

FOR THE RECORD

Lucía Cifuentes,¹ M.Sc; Mónica Acuña,¹ M.Sc; and Donisia Sepúlveda,² C.T.

Allele Frequencies for Six STR in a Chilean Population

KEYWORDS: forensic science, DNA typing, population genetics, short tandem repeat, allele frequencies, forensic science, D3S1358, FGA, D8S1179, D21S11, D18S51, D5S818

A sample of Chilean individuals from the northern area of Santiago, the capital of Chile, was studied. The current Chilean population was sprung from the admixture between aborigine populations of mongoloid origin (Amerindians) and Spanish conquerors of Caucasian origin. Blood samples from unrelated blood donors were randomly collected in the Hospital San José. An appropriate informed consent was obtained from all of them according to the Ethical Board of the Medicine School of the University of Chile.

DNA was extracted using the organic method described by Comey et al. (1). D3S1358, FGA, D8S1179, D21S11, D18S51, and D5S818 STRs were amplified using the AmpF ℓ STR[®] Profiler Plus™ kit from Applied Biosystems. DNA fragments were electrophoresed on the ABI PRISM 310 genetic analyzer from Applied Biosystems-Perkin Elmer using the POP 4 310 GA polymer. Data were collected using the GeneScan 3.1 and Genotyper softwares from Applied Biosystems. The allele frequencies were estimated by simple counting, and the heterozygosity was estimated according to methods described previously (2,3). The expected and observed heterozygotes frequencies were compared by means of a homogeneity χ^2 test (3,4).

¹ Programa de Genética Humana, ICBM, Facultad de Medicina, Universidad de Chile PO. Box 70061-Santiago 7 Chile.

² Laboratorio de Biología Molecular, Genética y Tecnología Ltda. Santiago, Chile.

The complete dataset can be obtained by contacting Lucia Cifuentes, M.Sc., Programa de Genética Humana, ICBM, Facultad de Medicina, Universidad de Chile, PO Box 70061-Santiago 7 Chile. Email: lcifuent@machi.med.uchile.cl

References

1. Comey CT, Koons BW, Smerick JV, Sbierski CA, Stamley DM. DNA extraction strategies for amplified fragments length polymorphism analysis. *J Forensic Sci* 1994;39:1254–69.
2. Edwards A, Hammond HA, Jin L, Caskey CT, Chakraborty R. Genetic variation at five trimeric and tetrameric repeat loci in four human population groups. *Genomics* 1992;12:241–53.
3. Nei M. Estimation of average heterozygosity and genetics distance from a small number of individuals. *Genetics* 1992;89:583–90.
4. Chakraborty R, Fonage M, Guegue R, Boerwinkle E. Population genetics of hypervariable loci: analysis of PCR based VNTR polymorphism within a population. In: Burke T, Dolf G, Jeffreys AJ, Wolff R, editors. *DNA fingerprinting: approaches and applications*, Birkhauser Verlag, Berlin, 1991;127–43.

Additional information and reprint requests:

Lucia Cifuentes, M.Sc., Programa de Genética Humana, ICBM
Facultad de Medicina
Universidad de Chile
PO Box 70061-Santiago 7
Chile
Email: lcifuent@machi.med.uchile.cl.

TABLE 1—*Gene frequencies and Hardy-Weinberg equilibrium for the D3S1358, FGA, D8S1179, D21S11, D18S51, D5S818 loci in a blood donor sample from the Hospital San José in Santiago, Chile.*

Loci	D3S1358	FGA	D8S1179	D21S11	D18S51	D5S818
Allele	G.F.	G.F.	G.F.	G.F.	G.F.	G.F.
5						
6						
6.3						
7						0.1049
8			0.0062			0.0062
9						0.0185
10			0.0432			0.0370
11			0.1111			0.4753
12			0.0741		0.1562	0.2346
13			0.3333		0.1125	0.1173
14	0.0813		0.2901		0.2437	0.0062
15	0.4187		0.1173		0.0937	
16	0.2062		0.0247		0.1125	
17	0.1813				0.1313	
18	0.1063	0.0185			0.0938	
19	0.0062	0.0803			0.0375	
20		0.0617			0.0188	
21		0.1049				
22		0.0988				
22.2		0.0062				
23		0.1605				
24		0.1173				
25		0.1790				
26		0.1235		0.0062		
27		0.0123		0.0250		
28		0.0247		0.1125		
28.2				0.0062		
29		0.0123		0.1688		
30				0.2874		
30.2				0.0250		
31				0.0688		
31.2				0.0688		
32				0.0375		
32.2				0.1375		
33.2				0.0500		
34.2				0.0063		
Total	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
% observed homozygosity	27.50	7.41	20.99	16.25	7.50	34.56
% expected homozygosity	26.87	11.91	22.94	15.74	14.57	30.75
Computed χ^2	0.0163	1.5673	0.1713	0.1743	3.2126	0.5544
p-value	0.8988	0.2107	0.6762	0.6760	0.0731	0.4565