



## Allele distribution of 15 STRs in a population from Extremadura (Central-Western Spain)

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### Abstract

Here we present allele frequencies for 15 STRs determined in samples from unrelated individuals from Extremadura using the Profiler Plus™, COfiler™, SGM Plus™ and PowerPlex™ 16 multiplex systems. Detection was made by capillary electrophoresis with Applied Biosystems ABI 310 Prism. Some statistical parameters of forensic interest such as observed/expected heterozygosity, mean exclusion chance, discrimination power and minimum frequencies were determined. Pairwise comparison with an Andalusian population was performed using the Chi-square test for homogeneity. © 2003 Elsevier Science B.V. All rights reserved.

*Keywords:* STR; CODIS; Population data; Central-Western Spain

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### 1. Materials and methods

#### 1.1. Population

Blood samples were selected from unrelated individuals from casework and paternity cases, living in Extremadura, a Central-Western region of Spain.

#### 1.2. Extraction

Either with phenol–chloroform–isoamyl alcohol followed by purification–concentration with Microcon 100 (Millipore, Bedford, MA, USA) or with GFX genomic purification columns (Amersham-Pharmacia-Biotech Piscataway, NJ, USA).

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Table 1  
Allele frequencies in a Central-Western Spain population

Alleles	D3	VWA	FGA	D8	D21	D18	D5	D13	D7	TH01	TPOX	CSF	D16	D2	D19	Penta D	Penta E
5										0.0073							0.0385
6										0.2445	0.0046						
7									0.0424	0.1241		0.0045				0.0089	0.1346
8				0.0036			0.0043	0.1473	0.0932	0.1533	0.5278		0.0224				0.0096
9				0.0214			0.0435	0.0268	0.1271	0.1496	0.0926	0.0136	0.1418			0.1964	0.0288
9.1									0.0042								
9.3										0.3102							
10				0.0607		0.0073	0.0739	0.0714	0.3093	0.0146	0.0741	0.2773	0.0634			0.1161	0.1635
11				0.0857		0.0073	0.3870	0.2857	0.2119		0.2731	0.3455	0.3097			0.2054	0.0865
12	0.0035			0.1500		0.1496	0.3348	0.2902	0.1695		0.0278	0.2955	0.2948		0.1074	0.2054	0.1442
12.2									0.0424						0.0041		
13	0.0035			0.2500		0.1606	0.1609	0.1250				0.0545	0.1567		0.2975	0.1696	0.1250
13.2															0.0083		
14	0.1154	0.1224		0.2214		0.1679	0.0043	0.0491				0.0045	0.0075		0.3223	0.0982	0.0673
14.2															0.0248		
15	0.2308	0.1294		0.1679		0.1350		0.0045				0.0045	0.0037	0.0083	0.1198	0.0089	0.0481
15.2															0.0537		
16	0.2692	0.2622		0.0321		0.1168								0.0375	0.0372		0.0769
16.2															0.0207		
17	0.2063	0.2448	0.0036	0.0071		0.1131								0.2625	0.0041		0.0288
18	0.1643	0.1329	0.0107			0.0803								0.0750			0.0192

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19	0.0070	0.0769	0.0821	0.0401	0.1208	0.0192
20		0.0210	0.1429	0.0219	0.1208	0.0096
21		0.0105	0.1714		0.0250	
21.2			0.0036			
22			0.1607			
22.2			0.0036		0.0458	
23			0.1857		0.0958	
24			0.1107		0.1042	
24.2			0.0036			
25			0.0786		0.0958	
25.2				0.0072		
26			0.0321	0.0036	0.0083	
27			0.0036	0.0290		
28			0.0036	0.0870		
29				0.2500		
30				0.2609		
30.2				0.0254		
31			0.0036	0.0471		
31.2				0.1341		
32				0.0072		
32.2				0.0942		
33				0.0036		
33.2				0.0471		
34.2				0.0036		

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Table 2  
Statistical parameters of genetic and forensic interest

	D3	VWA	FGA	D8	D21	D18	D5	D13	D7	TH01	TPOX	CSF	D16	D2	D19	Penta D	Penta E
HWE- Fisher( $p$ )	0.916	0.505	0.428	0.157	0.909	0.668	0.714	0.417	0.196	0.005	0.123	0.214	0.319	0.980	0.834	0.403	0.279
HWE- CHI( $p$ )	0.880	0.653	0.827	0.125	0.623	0.787	0.643	0.273	0.012	0.061	0.017	0.130	0.419	0.939	0.841	0.540	0.527
Ho	0.804	0.818	0.871	0.864	0.797	0.891	0.678	0.768	0.788	0.672	0.556	0.718	0.754	0.883	0.777	0.786	0.923
He	0.794	0.818	0.867	0.828	0.832	0.874	0.708	0.792	0.806	0.785	0.635	0.717	0.771	0.866	0.800	0.832	0.903
EC	0.627	0.651	0.748	0.735	0.615	0.785	0.428	0.565	0.599	0.418	0.275	0.486	0.542	0.771	0.580	0.595	0.847
DP	0.920	0.936	0.959	0.937	0.948	0.962	0.870	0.923	0.928	0.918	0.815	0.852	0.907	0.965	0.918	0.936	0.962
$n$	143	143	140	140	138	137	115	112	118	137	108	110	134	120	121	56	52
Minimum frequency	0.0104	0.0104	0.0106	0.0106	0.0108	0.0109	0.0129	0.0133	0.0126	0.0109	0.0138	0.0135	0.0111	0.0124	0.0123	0.0264	0.0284

### 1.3. Quantitation

Quantiblot® (PE Applied BioSystems, Foster City, CA, USA).

### 1.4. PCR

According to manufacturers' protocols of commercially available kits: AmpF/STR Profiler Plus™, COfiler™ and SGM Plus™ (PE Applied Biosystems). PowerPlex™ 16 (Promega, Madison, WI, USA).

### 1.5. Typing

ABI PRISM™ 310 and sequenced ladders. Genescan® 2.1 and Genotyper® 2.0 softwares were used for the analysis of typing results.

### 1.6. Quality control

Proficiency testing of the GEP-ISFG working group.

### 1.7. Analysis of data

GDA version 1.0 (d16c) [1]. Exact tests with 2000 shufflings. Minimum frequencies were calculated as  $1 - \alpha^{1/2n}$  according to Budowle et al. [2]. Pairwise comparisons between loci were assessed by Fisher and  $\chi^2$  tests ( $p > 0.05$ ). Excel software was used for additional statistics.

## 2. Results and discussion

Allele frequencies for D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, TH01, TPOX, CSF1PO, D16S539, D2S1338, D19S433, Penta D and Penta E are shown in Table 1. Table 2 shows statistical parameters of genetic and forensic interest.

A rare variant allele, 9.1 in D7S820, already described in STRbase (<http://www.cstl.nist.gov/biotech/strbase>) and in a Hungarian population [3] was found. No differences among the different kits were observed in the typing results of the shared loci. Nevertheless, amplification efficiency with PowerPlex™ kit was occasionally lower than with the other kits.

## References

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