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FOR THE RECORD

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Population Genetic Analysis of Moroccans Residing in Belgium Using 15 STRs of the Identifiler® Kit

POPULATION: 205 unrelated Moroccan immigrants living in Belgium.

KEYWORDS: forensic science, population genetics, short tandem repeats, CSF1PO, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D21S11, vWA, FGA, TH01, TPOX, D2S1338, D19S433, Moroccan population, Belgium

As a consequence of immigration starting in the 1960s, some 155,000 people of Moroccan origin presently reside in Belgium, thus making up the largest fraction (55%) of the 283,000 non-European Union foreigners living in Belgium (total population 10.4 million in 2002) (1). The aim of this study was to establish a database of the Moroccan population of Belgium. We therefore applied the AmpFlSTR Identifiler PCR Amplification kit (Applied Biosystems, Foster City, CA) that co-amplifies the 13 Combined DNA Index System (CODIS) STR loci (CSF1PO, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D21S11, vWA, FGA, TH01, TPOX) and in addition the two tetrameric markers D2S1338 and D19S433, as well as the amelogenin locus for gender identification.

Buccal swabs were collected from 205 unrelated individuals of Moroccan origin living in Belgium, representing the mother (101 females) or alleged father (104 males) from paternity cases. DNA was extracted using the Qiamp DNA kit (Qiagen, Venlo, the Netherlands) (2). PCR amplification was performed following the instructions of the Identifiler kit using a PE 9700 thermal cycler. PCR products were subsequently analyzed by capillary electrophoresis on an ABI 3100 Genetic Analyzer (Applied Biosystems) (3). Alleles were named according to the recommendations of the DNA Commission of the International Society for Forensic Genetics (4). Allelic frequencies were estimated by direct gene counting. Conformity of the observed genotype frequencies with Hardy–Weinberg expectations (HWE) was examined by the exact

TABLE 1—*Allele frequencies for 15 STR loci in a sample (n = 205) of Moroccans residing in Belgium.*

Allele	TH01	CSF1PO	D16S539	D13S317	D7S820	vWA	D8S1179	D21S11	D3S1358	D2S1338	D19S433	TPOX	D18S51	D5S818	FGA
6	0.190											0.010			
7	0.200	0.019	0.005		0.019							0.019			
8	0.162	0.014	0.024	0.086	0.138		0.005					0.471		0.052	
9	0.281	0.024	0.157	0.024	0.100							0.176		0.029	
9.3	0.100														
10	0.067	0.252	0.086	0.038	0.290		0.110					0.090		0.081	
11		0.310	0.267	0.295	0.243		0.129		0.005		0.005	0.219		0.276	
12		0.329	0.229	0.348	0.186		0.124				0.105	0.014	0.133	0.376	
13		0.029	0.200	0.154	0.019	0.005	0.281				0.219		0.157	0.181	
13.2											0.024				
14		0.024	0.029	0.057		0.124	0.200		0.076		0.319		0.119	0.005	
14.2											0.062				
15			0.005		0.005	0.152	0.119		0.224		0.100		0.090		
15.2											0.081				
16						0.224	0.029		0.319	0.057	0.043		0.133		
16.2											0.010				
17						0.276	0.005		0.233	0.300	0.010		0.205		0.005

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TABLE 1—*Continued.*

Allele	TH01	CSF1PO	D16S539	D13S317	D7S820	vWA	D8S1179	D21S11	D3S1358	D2S1338	D19S433	TPOX	D18S51	D5S818	FGA
17.2											0.005				
18						0.138			0.129	0.086			0.076		
18.2											0.005				
19						0.057			0.010	0.157			0.052		0.038
20						0.014			0.005	0.152			0.014		0.167
21						0.010				0.033			0.010		0.148
21.2															0.005
22										0.052			0.005		0.171
22.2															0.010
23										0.043					0.176
24										0.086			0.005		0.110
24.2								0.005							
25										0.029					0.095
26										0.005					0.057
27								0.043							0.019
28								0.138							
29								0.229							
30								0.190							
30.2								0.019							
31								0.081							
31.2								0.100							
32.2								0.119							
33.2								0.057							
34.2								0.010							
35								0.005							
35.2								0.005							

TABLE 2—*Testing for HWE and statistical parameters of forensic interest.*

	STR locus														
Statistic	TH01	CSF1PO	vWA	D8S1179	D21S11	D7S820	D3S1358	D13S317	D16S539	D2S1338	D19S433	TPOX	D18S51	D5S818	FGA
H_{obs}	0.714	0.714	0.752	0.771	0.867	0.771	0.733	0.790	0.800	0.838	0.838	0.733	0.838	0.771	0.905
H_{exp}	0.811	0.734	0.818	0.826	0.860	0.796	0.775	0.763	0.807	0.843	0.824	0.698	0.871	0.743	0.869
P	0.280	0.772	0.013	0.203	0.051	0.748	0.629	0.421	0.653	0.445	0.445	0.260	0.912	0.834	0.318
MP	0.070	0.121	0.078	0.058	0.046	0.083	0.087	0.101	0.071	0.049	0.061	0.153	0.034	0.113	0.041
PIC	0.77	0.68	0.77	0.80	0.84	0.76	0.74	0.72	0.77	0.82	0.79	0.64	0.85	0.70	0.85
PEX	0.445	0.455	0.446	0.533	0.731	0.579	0.473	0.612	0.609	0.645	0.679	0.431	0.629	0.548	0.792
MPI	1.73	1.77	1.73	2.11	3.80	2.37	1.84	2.59	2.57	2.85	3.17	1.68	2.71	2.19	4.92

H_{obs}, observed heterozygosity; H_{exp}, expected heterozygosity; *p*-value for exact test for HWE; MP, matching probability; PIC, polymorphism information content; PEX, power of exclusion; MPI, mean paternity index.

test from Guo and Thompson (5) using the Arlequin software (6). The parameters relevant for forensic casework (matching probability, power of exclusion, mean paternity index and polymorphism information content) were determined using the Powerstat worksheet (Promega, Madison, WI) (7).

Allelic frequencies in this Moroccan population sample typed for the 15 Identifiler STRs are given in Table 1; results of testing for HWE and the statistical parameters of forensic interest are shown in Table 2. Regarding the test results for HWE, a *p*-value > 0.05 was obtained for all STRs except one. For vWA the exact test yielded a *p*-value of 0.013. To judge whether to reject the null hypothesis (population equilibrium) based on the magnitude of the smallest of multiple *p*-values, it is necessary to apply the Bonferroni (8) correction to the chosen significance threshold, which is typically 0.05. Considering the Bonferroni procedure and the fact that 15 tests for HWE were simultaneously performed on the same population sample, the significance threshold is adjusted from $\alpha = 0.05$ to $0.05/15 = 0.0033$, which is clearly below the *p*-value of 0.013 that was observed for vWA. Hence, this single *p*-value gives no reason to reject the null hypothesis.

Combined, the 15 STRs result in a Matching Probability of 1 in 144×10^{15} and a Power of Exclusion of 99.99984%, which should be effective in the resolution of most forensic and paternity cases.

The complete dataset is available upon request to the corresponding author, Gerhard Mertens, via e-mail: gerhard.mertens@uza.be.

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