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FOR THE RECORD

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Guatemala Mestizo Population Data on 15 STR Loci (Identifiler® Kit)

POPULATION: Guatemala mestizo.

KEYWORDS: forensic science, DNA typing, population genetics, Guatemala, Identifiler® kit, D3S1358, TH01, D21S11, D18S51, D2S1338, D5S818, D13S317, D7S820, D16S539, CSF1PO, D19S433, vWA, D8S1179, TPOX, FGA

Sample Preparation

Blood samples were obtained by venipuncture from unrelated individuals ($n = 200$) living in the State of Guatemala, and spotted on an FTA paper (Whatman, Florham Park, NJ).

PCR

Approximately 1 ng of DNA was used in each amplification. The samples were amplified using the AmpF*l*STR® Identifiler® kit (Applied Biosystems, Foster City, CA). The alleles were separated and detected using an Applied Biosystems ABI310 genetic analyzer.

Analysis of Data

The frequency of each allele for each locus was calculated from the numbers of each genotype in the sample set (i.e., the gene count method). Unbiased estimates of expected heterozygosity were computed as described by Edwards et al. (1). Possible divergence from Hardy–Weinberg expectations (HWE) was tested by calculating the unbiased estimate of the expected homozygote/heterozygote frequencies (1–4) and the exact test (5), based on 2000 shuffling experiments. The program for this analysis was kindly provided by R. Chakraborty (University of Cincinnati, Center for Genome Research, Department of Environmental Health, Cincinnati, OH).

The distributions of the observed allele frequencies for the 15 STR loci are shown in Table 1. The most informative loci are FGA and D18S51, and the least discriminating are TPOX and D3S1358. There were no detectable departures from HWE for the 15 loci. The combined power of discrimination is >0.99999999, and the combined power of exclusion is 0.99999875.

The complete data are available either by accessing http//:www.lorgen.com/forense or emailing the contact author (jlorente@ugr.es).

TABLE 1—*Observed allele frequencies for the 15 Identifiler® loci.*

Allele	D3S1358	TH01	D21S11	D18S51	D2S1338	D5S818	D13S317
4		0.0050					
5		0.0025					
6		0.4200					
7		0.2500				0.0675	
8		0.0500				0.0050	0.0550
9		0.0900		0.0025		0.0825	0.2475
9.3		0.1675					
10		0.0150				0.0425	0.1175
11				0.0025		0.4475	0.1850
12				0.1000		0.2400	0.1900
13	0.0025			0.1150		0.1050	0.1375

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TABLE 1— *Continued.*

Allele	D3S1358	TH01	D21S11	D18S51	D2S1338	D5S818	D13S317
14	0.0600			0.2300		0.0100	0.0675
15	0.4825			0.1475	0.0025		
16	0.2375			0.0875	0.0075		
16.2	0.0025						
17	0.1250			0.1450	0.1150		
18	0.0850			0.0700	0.0325		
19	0.0050			0.0475	0.1800		
20				0.0225	0.1600		
21				0.0225	0.0225		
22				0.0050	0.1225		
23				0.0025	0.2350		
24					0.0625		
25					0.0450		
26			0.0025		0.0150		
27			0.0050				
28			0.0750				
29			0.2550				
30			0.2350				
30.2			0.0025				
31			0.0525				
31.2			0.1425				
32			0.0100				
32.2			0.1475				
33			0.0025				
33.2			0.0575				
34			0.0025				
34.2			0.0050				
35			0.0050				
Homozygosity test*	0.855	0.728	0.392	0.463	0.189	0.884	0.447
Exact test†	0.750	0.381	0.203	0.056	0.331	0.522	0.204
PD	0.85800000	0.87855000	0.94850000	0.96040000	0.95690000	0.87745000	0.94460000
PE	0.45403932	0.49390020	0.65700908	0.73085064	0.70273600	0.50223640	0.65646563

Allele	D7S820	D16S539	CSF1PO	D19S433	vWA	D8S1179	TPOX	FGA
7	0.0075		0.0050					
8	0.0675	0.0050	0.0100			0.0050	0.4975	
9	0.0475	0.1125	0.0225			0.0075	0.0450	
10	0.2075	0.2400	0.2350	0.0050		0.0600	0.0425	
10.2				0.0025				
10.3	0.0050							
11	0.3075	0.2550	0.2625	0.0075		0.0400	0.2575	
11.2				0.0025				
12	0.2825	0.2550	0.4000	0.0625		0.1425	0.1525	
12.2				0.0150				
13	0.0675	0.1200	0.0600	0.2100	0.0050	0.3300	0.0050	
13.2				0.1600				
14	0.0075	0.0100	0.0025	0.2600	0.0800	0.2650		
14.2				0.0400				
15		0.0025	0.0025	0.1175	0.0775	0.1175		
15.2				0.0850				
16				0.0175	0.3675	0.0300		
16.2				0.0100				
17				0.0050	0.3100	0.0025		
18					0.1050			0.0025
19					0.0425			0.0975
20					0.0100			0.0500
21					0.0025			0.0850
22								0.1200
23								0.1175
24								0.1675
24.2								0.0050
25								0.1700
26								0.1450
27								0.0350
28								0.0025
>30								0.0025
Homozygosity test*	0.437	0.921	0.565	0.774	0.754	0.145	0.241	0.653
Exact test†	0.131	0.348	0.463	0.473	0.953	0.694	0.242	0.660
PD	0.90845000	0.91390000	0.86970000	0.95035000	0.89700000	0.91970000	0.82615000	0.96735000
PE	0.56031198	0.57576700	0.46487616	0.67634348	0.52640202	0.58221995	0.41414762	0.74300963

*χ^2_{idf} based on unbiased estimate with 2000 shufflings.
†Exact test based on 2000 shufflings.
PD, power of discrimination; PE, power of exclusion.

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References

1. Edwards A, Hammond HA, Jin L, Caskey CT, Chakraborty R. Genetic variation at five trimeric and tetrameric tandem repeat loci in four human population groups. Genomics 1992;12:241–53.
2. Chakraborty R, Smouse PE, Neel JV. Population amalgamation and genetic variation: observations on artificially agglomerated tribal populations of Central and South America. Am J Hum Genet 1988;43:709–25.
3. Chakraborty R, Fornage 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. Berlin: Birkhauser Verlag, 1991: 127–43.
4. Nei M, Roychoudjury AK. Sampling variances of heterozygosity and genetic distance. Genetics 1974;76:379–90.
5. Guo SW, Thompson EA. Performing the exact test of Hardy–Weinberg proportion for multiple alleles. Biometrics 1992;48:361–72.

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