

## STR data (AmpF/STR Profiler Plus) from North Portugal

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### D3S1358

Genot.	Obs.	Expect.	Genot.	Obs.	Expect.	Genot.	Obs.	Expect.
12-12	0	0.000	17-12	0	0.194	19-14	0	0.617
13-12	0	0.003	17-13	1	0.387	19-15	4	1.738
13-13	0	0.001	17-14	19	14.907	19-16	1	1.450
14-12	0	0.103	17-15	40	42.009	19-17	1	1.162
14-13	1	0.206	17-16	40	35.040	19-18	0	0.953
14-14	6	3.907	17-17	11	13.939	19-19	0	0.020
15-12	1	0.290	18-12	0	0.159	20-12	0	0.003
15-13	0	0.579	18-13	0	0.318	20-13	0	0.005
15-14	20	22.308	18-14	13	12.234	20-14	0	0.206
15-15	34	31.290	18-15	38	34.477	20-15	1	0.579
16-12	0	0.242	18-16	31	28.757	20-16	0	0.483
16-13	0	0.483	18-17	22	23.037	20-17	0	0.387
16-14	12	18.607	18-18	7	9.374	20-18	1	0.318
16-15	45	52.439	19-12	0	0.008	20-19	0	0.016
16-16	26	21.749	19-13	0	0.016	20-20	0	0.001

Expected number of homozygotes: 80.28038

Observed number of homozygotes: 84

Expected number of heterozygotes: 294.7196

Observed number of heterozygotes: 291

Unbiased estimates of Hardy-Weinberg exact P-values by the Markov chain method.

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Markov chain parameters:

Dememorization: 6000

Batches: 300

Iterations per batch: 6000

Probability test: P-value= 0.508996 (S.E.: 0.008255)

### VWA

Genot.	Obs.	Expect.	Genot.	Obs.	Expect.	Genot.	Obs.	Expect.
13-13	0	0.000	18-17	43	40.328	21-14	0	0.206
14-13	0	0.103	18-18	16	17.240	21-15	1	0.256
14-14	6	4.488	19-13	0	0.068	21-16	0	0.506
15-13	0	0.128	19-14	6	5.984	21-17	0	0.469
15-14	9	11.245	19-15	7	7.411	21-18	1	0.403
15-15	4	6.900	19-16	15	14.687	21-19	0	0.136
16-13	0	0.253	19-17	15	13.599	21-20	0	0.016
16-14	24	22.284	19-18	11	11.695	21-21	0	0.001

16-15	25	27.601
16-16	31	27.222
17-13	1	0.234
17-14	20	20.633
17-15	29	25.557
17-16	47	50.645
17-17	21	23.329
18-13	0	0.202
18-14	17	17.744
18-15	26	21.979
18-16	42	43.555

19-19	2	1.938
20-13	0	0.008
20-14	0	0.722
20-15	3	0.894
20-16	1	1.773
20-17	3	1.641
20-18	0	1.411
20-19	0	0.476
20-20	0	0.025
21-13	0	0.002

22-13	0	0.001
22-14	0	0.103
22-15	1	0.128
22-16	0	0.253
22-17	0	0.234
22-18	0	0.202
22-19	0	0.068
22-20	0	0.008
22-21	0	0.002
22-22	0	0.000

Expected number of homozygotes: 81.14303

Observed number of homozygotes: 80

Expected number of heterozygotes: 345.857

Observed number of heterozygotes: 347

Unbiased estimates of Hardy-Weinberg exact P-values by the Markov chain method.

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 Markov chain parameters:

Dememorization: 6000

Batches: 300

Iterations per batch: 6000

Probability test: P-value= 0.897011 (S.E.: 0.005296)

### FGA

Genot.	Obs.	Expect.
17-17	0	0.000
18-17	0	0.017
18-18	0	0.100
19-17	0	0.059
19-18	0	0.766
19-19	1	1.325
20-17	0	0.123
20-18	1	1.598
20-19	7	5.654
20-20	5	5.839
20.2-17	0	0.000
20.2-18	0	0.000
20.2-19	0	0.000
20.2-20	0	0.000
20.2-20.2	0	0.000
21-17	0	0.191
21-18	3	2.480
21-19	8	8.776
21-20	23	18.315
21-20.2	0	0.000
21-21	10	14.118

Genot.	Obs.	Expect.
23.2-22	1	0.507
23.2-22.2	0	0.035
23.2-23	0	0.519
23.2-23.2	0	0.004
24-17	0	0.142
24-18	1	1.848
24-19	7	6.538
24-20	13	13.644
24-20.2	0	0.000
24-21	25	21.177
24-22	15	18.761
24-22.2	0	1.279
24-23	20	19.187
24-23.2	0	0.426
24-24	9	7.817
24.2-17	0	0.001
24.2-18	0	0.017
24.2-19	0	0.059
24.2-20	0	0.123
24.2-20.2	0	0.000
24.2-21	0	0.191

Genot.	Obs.	Expect.
26-24.2	0	0.035
26-25	3	1.729
26-26	0	0.449
27-17	0	0.006
27-18	0	0.083
27-19	1	0.294
27-20	1	0.615
27-20.2	0	0.000
27-21	0	0.954
27-22	0	0.845
27-22.2	0	0.058
27-23	0	0.864
27-23.2	0	0.019
27-24	1	0.711
27-24.2	0	0.006
27-25	0	0.320
27-26	2	0.173
27-27	0	0.013
28-17	0	0.003
28-18	0	0.033
28-19	0	0.118

22-17	0	0.169	24.2-22	1	0.169	28-20	0	0.246
22-18	2	2.197	24.2-22.2	0	0.012	28-20.2	0	0.000
22-19	5	7.775	24.2-23	0	0.173	28-21	0	0.382
22-20	16	16.225	24.2-23.2	0	0.004	28-22	1	0.338
22-20.2	0	0.000	24.2-24	0	0.142	28-22.2	0	0.023
22-21	23	25.183	24.2-24.2	0	0.000	28-23	0	0.346
22-22	16	11.070	25-17	0	0.064	28-23.2	0	0.008
22.2-17	0	0.012	25-18	0	0.832	28-24	1	0.284
22.2-18	1	0.150	25-19	2	2.945	28-24.2	0	0.003
22.2-19	1	0.530	25-20	6	6.146	28-25	0	0.128
22.2-20	0	1.106	25-20.2	0	0.000	28-26	0	0.069
22.2-20.2	0	0.000	25-21	10	9.539	28-27	0	0.013
22.2-21	2	1.717	25-22	9	8.451	28-28	0	0.001
22.2-22	1	1.521	25-22.2	2	0.576	29-17	0	0.003
22.2-22.2	0	0.046	25-23	7	8.643	29-18	0	0.033
23-17	1	0.173	25-23.2	0	0.192	29-19	0	0.118
23-18	5	2.247	25-24	7	7.106	29-20	0	0.246
23-19	10	7.951	25-24.2	0	0.064	29-20.2	0	0.000
23-20	16	16.594	25-25	2	1.569	29-21	1	0.382
23-20.2	0	0.000	26-17	0	0.035	29-22	0	0.338
23-21	27	25.755	26-18	0	0.449	29-22.2	0	0.023
23-22	21	22.817	26-19	3	1.590	29-23	1	0.346
23-22.2	2	1.556	26-20	3	3.319	29-23.2	0	0.008
23-23	11	11.581	26-20.2	0	0.000	29-24	0	0.284
23.2-17	0	0.004	26-21	5	5.151	29-24.2	0	0.003
23.2-18	0	0.050	26-22	5	4.563	29-25	0	0.128
23.2-19	0	0.177	26-22.2	0	0.311	29-26	0	0.069
23.2-20	0	0.369	26-23	3	4.667	29-27	0	0.013
23.2-20.2	0	0.000	26-23.2	0	0.104	29-28	0	0.005
23.2-21	2	0.572	26-24	3	3.837	29-29	0	0.001

Expected number of homozygotes : 53.93342

Observed number of homozygotes : 54

Expected number of heterozygotes: 337.0667

Observed number of heterozygotes: 337

Unbiased estimates of Hardy-Weinberg exact P-values by the Markov chain method.

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Markov chain parameters:

Dememorization: 8000

Batches: 400

Iterations per batch: 8000

Probability test: P-value= 0.950417 (S.E.: 0.003340)

### D8S1179

Genot.	Obs.	Expect.
8-8	0	0.013
9-8	0	0.053

Genot.	Obs.	Expect.
13-12	32	29.570
13-13	34	33.945

Genot.	Obs.	Expect.
16-10	3	2.131
16-11	3	1.907

9-9	0	0.037
10-8	0	0.507
10-9	0	0.812
10-10	3	3.805
11-8	1	0.454
11-9	0	0.726
11-10	5	6.900
11-11	4	3.041
12-8	0	0.654
12-9	1	1.047
12-10	8	9.944
12-11	9	8.897
12-12	7	6.346
13-8	3	1.509
13-9	3	2.414
13-10	23	22.932
13-11	23	20.518

14-8	1	1.035
14-9	2	1.656
14-10	21	15.728
14-11	14	14.072
14-12	23	20.280
14-13	39	46.769
14-14	15	15.935
15-8	0	0.614
15-9	2	0.983
15-10	10	9.335
15-11	5	8.352
15-12	9	12.037
15-13	29	27.760
15-14	20	19.039
15-15	7	5.589
16-8	0	0.140
16-9	0	0.224

16-12	2	2.748
16-13	6	6.336
16-14	5	4.346
16-15	2	2.579
16-16	0	0.280
17-8	0	0.007
17-9	0	0.011
17-10	0	0.101
17-11	0	0.091
17-12	0	0.131
17-13	0	0.302
17-14	0	0.207
17-15	1	0.123
17-16	0	0.028
17-17	0	0.000

Expected number of homozygotes : 68.99199

Observed number of homozygotes : 70

Expected number of heterozygotes: 306.0081

Observed number of heterozygotes: 305

Unbiased estimates of Hardy-Weinberg exact P-values by the Markov chain method.

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Markov chain parameters:

Dememorization: 6000

Batches: 3000

Iterations per batch: 6000

Probability test: P-value= 0.993779 (S.E.: 0.000164)

<b>D21S11</b>
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Genot.	Obs.	Expect.
24.2-24.2	0	0.008
25-24.2	0	0.005
25-25	0	0.000
26-24.2	0	0.005
26-25	0	0.001
26-26	0	0.000
27-24.2	0	0.090
27-25	0	0.022
27-26	0	0.022
27-27	0	0.180
28-24.2	0	0.692
28-25	0	0.173
28-26	0	0.173
28-27	1	2.942
28-28	10	11.248

Genot.	Obs.	Expect.
31-26	0	0.071
31-27	1	1.213
31-28	13	9.345
31-29	7	10.343
31-29.2	0	0.071
31-29.3	0	0.143
31-30	15	12.911
31-30.2	1	1.783
31-31	2	1.890
31.2-24.2	0	0.460
31.2-25	0	0.115
31.2-26	1	0.115
31.2-27	4	1.954
31.2-28	10	15.055
31.2-29	17	16.664

Genot.	Obs.	Expect.
33-30.2	0	0.066
33-31	0	0.143
33-31.2	1	0.230
33-32	0	0.024
33-32.2	0	0.193
33-33	0	0.001
33.2-24.2	0	0.106
33.2-25	0	0.026
33.2-26	0	0.026
33.2-27	0	0.449
33.2-28	5	3.461
33.2-29	4	3.831
33.2-29.2	0	0.026
33.2-29.3	1	0.053
33.2-30	3	4.782

29-24.2	1	0.766	31.2-29.2	0	0.115	33.2-30.2	1	0.661
29-25	1	0.192	31.2-29.3	0	0.230	33.2-31	1	1.427
29-26	0	0.192	31.2-30	26	20.802	33.2-31.2	1	2.299
29-27	2	3.256	31.2-30.2	3	2.873	33.2-32	0	0.238
29-28	25	25.092	31.2-31	3	6.206	33.2-32.2	4	1.929
29-29	16	13.791	31.2-31.2	4	4.942	33.2-33	0	0.053
29.2-24.2	0	0.005	32-24.2	0	0.048	33.2-33.2	0	0.251
29.2-25	0	0.001	32-25	0	0.012	34.2-24.2	0	0.016
29.2-26	0	0.001	32-26	0	0.012	34.2-25	0	0.004
29.2-27	0	0.022	32-27	1	0.202	34.2-26	0	0.004
29.2-28	1	0.173	32-28	2	1.557	34.2-27	0	0.067
29.2-29	0	0.192	32-29	0	1.724	34.2-28	0	0.519
29.2-29.2	0	0.000	32-29.2	0	0.012	34.2-29	0	0.575
29.3-24.2	0	0.011	32-29.3	0	0.024	34.2-29.2	0	0.004
29.3-25	0	0.003	32-30	1	2.152	34.2-29.3	0	0.008
29.3-26	0	0.003	32-30.2	0	0.297	34.2-30	0	0.717
29.3-27	0	0.045	32-31	1	0.642	34.2-30.2	0	0.099
29.3-28	1	0.346	32-31.2	3	1.034	34.2-31	2	0.214
29.3-29	0	0.383	32-32	0	0.048	34.2-31.2	0	0.345
29.3-29.2	0	0.003	32.2-24.2	2	0.386	34.2-32	0	0.036
29.3-29.3	0	0.001	32.2-25	0	0.096	34.2-32.2	1	0.289
30-24.2	0	0.956	32.2-26	0	0.096	34.2-33	0	0.008
30-25	0	0.239	32.2-27	0	1.639	34.2-33.2	0	0.079
30-26	0	0.239	32.2-28	16	12.633	34.2-34.2	0	0.004
30-27	5	4.065	32.2-29	16	13.983	35-24.2	0	0.011
30-28	32	31.322	32.2-29.2	0	0.096	35-25	0	0.003
30-29	32	34.670	32.2-29.3	0	0.193	35-26	0	0.003
30-29.2	0	0.239	32.2-30	11	17.454	35-27	0	0.045
30-29.3	0	0.478	32.2-30.2	1	2.411	35-28	0	0.346
30-30	25	21.519	32.2-31	5	5.207	35-29	0	0.383
30.2-24.2	0	0.132	32.2-31.2	10	8.390	35-29.2	0	0.003
30.2-25	0	0.033	32.2-32	1	0.868	35-29.3	0	0.005
30.2-26	0	0.033	32.2-32.2	3	3.472	35-30	2	0.478
30.2-27	3	0.561	33-24.2	0	0.011	35-30.2	0	0.066
30.2-28	5	4.326	33-25	0	0.003	35-31	0	0.143
30.2-29	7	4.789	33-26	0	0.003	35-31.2	0	0.230
30.2-29.2	0	0.033	33-27	0	0.045	35-32	0	0.024
30.2-29.3	0	0.066	33-28	0	0.346	35-32.2	0	0.193
30.2-30	4	5.978	33-29	1	0.383	35-33	0	0.005
30.2-30.2	0	0.396	33-29.2	0	0.003	35-33.2	0	0.053
31-24.2	1	0.285	33-29.3	0	0.005	35-34.2	0	0.008
31-25	0	0.071	33-30	0	0.478	35-35	0	0.001

Expected number of homozygotes : 57.75298

Observed number of homozygotes : 60

Expected number of heterozygotes: 321.2472

Observed number of heterozygotes: 319

Unbiased estimates of Hardy-Weinberg exact P-values by the Markov chain method.

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Markov chain parameters:

Dememorization: 9000  
 Batches: 450  
 Iterations per batch: 9000

Probability test: P-value= 0.233866 (S.E.: 0.009840)

<b>D18S51</b>
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Genot.	Obs.	Expect.	Genot.	Obs.	Expect.	Genot.	Obs.	Expect.
10-10	0	0.124	17-17	5	3.796	21-14	1	1.335
11-10	0	0.077	18-10	2	0.996	21-15	0	1.094
11-11	0	0.008	18-11	0	0.285	21-16	1	1.313
12-10	2	1.839	18-12	15	6.829	21-17	2	0.821
12-11	0	0.525	18-13	2	6.829	21-18	0	0.569
12-12	6	6.238	18-14	5	8.679	21-19	1	0.263
13-10	2	1.839	18-15	11	7.114	21-20	0	0.197
13-11	0	0.525	18-16	7	8.536	21-21	0	0.038
13-12	17	12.607	18-17	6	5.335	22-10	0	0.038
13-13	10	6.238	18-18	1	1.814	22-11	0	0.011
14-10	1	2.337	19-10	0	0.460	22-12	0	0.263
14-11	1	0.668	19-11	0	0.131	22-13	0	0.263
14-12	10	16.022	19-12	2	3.152	22-14	1	0.334
14-13	17	16.022	19-13	3	3.152	22-15	0	0.274
14-14	7	10.097	19-14	5	4.005	22-16	0	0.328
15-10	4	1.915	19-15	2	3.283	22-17	1	0.205
15-11	0	0.547	19-16	3	3.940	22-18	0	0.142
15-12	12	13.133	19-17	1	2.462	22-19	0	0.066
15-13	10	13.133	19-18	2	1.707	22-20	0	0.049
15-14	24	16.689	19-19	1	0.378	22-21	0	0.022
15-15	4	6.772	20-10	0	0.345	22-22	0	0.001
16-10	2	2.298	20-11	1	0.098	23-10	0	0.019
16-11	2	0.657	20-12	2	2.364	23-11	0	0.005
16-12	15	15.759	20-13	2	2.364	23-12	0	0.131
16-13	10	15.759	20-14	2	3.004	23-13	0	0.131
16-14	29	20.027	20-15	1	2.462	23-14	0	0.167
16-15	19	16.416	20-16	5	2.955	23-15	0	0.137
16-16	7	9.767	20-17	1	1.847	23-16	0	0.164
17-10	1	1.436	20-18	0	1.280	23-17	0	0.103
17-11	0	0.410	20-19	2	0.591	23-18	0	0.071
17-12	8	9.850	20-20	1	0.209	23-19	1	0.033
17-13	11	9.850	21-10	0	0.153	23-20	0	0.025
17-14	12	12.517	21-11	0	0.044	23-21	0	0.011
17-15	9	10.260	21-12	1	1.051	23-22	0	0.003
17-16	13	12.312	21-13	2	1.051	23-23	0	0.000

Expected number of homozygotes : 45.48153  
 Observed number of homozygotes : 42  
 Expected number of heterozygotes: 320.5185  
 Observed number of heterozygotes: 324

Unbiased estimates of Hardy-Weinberg exact P-values by the Markov chain method.

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 Markov chain parameters:  
 Dememorization: 3000  
 Batches: 150  
 Iterations per batch: 3000

Probability test: P-value= 0.069267 (S.E.: 0.008285)

**D5S818**

Genot.	Obs.	Expect.
8-8	0	0.060
9-8	0	0.348
9-9	0	0.435
10-8	0	0.562
10-9	5	1.462
10-10	2	1.153
11-8	2	3.467
11-9	8	9.015
11-10	13	14.562
11-11	42	44.727

Genot.	Obs.	Expect.
12-8	7	3.748
12-9	9	9.746
12-10	13	15.743
12-11	112	97.082
12-12	48	52.289
13-8	1	1.633
13-9	3	4.246
13-10	7	6.859
13-11	37	42.300
13-12	40	45.730

Genot.	Obs.	Expect.
13-13	16	9.881
14-8	0	0.120
14-9	1	0.313
14-10	0	0.506
14-11	3	3.120
14-12	3	3.373
14-13	2	1.470
14-14	0	0.048

Expected number of homozygotes : 108.593  
 Observed number of homozygotes : 108  
 Expected number of heterozygotes: 265.407  
 Observed number of heterozygotes: 266

Unbiased estimates of Hardy-Weinberg exact P-values by the Markov chain method.

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 Markov chain parameters:  
 Dememorization: 6000  
 Batches: 300  
 Iterations per batch: 6000

Probability test: P-value= 0.239714 (S.E.: 0.004546)

**D13S317**

Genot.	Obs.	Expect.
8-8	6	6.662
9-8	5	6.326
9-9	0	1.455
10-8	3	5.384
10-9	2	2.530
10-10	3	1.050
11-8	35	33.513
11-9	13	15.751
11-10	13	13.405
11-11	40	41.556

Genot.	Obs.	Expect.
12-8	38	25.437
12-9	16	11.956
12-10	8	10.175
12-11	66	63.339
12-12	20	23.911
13-8	5	10.767
13-9	6	5.061
13-10	4	4.307
13-11	28	26.810
13-12	15	20.350

Genot.	Obs.	Expect.
13-13	8	4.253
14-8	2	5.249
14-9	5	2.467
14-10	4	2.100
14-11	14	13.070
14-12	6	9.921
14-13	6	4.199
14-14	1	0.997

Expected number of homozygotes : 79.88425

Observed number of homozygotes : 78  
 Expected number of heterozygotes: 292.1157  
 Observed number of heterozygotes: 294

Unbiased estimates of Hardy-Weinberg exact P-values by the Markov chain method.

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 Markov chain parameters:  
 Dememorization: 3000  
 Batches: 150  
 Iterations per batch: 3000

Probability test: P-value= 0.051602 (S.E.: 0.003674)

<b>D7S820</b>
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Genot.	Obs.	Expect.	Genot.	Obs.	Expect.	Genot.	Obs.	Expect.
6.3-6.3	0	0.000	10-8	23	26.820	12-9	19	21.641
7-6.3	0	0.022	10-9	24	29.915	12-10	39	35.073
7-7	1	0.165	10-10	29	24.112	12-11	29	28.170
8-6.3	0	0.143	11-6.3	0	0.207	12-12	13	12.593
8-7	2	2.283	11-7	2	3.314	13-6.3	1	0.025
8-8	6	7.347	11-8	24	21.542	13-7	0	0.395
9-6.3	0	0.159	11-9	20	24.027	13-8	6	2.568
9-7	3	2.546	11-10	39	38.941	13-9	2	2.864
9-8	22	16.549	11-11	17	15.535	13-10	2	4.642
9-9	13	9.150	12-6.3	0	0.187	13-11	3	3.728
10-6.3	0	0.258	12-7	4	2.985	13-12	4	3.358
10-7	3	4.126	12-8	15	19.402	13-13	0	0.210

Expected number of homozygotes : 69.11111  
 Observed number of homozygotes : 79  
 Expected number of heterozygotes: 295.8889  
 Observed number of heterozygotes: 286

Unbiased estimates of Hardy-Weinberg exact P-values by the Markov chain method.

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 Markov chain parameters:  
 Dememorization: 6000  
 Batches: 300  
 Iterations per batch: 6000

Probability test: P-value= 0.249529 (S.E.: 0.005630)