cofiler kit from a sample of 245 unrelated individuals from routine casework, paternity testing and from volunteers in the Canary Islands population.

2. Material and methods

DNA was extracted from air dried bloodstains and from saliva using a phenol–clorophorm extraction procedure and quantified by using direct dot blot hybridisation to D17Z1 probe (Quantiblot kit, Applied Biosystem).

The amplification conditions were performed according to the manufacturer's recomendations using the AmpF*l*STR Cofiler Amplification kit in a 2400-thermal cycler.

Amplified fragments were separated by capillary electrophoresis in an Applied Biosystems ABI 310 instrument. Allele size and genotyping were performed by comparison to amplified fragments with internal size standards and allelic ladders.

Hardy–Weinberg equilibrium [1], minimum allele frequencies [2–4] and other statistical parameters [5,6] were estimated.

3. Results

The observed genotype and the allele frequencies for these systems are shown in Tables 1 and 2. Statistical parameters are summarised in Table 3. The loci studied do not deviate from HWE in the population analysed. Combined PD and EC are 99.99987% and 98.8667%, respectively. Independence between loci has been estimated by χ^2 test and no statistically significant differences were found.

Table 1
Allele frequencies

Allele	D3S1358 ($n=239$)	D16S539 ($n=229$)	TH01 ($n=229$)	TPOX ($n=229$)	CSF1PO ($n=225$)	D7S820 ($n=238$)
6			0.2118	0.0065		
7			0.1921	0.0022	0.0044	0.0063
8		0.0284	0.1288	0.5328	0.0044	0.1554
9		0.0939	0.2009	0.1092	0.0356	0.1218
9.3			0.2576			
10		0.0546	0.0087	0.0655	0.3044	0.3151
11		0.3341		0.2598	0.3089	0.2101
12	0.0021	0.2576		0.0240	0.2867	0.1702
13	0.0063	0.1987			0.0533	0.0189
14	0.0795	0.0328			0.0022	0.0021
15	0.2636					
16	0.2510					
17	0.2008					
18	0.1904					
19	0.0063					
Min. frequency	0.0124	0.0127	0.0132	0.0016	0.0121	0.0118

Table 2
Observed genotypes

Genotype	Observed	Genotype	Observed
D3S1358			
12–15	1	15–17	32
13–14	1	15–18	15
13–15	1	15–19	1
13–18	1	16–16	16
14–14	1	16–17	16
14–15	10	16–18	25
14–16	9	16–19	2
14–17	10	17–17	6
14–18	6	17–18	26
15–15	15	18–18	9
15–16	36		
D16S538			
8–9	3	10–12	6
8–11	4	10–13	3
8–12	3	10–14	1
8–13	2	11–11	21
8–14	1	11–12	47
9–9	1	11–13	30
9–10	2	11–14	6
9–11	15	12–12	14
9–12	10	12–13	23
9–13	10	12–14	1
9–14	1	13–13	10
10–10	2	13–14	3
10–11	9	14–14	1
D7S820			
7–10	2	9–12	11
7–12	1	9–13	2
8–8	7	10–10	32
8–9	8	10–11	27
8–10	19	10–12	20
8–11	25	10–13	3
8–12	7	11–11	7
8–13	1	11–12	18
9–9	5	11–13	3
9–10	15	11–14	1
9–11	12	12–12	12
CSF1PO			
7–10	1	11–11	20
7–11	1	11–12	45
8–11	2	11–13	7
9–9	3	11–14	1
9–10	4	12–12	20
9–11	4	12–13	4
9–12	2	13–13	3

Table 2 (*continued*)

Genotype	Observed	Genotype	Observed
CSF1PO			
10–10	24		
10–11	39		
10–12	38		
10–13	7		
TPOX			
6–9	2	10–11	6
6–10	1	10–12	1
7–8	1	11–11	14
8–8	63	11–12	2
8–9	27		
8–10	15		
8–11	70		
8–12	5		
9–9	1		
9–10	3		
9–11	13		
9–12	3		
10–10	2		
TH01			
6–6	8	8–9	7
6–7	17	8–9.3	19
6–8	12	9–9	9
6–9	21	9–9.3	23
6–9.3	31	9.3–9.3	14
7–7	6	9.3–10	1
7–8	17		
7–9	23		
7–9.3	16		
7–10	3		
8–8	2		

Table 3
Statistics parameters

	χ^2	Exact test	Observed heteroz	Experimental heteroz	PIC	EC	PD
D3S1358	0.3015	0.1635	0.8033	0.7862	0.7499	0.6053	0.9120
D16S539	0.6355	0.5240	0.7860	0.7706	0.7340	0.5734	0.9042
TH01	0.1570	0.1715	0.8297	0.7966	0.7624	0.6553	0.9192
TPOX	0.2575	0.2220	0.6587	0.6332	0.5816	0.3561	0.8039
CSF1PO	0.0555	0.0895	0.6889	0.7272	0.6747	0.4113	0.8708
D7S820	0.1915	0.1105	0.7353	0.7898	0.7568	0.4849	0.9230

Number of random shuffles performed: 2000. EC: exclusion chance. DP: discrimination power. PIC: polymorphic information content [7].

References

[1] S.W. Guo, E.A. Thompson, Performing the exact test of Hardy–Weinberg proportion for multiple alleles, Biometrics 48 (1992) 361–372.

[2] B. Budowle, K.L. Monson, R. Chakraborty, Estimating minimum allele frequencies for DNA profile frequency estimates for PCR-based loci, Int. J. Legal Med. 108 (1996) 173–176.

[3] R. Chakraborty, A class of population genetic questions formulated as the generalized occupancy problem, Genetics 134 (1993) 953–958.

[4] B.S. Weir, Independence of VNTR alleles defined by fixed bins, Genetics 130 (1992) 873–887.

[5] P.P. Lewis, D. Zaykin, Genetic Data Analysis: Computer program for the analysis of allelic data. Version 1.0 (d16c). Free program distributed by the authors over the internet from http://lewis.eeb.uconn.edu/lewishome/software.html, 2001.

[6] A. Tereba, Tools for Analysis of Population Statistics. Profiles in DNA, 2(3). Free program distributed by the author over the internet from http://www.promega.com/geneticidtools/powerstats, 1999.

[7] D. Botstein, R.L. White, M. Skolnick, R.W. Davis, Construction of a genetic linkage map in man using restriction fragment length polymorphisms, Am. J. Hum. Genet. 32 (1998) 314–331.