Allele frequencies for 12 autosomal short tandem repeat loci in two Bolivian populations

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ABSTRACT. Two hundred and sixty unrelated subjects who asked for paternity testing at two Bolivian Laboratories in La Paz and Santa Cruz were studied. The loci D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, TH01, TPOX, and CSF1PO were typed from blood samples, amplifying DNA by polymerase chain reactions and electrophoresis. Allele frequencies were estimated by simple counting and the unbiased heterozygosity was calculated. Hardy-Weinberg equilibrium was studied and gene frequencies were compared between the two samples. All loci conformed to the Hardy-Weinberg law and allele frequencies were similar in samples from the two cities. The Bolivian gene frequencies estimated were significantly different from those described for Chile and the United States Hispanic-Americans for most of the loci.

Key words: DNA typing; Population genetics; Short tandem repeat; Allele frequencies; Forensic science; Bolivian population

INTRODUCTION

The usefulness of genetic markers for identity testing and paternity analysis is based on known allele frequencies for the genetic markers analyzed. Yet, there is no information published about gene frequencies of multiallelic loci in the Bolivian population.

The current Bolivian population arose from the admixture between aborigine populations of Mongoloid origin (Amerindians) and Spanish conquerors of Caucasian origin.

The present study describes the allele frequencies for twelve short tandem repeat (STR) loci (D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, TH01, TPOX, CSF1PO) in two urban populations from La Paz and Santa Cruz, Bolivia, and compares these frequencies with data published from other populations.

SUBJECTS AND METHODS

Blood samples were collected from 176 unrelated Bolivian individuals from the cities of La Paz (N = 176) and Santa Cruz (N = 84), Bolivia, who asked for paternity testing from 1999 to 2005. Genomic DNA was obtained by the organic extraction method described by Comey et al. (1994). The vWA, CSF1PO, TPOX, and TH01 STRs analyzed before November 2000 were amplified using 1 ng DNA for each polymerase chain reaction, and the fragments were electrophoresed on 6% acrylamide gels and silver stained (GenePrint™ STR systems, 1997). The D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, TH01, TPOX, and CSF1PO loci studied after November 2000 were amplified using the AmpFl 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 obtained using the GeneScan 3.1, and Genotyper software from Applied Biosystems.

The allele frequencies were estimated by simple counting and the unbiased heterozygosity was calculated (Nei, 1992; Edwards et al., 1992). Both gene frequencies (expected according the Hardy-Weinberg equilibrium and those actually observed) were compared using the homogeneity χ^2 test (Chakraborty et al., 1991; Nei, 1992). Comparisons of gene frequencies among populations were made by means of the non-parametric method described by Roff and Bentzen et al. (1989).

RESULTS AND DISCUSSION

The gene frequencies estimated for the La Paz and Santa Cruz samples were similar (P > 0.05) and therefore pooled in Table 1. Every locus analyzed fit the Hardy-Weinberg equilibrium (P > 0.05). The lowest observed heterozygosity was 0.63 for the TPOX locus, while the highest observed heterozygosity was for the FGA locus (0.92). These gene frequencies are significantly different from those described for Chile (Figueroa et al., 2000; Cifuentes et al., 2002) and the United States Hispanic-Americans published by GenePrint™ STR systems (1997) for every locus (P < 0.05 for all of them) with the exceptions of D3S1358, D18S51, TPOX, and CSF1PO loci.

Table 1. Gene frequencies (G.F.) for the D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, TH01, TPOX, and CSF1PO loci in two samples from Bolivia.

Loci	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51
Homozygotes	31	44	8	18	14	13
Heterozygotes	74	132	98	95	93	81
Total	105	176	106	113	107	94
Allele	G.F.	G.F.	G.F.	G.F.	G.F.	G.F.
6						
6.3						
7						
8						
9				0.0044		0.0053
9.3				0.0000		0.0000
10				0.0752		0.0160
11				0.0619		0.0106
12				0.1327		0.1436
13	0.0048	0.0028		0.3097		0.1117
14	0.0333	0.0426		0.2257		0.2021
15	0.4143	0.0966		0.1593		0.1649
16	0.3095	0.3352		0.0265		0.1223
16.5	0.0000	0.0000		0.0000		0.0000
17	0.1524	0.3494		0.0044		0.0957
18	0.0762	0.1080	0.0094			0.0798
19	0.0048	0.0597	0.1698			0.0213
20	0.0000	0.0028	0.1038			0.0053
21	0.0048	0.0000	0.0566			0.0213
21.2			0.0000			
22			0.0991			
22.2			0.0047			
23			0.1321			
23.2			0.0000			
24			0.1415			
24.2			0.0000			
25			0.1745			
26			0.0849			
27			0.0236		0.0140	
28					0.0514	
29					0.1869	
30					0.2103	
30.2					0.0421	
31					0.0794	
31.2					0.1215	
32					0.0047	
32.2					0.2056	
33					0.0000	
33.2					0.0841	
34.2					0.0000	
Total	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
Observed heterozygosity	0.7	0.75	0.92	0.84	0.87	0.86
Gene diversity	0.7	0.74	0.87	0.80	0.86	0.87

Table 1. Continued.

Loci	D5S818	D13S317	D7S820	TH01	TPOX	CSF1PO
Homozygotes	22	13	18	25	33	22
Heterozygotes	83	92	83	60	57	62
Total	105	105	101	85	90	84
Allele	G.F.	G.F.	G.F.	G.F.	G.F.	G.F.
6				0.2590	0.0111	
6.3				0.0000	0.0000	
7	0.1571	0.0084	0.0050	0.4000	0.0167	
8	0.0095	0.0714	0.0495	0.0471	0.5440	
9	0.0762	0.2333	0.0644	0.0647	0.0611	0.0179
9.3	0.0000	0.0000	0.0000	0.2353	0.0111	0.0000
10	0.0238	0.0857	0.3218		0.0333	0.2143
11	0.4190	0.1857	0.3119		0.1944	0.2738
12	0.2190	0.1714	0.2079		0.1278	0.3988
13	0.0857	0.1333	0.0396			0.0714
14	0.0095	0.1095				0.0179
15		0.0048				0.0060
16						
16.5						
17						
18						
19						
20						
21						
21.2						
22						
22.2						
23						
23.2						
24						
24.2						
25						
26						
27						
28						
29						
30						
30.2						
31						
31.2						
32						
32.2						
33						
33.2						
34.2						
35						
Total	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
Observed heterozygosity	0.79	0.88	0.82	0.71	0.63	0.74
Gene diversity	0.74	0.84	0.75	0.71	0.64	0.71

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