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FOR THE RECORD

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Gene Frequencies for Three Hypervariable DNA Loci in a Chilean Population of Mixed Ancestry

POPULATION: Amerindian and Caucasian ancestral mix

KEYWORDS: forensic science, DNA typing, population genetics, polymorphisms, Chile, short tandem repeats, D16S539, D7S820, D13S317

Blood samples were collected in tubes containing ACD from 121 unrelated individuals who asked paternity analysis in The Clinical Hospital of the University of Chile during the years 2000 and 2001. The method presented by Comey (1) was used to remove DNA from the samples. The three STR were amplified using 1 ng of DNA for each PCR reaction, and the fragments electrophoresed through 6% acrylamide gels and silver stained, according to the manufacturer's recommendations (2).

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TABLE 1—*Gene frequencies and Hardy-Weinberg equilibrium for the D16S539, D7S820, and D13S317 loci.*

	D16S539	D13S317	D7S820
Homozygotes	25	17	25
Heterozygotes	96	102	95
All	121	119	120
Allele	frequency	frequency	frequency
6			
7			0.0125
8	0.0165	0.1345	0.0917
9	0.1240	0.1387	0.0875
10	0.0992	0.0546	0.2708
11	0.3595	0.1891	0.3167
12	0.2727	0.2395	0.1625
13	0.1198	0.1303	0.0542
14	0.0083	0.1135	0.0042
15			
	1.0000	1.0002	1.0001
% of observed homozygosity	20.66	14.29	28.83
% of expected homozygosity	24.35	16.32	21.92
Computed X^2	0.895	0.362	0.083
p-value	0.344	0.548	0.774

By simple counting, it was possible to estimate the allele frequencies. The calculation of the unbiased heterozygosity was done using the previously mentioned methods (3,4). Both gene frequencies (expected according to the Hardy-Weinberg equilibrium and those observed) were compared using the homogeneity X^2 test (4,5).

The gene frequencies estimated are significantly different from those described for USA Caucasians and Hispanic-Americans published by Promega (2). The computed X^2 for these comparisons were 33.70, 49.88 and 94.27 for D16S539, D7S820, and D13S317, respectively ($p < 0.005$ for all of them).

Table 1 contains the summary of frequencies. The complete data file is available upon request.

References

1. Comey CT, Koons BW, Smerick JV, Sobieralski CA, Stamley DM. DNA extraction strategies for amplified fragment length polymorphism analysis. J Forensic Sci 1994;39:1254–69.
2. GenePrint™ STR systems. Technical manual Promega. 1998.
3. 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.
4. Nei M. Estimation of average heterozygosity and genetic distance from a small number of individuals. Genetics 1992;89:583–90.
5. Chakraborty R, Fornage M, Guegue R, Boewinkle E. Population genetics of hypervariable loci: analysis of PCR based VNTR polymorphism within a population. In: Burke T, Dolf G, Jeffreys AJ, Wolff R, eds. DNA fingerprinting: approaches and applications. Birkhauser Verlag, Berlin, 1991;127–43.

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