J Forensic Sci, March 2006, Vol. 51, No. 2
doi:10.1111/j.1556-4029.2006.00089.x
Available online at: www.blackwell-synergy.com

FOR THE RECORD

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Allele Frequency Data for 19 Short Tandem Repeats (PowerPlex® 16 and FFFl) in a Belgian Population Sample

POPULATION: Belgian Caucasians (Dutch speaking; $n = 198$).

KEYWORDS: forensic science, DNA typing, population genetics, D3S1338, vWA, D16S539, D8S1179, D21S11, D18S51, TH01, FGA, TPOX, CSF1PO, D5S818, D13S317, D7S820, Penta D, Penta E, F13A01, F13B, FESFPS, LPL

A short tandem repeat (STR) database for paternity investigations was created for a Belgian Caucasian population group. Whole blood samples on ethylene diamine tetraacetic acid from 198 individuals were collected by the Red Cross Bloodtransfusion Center of Leuven, and DNA was isolated as described by De Maesschalck et al. (1). The allele distribution for 19 STRs was determined with two polymerase chain reaction (PCR) amplifications on a GeneAmp 9700 PCR System (Applied Biosystems, Foster City, CA): the coamplification of the STRs D3S1338, vWA, D16S539, D8S1179, D21S11, D18S51, TH01, FGA, TPOX, CSF1PO, D5S818, D13S317, D7S820, Penta D, and Penta E with the PowerPlex® 16 System (Promega, Madison, WI), and the coamplification of the STRs F13A01, F13B, FESFPS, and LPL was carried out with the FFFl Fluorescent STR System (Promega). The manufacturer's recommendations concerning the amplification conditions were followed except for the total reaction volume, which was performed in 12.5 μL with 1 ng of DNA. After quality control of the PCR products (5 μL) on 6% PAGE gels, 1 μL of PCR product was analyzed on the ABI PRISM® 3100 Genetic Analyzer (Applied Biosystems) with a 37 cm capillary and using POP-6™ as separation medium (Decorte et al, in preparation). Fragment size determination was done with GeneScan v. 3.7 and ILS600 [CXR] as the internal size standard. Genotyper v. 3.7 was used for allele designation with respect to the allelic ladders included respectively in the PowerPlex® 16 System and FFFl Fluorescent STR System with the PowerTyper™ 16 Macro and a customized FFFl Macro. All alleles were designated according to the number of repeat units as recommended by the DNA commission of the International Society for Forensic Genetics (2).

The allele frequency distributions for the different STRs are summarized in Tables 1 and 2. Observed heterozygosity (H_o), expected heterozygosity (H_e), and Hardy–Weinberg equilibrium

TABLE 1—*Allele frequency data for the PowerPlex® 16 STR loci (n = 198).*

Allele	D3S1358	CSF1PO	D5S818	D7S820	D8S1179	D13S317	D16S539	D18S51	D21S11	FGA	TH01	vWA	TPOX	Penta D	Penta E
5	–	–	–	–	–	–	–	–	–	–	0.003	–	–	–	0.071
6	–	–	–	–	–	–	–	–	–	–	0.220	–	–	–	–
7	–	–	–	0.013	–	–	–	–	–	–	0.192	–	–	0.008	0.174
8	–	–	0.008	0.141	0.033	0.111	0.018	–	–	–	0.136	–	0.512	0.013	0.030
9	–	0.025	0.035	0.197	0.010	0.086	0.116	–	–	–	0.121	–	0.126	0.159	0.005
9.3	–	–	–	–	–	–	–	–	–	–	0.315	–	–	0.126	–
10	–	0.253	0.051	0.225	0.071	0.078	0.056	0.005	–	–	0.013	–	0.068	0.119	0.096
11	0.003	0.328	0.376	0.192	0.063	0.313	0.330	0.010	–	–	–	–	0.253	0.214	0.111
12	–	0.305	0.338	0.189	0.139	0.283	0.265	0.131	–	–	–	–	0.038	0.242	0.204
13	0.003	0.071	0.179	0.040	0.348	0.086	0.187	0.174	–	–	–	–	0.003	0.091	0.104
14	0.157	0.015	0.010	0.003	0.220	0.043	0.028	0.146	–	–	–	0.104	–	0.025	0.035
15	0.220	0.003	0.003	–	0.101	–	–	0.164	–	–	–	0.124	–	0.003	0.040
16	0.241	–	–	–	–	–	–	0.114	–	–	–	0.217	–	–	0.045
16.1	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.003
17	0.232	–	–	–	–	–	–	0.134	–	–	–	0.264	–	–	0.030

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TABLE 1—*Continued.*

Allele	D3S1358	CSF1PO	D5S818	D7S820	D8S1179	D13S317	D16S539	D18S51	D21S11	FGA	TH01	vWA	TPOX	Penta D	Penta E
18	0.126	–	–	–	–	–	–	0.043	–	0.018	–	0.197	–	–	0.025
19	0.015	–	–	–	–	–	–	0.040	–	0.066	–	0.078	–	–	0.013
19.2	–	–	–	–	–	–	–	–	–	0.008	–	0.013	–	–	–
20	0.003	–	–	–	–	–	–	0.015	–	0.131	–	–	–	–	0.008
20.2	–	–	–	–	–	–	–	–	–	0.003	–	0.003	–	–	–
21	–	–	–	–	–	–	–	0.013	–	0.171	–		–	–	0.003
22	–	–	–	–	–	–	–	0.005	–	0.169	–	–	–	–	0.003
22.2	–	–	–	–	–	–	–	–	–	0.018	–	–	–	–	–
23	–	–	–	–	–	–	–	0.003	–	0.173	–	–	–	–	–
23.2	–	–	–	–	–	–	–	–	–	0.005	–	–	–	–	–
24	–	–	–	–	–	–	–	0.003		0.121	–	–	–	–	–
24.2	–	–	–	–	–	–	–	–	0.005	0.003	–	–	–	–	–
25	–	–	–	–	–	–	–	–	–	0.081	–	–	–	–	–
26	–	–	–	–	–	–	–	–	0.005	0.033	–	–	–	–	–
27	–	–	–	–	–	–	–	–	0.033	–	–	–	–	–	–
28	–	–	–	–	–	–	–	–	0.154	–	–	–	–	–	–
28.2	–	–	–	–	–	–	–	–	0.003	–	–	–	–	–	–
29	–	–	–	–	–	–	–	–	0.184	–	–	–	–	–	–
29.2	–	–	–	–	–	–	–	–	0.005	–	–	–	–	–	–
30	–	–	–	–	–	–	–	–	0.262	–	–	–	–	–	–
30.2	–	–	–	–	–	–	–	–	0.045	–	–	–	–	–	–
31	–	–	–	–	–	–	–	–	0.083	–	–	–	–	–	–
31.2	–	–	–	–	–	–	–	–	0.114	–	–	–	–	–	–
32	–	–	–	–	–	–	–	–	0.005	–	–	–	–	–	–
32.2	–	–	–	–	–	–	–	–	0.066	–	–	–	–	–	–
33	–	–	–	–	–	–	–	–	0.003	–	–	–	–	–	–
33.2	–	–	–	–	–	–	–	–	0.030	–	–	–	–	–	–
34.2	–	–	–	–	–	–	–	–	0.003	–	–	–	–	–	–
PE	0.598	0.484	0.462	0.631	0.604	0.594	0.556	0.736	0.696	0.733	0.574	0.627	0.411	0.663	0.767
PD	0.929	0.878	0.864	0.940	0.930	0.925	0.911	0.969	0.959	0.968	0.919	0.938	0.831	0.950	0.976
H_o	0.838	0.758	0.687	0.747	0.793	0.793	0.773	0.869	0.838	0.888	0.848	0.838	0.626	0.803	0.859
H_e	0.800	0.731	0.710	0.818	0.792	0.789	0.770	0.871	0.847	0.869	0.784	0.813	0.653	0.833	0.885
p	0.341	0.733	0.263	0.018	0.944	0.983	0.297	0.363	0.703	0.612	0.078	0.781	0.426	0.770	0.148

PE, power of exclusion; PD, power of discrimination; H_o, heterozygosity observed; H_e, heterozygosity expected; p, Hardy–Weinberg equilibrium, exact test.

TABLE 2—*Allele frequency data for the FFFl STR loci (n = 198).*

Allele	LPL	FESFPS	F13B	F13A
3.2	–	–	–	0.071
4	–	–	–	0.028
5	–	–	0.003	0.184
6	–	–	0.071	0.313
7	–	–	0.003	0.355
8	–	0.008	0.255	0.003
9	0.045	–	0.212	–
10	0.385	0.305	0.456	–
10.3	–	0.003	–	–
11	0.295	0.416	–	0.005
12	0.237	0.230	–	0.003
13	0.030	0.038	–	–
14	0.008	–	–	0.010
15	–	–	–	0.018
16	–	–	–	0.010
PE	0.450	0.410	0.420	0.506
PD	0.859	0.836	0.841	0.887
H_o	0.667	0.737	0.697	0.712
H_e	0.708	0.680	0.678	0.737
p	0.195	0.011	0.139	0.603

PE, power of exclusion; PD, power of discrimination; H_o, heterozygosity observed; H_e, heterozygosity expected; p, Hardy–Weinberg equilibrium, exact test.

(exact test) were calculated with Genepop v. 3.3 software (3). No deviation from Hardy–Weinberg equilibrium was observed after Bonferroni correction for multiple testing (4). The power of discrimination according to Jones (5) and the power of exclusion according to Fisher (6) were calculated for each locus. The combined match probability was one in 1.759×10^{18}, while the combined power of exclusion was 0.999999931. The results of this population study should be useful for paternity investigations and human identification.

The complete data set (genotypes) is available to any interested party upon request to corresponding author Ronny Decorte at ronny.decorte@med.kuleuven.be.

Acknowledgments

We would like to thank Dr. M.-P. Emonds (Bloodtransfusion Centre of Leuven, Belgium) for providing the population sample. J.-J. Cassiman is a holder of the "Arthur Bax and Anna Vanluffelen chair of Human Genetics."

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