

## FOR THE RECORD

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# STR Data for the PowerPlex<sup>®</sup> 16 Loci in Buenos Aires Population (Argentina)

**KEYWORDS:** forensic science, DNA typing, population genetics, short tandem repeats, D3S1358, TH01, D21S11, D18S51, PENTA E, D5S818, D13S317, D7S820, D16S539, CSF1PO, PENTA D, vWA, D8S1179, TPOX, FGA, Argentina

DNA samples from 101 unrelated individuals were extracted by Chelex procedure (1) and then quantified using QuantiBlot<sup>®</sup> Human DNA Quantitation Kit according to the manufacturer's instructions (2). DNA samples (1 ng) were amplified and typed by PowerPlex<sup>®</sup> 16 System (3). The electrophoresis was carried out on the ABI PRISM<sup>®</sup> 377 DNA Sequencer using GeneScan<sup>®</sup> Genotyper<sup>®</sup> and PowerTyper<sup>TM</sup> 16 Macro software. Data were analyzed using a program provided by R. Chakraborty (University of Texas School of Biomedical Sciences, Houston, Texas). Interclass corre-

lations yielding  $p < 0.05$  for pairwise comparisons: TH01/D7S820, TH01/D8S1179, D18S51/D5S818, D18S51/D7S820, PentaE/PentaD, and D5S818/D16S539.

The complete data are available to any interested researcher by accessing <http://www.cnea.gov.ar/cac/radiobiologia/abidefinitivo.xls>

## References

- Walsh PS, Metzger DA, Higuchi R. Chelex 100 as a medium for simple extraction of DNA for PCR-based from forensic material. *Biotechniques* 1991;10:506–13.
- Perkin Elmer. QuantiBlot<sup>®</sup> Human DNA Quantitation Kit, Revised ed., May 1996.
- PowerPlex<sup>®</sup> 16 System, Technical Manual Part TMD012 Revised ed., March 2001.

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TABLE 1—Allele frequencies for STR data for the PowerPlex® 16 loci in Argentina population.

Allele	D3S1358	TH01	D21S11	D18S51	PENTA E	D5S818	D13S317
2.2					0.035		
5							
6		0.267					
7		0.312			0.109	0.064	
8		0.099			0.010		0.163
9		0.134			0.010	0.045	0.193
9.3		0.183					
10		0.005			0.064	0.035	0.045
11				0.020	0.099	0.455	0.193
12				0.119	0.218	0.267	0.218
13				0.084	0.084	0.129	0.104
14	0.094			0.149	0.069	0.005	0.084
15	0.312			0.173	0.114		
16	0.267			0.168	0.030		
17	0.163			0.114	0.050		
18	0.149			0.064	0.040		
19	0.010			0.050	0.015		
20	0.005			0.030	0.020		
21				0.025	0.015		
22				0.005	0.010		
23					0.005		
24							
25					0.005		
26			0.005				
27			0.010				
28			0.129				
29			0.158				
30			0.228				
30.2			0.030				
31			0.054				
31.2			0.183				
32			0.010				
32.2			0.158				
33.2			0.035				
Homozygosity test*	0.042	0.016	0.337	0.540	0.790	0.210	0.666
Exact test**	0.055	0.109	0.345	0.936	0.453	0.231	0.153
PD	0.89520635	0.90775414	0.94618175	0.96716008	0.97363004	0.87069895	0.93931967
PE	0.55995084	0.55237420	0.68473614	0.75145012	0.79136515	0.46643097	0.66091772

TABLE 1—*continued.*

Allele	D7S820	D16S539	CSF1PO	PENTA D	vWA	D8S1179	TPOX	FGA
2.2				0.005				
5								
6								
7	0.015						0.005	
8	0.109	0.030		0.010			0.490	
9	0.084	0.183	0.020	0.213		0.010	0.084	
9.3								
10	0.297	0.064	0.292	0.149		0.069	0.050	
11	0.233	0.267	0.252	0.134		0.074	0.292	
12	0.218	0.287	0.347	0.228		0.168	0.079	
13	0.040	0.149	0.079	0.178			0.272	
14	0.005	0.015	0.010	0.054	0.079		0.248	
15		0.005		0.025	0.114		0.139	
16				0.005	0.272		0.015	
17					0.267		0.005	
18					0.193			0.020
19					0.059			0.119
20					0.010			0.114
21					0.005			0.144
22								0.163
23								0.094
24								0.114
25								0.163
26								0.059
27								0.010
28								
29								
30								
30.2								
31								
31.2								
32								
32.2								
33.2								
Homozygosity test*	0.207	0.942	0.738	0.017	0.924	0.770	0.383	0.305
Exact test**	0.801	0.918	0.595	0.226	0.537	0.642	0.888	0.247
PD	0.92559553	0.91892952	0.86756200	0.94363298	0.92010587	0.92912460	0.83070287	0.95951377
PE	0.58935836	0.58076682	0.47503097	0.65438853	0.59747357	0.61972987	0.41436402	0.74182206

PD=power of discrimination.

PE=power of exclusion.

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

\*\* Exact test based on 2000 shufflings.