

FOR THE RECORD

Luis J. Martínez-Gonzalez,¹ M.S.; Esther Martinez-Espin,¹ M.S.; Francisco Fernandez-Rosado,¹ M.S.; Mayra A. Moguel,² M.S.; Carmen Entrala,¹ Ph.D.; J. Carlos Alvarez,¹ Ph.D.; Jose A. Lorente,¹ M.D., Ph.D.; and Bruce Budowle,³ Ph.D.

Mexican Population Data on Fifteen STR Loci (Identifiler® Kit) in a Chihuahua (North Central Mexico) Sample

POPULATION: Chihuahua, Northern Mexico, Mexico

KEYWORDS: forensic science, DNA typing, population genetics, Mexico, Identifiler

Sample preparation—Blood samples were obtained by venipuncture from unrelated individuals ($n = 161$) living in the State of Chihuahua, North Central Mexico, and spotted on FTA paper (Whatman, Clifton, NJ).

PCR—Approximately 1 ng of DNA were used in each amplification. The samples were amplified using the AmpFISTR® Identifiler® kit (Applied Biosystems, Foster City, CA) and 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 shufflings experiments. An interclass correlation criterion (6) for two-locus associations was used for detecting disequilibrium between the STR loci. The program for this analysis was kindly provided by R. Chakraborty (University of Texas, School of Biomedical sciences, Houston Texas).

The distributions of the observed allele frequencies for the 15 STR loci are shown in Table 1. The most informative loci are D18S51 and FGA, and the least discriminating are TPOX and CSF1PO. The fifteen loci meet Hardy-Weinberg expectations. The combined power of discrimination is >0.99999999 , and the combined power of exclusion is 0.99999926. The complete data are

available either by accessing <http://www.gitad.org/poblaciones> or emailing the corresponding author.

Acknowledgment

This study was partially supported by the “Fundacion M. Botin”, Santander, Spain. We thank Applied Biosystems for kindly providing the Identifiler® kit.

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. [PubMed]
2. Chakraborty R, Smouse PE, Neel JV. Population amalgamation and genetic variation: observations on artificially agglomerated tribal populations of Central and South America. Amer J Hum Genet 1988;43:709–25. [PubMed]
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. [PubMed]
4. Nei M, Roychoudhury AK. Sampling variances of heterozygosity and genetic distance. Genetics 1974;76:379–90. [PubMed]
5. Guo SW, Thompson EA. Performing the exact test of Hardy Weinberg proportion for multiple alleles. Biometrics 1992;48:361–72. [PubMed]
6. Karlin S, Cameron EC, Williams PT. Sibling and parent-offspring, correlation estimation with variable family size. Proc Natl Acad Sci USA 1981;78:2664–8. [PubMed]

¹ Laboratory of Genetic Identification. Dept. de Medicina Legal. Facultad de Medicina. Universidad de Granada. E-18012 Granada, Spain.

² DNA Laboratory. D.G. Servicios Periciales. P.G.J. del Estado de Chihuahua. Chihuahua, Mexico.

³ FBI Laboratory Division. Quantico, VA 22135.

Additional information and reprint requests:
Prof. Dr. Jose A. Lorente
Department of Medicina Legal—University of Granada
Av. Madrid 11
E-18012 Granada
Spain

TABLE 1—*Observed allele frequencies for the fifteen Identifier® loci.*

Allele	D3S1358	TH01	D21S11	D18S51	D2S1338	D5S818	D13S317
2.2							
<5		0.00311					
5							
6		0.23913					
7		0.30435				0.05901	
8		0.06832				0.01553	0.06832
9		0.16460				0.04037	0.22981
9.3		0.21118					
10		0.00621		0.01863		0.05590	0.09627
>10		0.00311					
11				0.02174		0.40994	0.26398
<12	0.00621						
12	0.00311			0.13975		0.29814	0.18012
13	0.00621			0.14286		0.11180	0.09627
14	0.05280			0.13975		0.00621	0.06522
15	0.31677			0.16460			0.00311
16	0.26087			0.13665	0.03106		
17	0.16770			0.10248	0.16460		
18	0.14596			0.06522	0.04348		
19	0.04037			0.03727	0.23913		
20				0.01863	0.17391		
21				0.00621	0.02795		
22				0.00311	0.06211		
23				0.00311	0.14286		
24					0.05901		
25					0.04348		
25.2		0.00311					
26					0.01242		
27		0.01863					
28		0.09317					
29		0.20807					
30		0.29503					
30.2		0.02795					
31		0.05901					
31.1		0.00311					
31.2		0.13043					
32		0.00311					
32.2		0.09006					
32.3		0.00311					
33		0.00311					
33.2		0.04658					
34.2		0.00932					
34.3		0.00311					
35.2		0.00311					
Homozygosity test*	0.762	0.446	0.148	0.680	0.228	0.342	0.301
Exact test**	0.017	0.459	0.116	0.824	0.972	0.073	0.012
PD	0.91007291	0.90675514	0.94649126	0.96909841	0.95675321	0.85405656	0.93368311
PE	0.57058241	0.55668406	0.66976540	0.75147290	0.70663845	0.49866824	0.64004831
Allele	D7S820	D16S539	CSF1PO	D19S433	vWA	D8S1179	TPOX
2.2							
3.2							
5							
6						0.00311	
7	0.01863						
8	0.14596	0.03416	0.00311			0.00621	0.58385
9	0.06832	0.11180	0.02484			0.00932	0.06832
10	0.30124	0.20186	0.28261			0.07143	0.05280
11	0.27019	0.21739	0.29193	0.00621	0.00311	0.05901	0.22671
11.2				0.01242			
12	0.16460	0.27640	0.34783	0.03727		0.11801	0.06211
12.2				0.01242			
13	0.02484	0.13975	0.04348	0.22360		0.30124	0.00311
13.2				0.07764			
14	0.00621	0.01863	0.00621	0.31056	0.07143	0.29193	
14.2				0.02484			
15				0.16770	0.07453	0.11801	
15.2				0.06211			
16				0.02484	0.29503	0.02174	
16.2				0.03416			
17					0.30745	0.00311	0.00311

TABLE 1—Continued.

Allele	D7S820	D16S539	CSF1PO	D19S433	vWA	D8S1179	TPOX	FGA
17.2				0.00621				
18					0.16149			0.01242
19					0.07143			0.09006
20					0.01242			0.08385
21					0.00311			0.09938
22								0.10870
22.2								
23								0.17391
23.2								0.00311
24								0.15839
25								0.14596
26								0.09317
27								0.02484
28								0.00311
Homozygosity test*	0.800	0.916	0.157	0.845	0.382	0.428	0.239	0.377
Exact test**	0.523	0.448	0.672	0.072	0.057	0.648	0.705	0.268
PD	0.91709425	0.92789630	0.85112457	0.92889935	0.90289726	0.92805062	0.79086455	0.96801821
PE	0.57759331	0.60855433	0.45289261	0.63921864	0.57252133	0.59304848	0.36674141	0.75055161

PD = power of discrimination.

PE = power of exclusion.

* $\chi^2_{\text{df}}^{\text{obs}}$ based on unbiased estimate with 2000 shufflings.

** Exact test based on 2000 shufflings.