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Analysis of 15 short tandem repeats reveals significant differences between the Arabian populations from Morocco and Syria

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Abstract

The short tandem repeat (STR) systems D3S1358, TH01, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, vWA, D8S1179, TPOX and FGA were studied in Arabian population samples from Morocco and Syria. No significant deviation from Hardy–Weinberg equilibrium could be observed in either preparation. Comparing the Moroccan and Syrian populations using the program R×C, no similarity could be observed at all 15 loci. In the Moroccan and Syrian populations the matching probability is 1 in 1.4×10^{17} and 1 in 2.6×10^{17} , respectively. Thus, the combination of these 15 STR loci is powerful tool for forensic identification in Arabian populations.

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1. Introduction

Short tandem repeat (STR) typing has become the state-of-the-art technique for forensic identification and paternity testing [1,2]. The aim of this work was to establish a STR database for the Arabian populations from Morocco and Syria, located at the very West and East of the Mediterranean Sea, respectively, and to check if they can be fused to a single Arabian database. Therefore, we have applied PowerPlex 16 System (Promega, Madison, WI) that amplifies the seven ENFSI STR loci as well as 13 CODIS STR loci in addition to the two pentanucleotide repeat loci, Penta E and Penta D, and the amelogenin locus for gender identification [3].

In this study we present the allele frequencies and forensic efficiency values for the 15 STR loci in the Moroccan and Syrian populations and compare them.

2. Materials and methods

The population samples examined have already been described elsewhere [4,5]. DNA from the blood or saliva samples was extracted by the proteinase K/chelex-100 method [6] and amplified according to the recommendations of the manufacturer for the PowerPlex 16 System (Promega) except for using 12.5 µl polymerase chain reaction (PCR) volumes in a GeneAmp 9600 (Applied Biosystems, Foster City, CA). PCR products were separated by capillary gel electrophoresis on an ABI PRISM 310 Genetic Analyzer with laser-induced fluorescence (LIF) detection. Evaluation of the Hardy–Weinberg equilibrium and

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Table 1

Allele frequencies and forensic efficiency parameters for 15 STR loci in a Moroccan population ($n = 138$)^a

Allele	D3S1358	TH01	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	vWA	D8S1179	TPOX	FGA
2.2											0.02				
5					0.032						0.004				
6		0.168			0						0			0.015	
7		0.193			0.143			0.004			0.012			0.019	
8		0.182			0.028	0.022	0.099	0.115	0.039	0.028	0.016		0.004	0.404	
9		0.336		0.008	0.032	0.033	0.047	0.133	0.098	0.02	0.159		0.007	0.135	
9.3		0.117		0	0	0	0	0	0	0	0		0	0	
10		0.004		0.004	0.103	0.069	0.044	0.311	0.051	0.276	0.134		0.067	0.077	
11				0.004	0.155	0.281	0.318	0.2	0.285	0.311	0.236		0.144	0.335	
12				0.146	0.179	0.372	0.339	0.204	0.313	0.339	0.122		0.104	0.015	
13				0.122	0.119	0.212	0.109	0.033	0.168	0.024	0.211	0.004	0.252		
14	0.073			0.138	0.02	0.011	0.044		0.047	0.004	0.077	0.134	0.244		
15	0.266			0.106	0.024						0.004	0.145	0.144		
16	0.255			0.159	0.04						0.004	0.236	0.03		
17	0.255			0.175	0.075							0.243	0.004		
18	0.131			0.061	0.032							0.159			
19	0.015			0.041	0.008							0.054			0.071
19.2	0			0	0							0			0.004
20	0.004			0.028	0.004							0.025			0.098
21				0.008	0.008										0.18
22															0.173
22.2															0.008
23															0.18
24															0.143
24.2			0.004												0
25			0												0.079
26			0												0.049
27			0.007												0.008
28			0.134												0.004
29			0.239												0.004
29.2			0.007												
30			0.228												
30.2			0.015												
31			0.063												
31.2			0.131												
32			0.007												
32.2			0.086												
33			0.004												
33.2			0.063												
35			0.011												

Table 1 (continued)

Allele	D3S1358	TH01	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	vWA	D8S1179	TPOX	FGA
<i>n</i>	137	137	134	123	126	137	137	135	128	127	123	138	135	130	133
H. obs	0.781	0.766	0.858	0.878	0.857	0.693	0.737	0.748	0.766	0.756	0.78	0.71	0.793	0.785	0.857
H. exp	0.779	0.778	0.843	0.875	0.89	0.734	0.759	0.793	0.78	0.714	0.838	0.821	0.822	0.703	0.864
HWE	0.304	0.111	0.496	0.215	0.638	0.414	0.109	0.441	0.903	0.692	0.233	0.002	0.144	0.499	0.848
PD	0.907	0.907	0.949	0.962	0.973	0.884	0.896	0.925	0.917	0.849	0.944	0.937	0.938	0.833	0.962
PE	0.564	0.538	0.711	0.751	0.709	0.418	0.488	0.507	0.537	0.52	0.563	0.444	0.585	0.571	0.709
PIC	0.74	0.74	0.82	0.86	0.88	0.69	0.72	0.76	0.74	0.66	0.81	0.79	0.79	0.65	0.85

^a H. obs, observed heterozygosity; H. exp, expected heterozygosity (unbiased); HWE, exact test probability performed by conventional Monte Carlo method; PD, power of discrimination; PE, power of exclusion; PIC, polymorphism information content.

Table 2

Allele frequencies and forensic efficiency parameters for 15 STR loci in a Syrian population ($n = 121$)^a

Allele	D3S1358	TH01	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	vWA	D8S1179	TPOX	FGA
2.2											0.004				
5					0.073						0.004				
6		0.267			0.004						0			0.004	
7		0.15			0.112		0.004	0.021			0.004			0.004	
8		0.154			0.017	0.013	0.147	0.13	0.027	0.004	0.017		0.008	0.45	
9		0.254			0	0.047	0.059	0.105	0.149	0.004	0.165		0.013	0.21	
9.3		0.133			0	0	0	0.004	0	0	0		0	0	
10		0.042		0.004	0.078	0.056	0.055	0.319	0.135	0.279	0.165		0.071	0.059	
11				0.022	0.138	0.333	0.332	0.273	0.23	0.274	0.152		0.058	0.248	
11.3				0	0	0	0	0	0	0	0		0.004	0	
12				0.159	0.185	0.316	0.252	0.13	0.279	0.381	0.178		0.125	0.025	
13	0.004			0.124	0.112	0.226	0.097	0.017	0.144	0.053	0.2	0.004	0.296		
14	0.025			0.208	0.034	0.009	0.055		0.032	0.004	0.074	0.087	0.2		
15	0.277			0.137	0.056				0.005		0.022	0.091	0.179		
16	0.277			0.124	0.03						0.013	0.269	0.042		
16.4	0			0	0.004							0	0		
17	0.231			0.084	0.047							0.331	0.004		
17.2	0			0.004	0							0			
18	0.164			0.071	0.047							0.161			0.013
19	0.021			0.035	0.026							0.037			0.071
20				0.013	0.026							0.021			0.05
21				0.009	0.009										0.172
21.2				0											0.021
22				0.004											0.139
22.2															0.017
23															0.172
24															0.239
24.2															0.004
25															0.08
26			0.004												0.013
27			0.022												0.008
28			0.088												
29			0.219												
29.2			0.004												
30			0.25												
30.2			0.066												
31			0.048												
31.2			0.083												
32.2			0.127												
33			0.018												
33.2			0.061												

Table 2 (continued)

Allele	D3S1358	TH01	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	vWA	D8S1179	TPOX	FGA
34			0.004												
35			0.004												
<i>n</i>	119	120	114	113	116	117	119	119	111	113	115	121	120	119	119
H. obs	0.731	0.825	0.754	0.858	0.897	0.709	0.723	0.756	0.775	0.673	0.774	0.835	0.817	0.664	0.815
H. exp	0.768	0.802	0.851	0.872	0.903	0.735	0.789	0.781	0.81	0.703	0.848	0.778	0.818	0.691	0.853
HWE	0.349	0.703	0.094	0.775	0.409	0.89	0.788	0.423	0.74	0.712	0.22	0.735	0.781	0.242	0.6
PD	0.902	0.924	0.953	0.963	0.974	0.885	0.928	0.92	0.934	0.854	0.951	0.909	0.938	0.852	0.957
PE	0.478	0.646	0.517	0.712	0.788	0.443	0.464	0.521	0.553	0.387	0.552	0.665	0.63	0.375	0.627
PIC	0.72	0.77	0.83	0.85	0.89	0.69	0.76	0.74	0.78	0.64	0.82	0.74	0.79	0.64	0.83

^a H. obs, observed heterozygosity; H. exp, expected heterozygosity (unbiased); HWE, exact test probability performed by conventional Monte Carlo method; PD, power of discrimination; PE, power of exclusion; PIC, polymorphism information content.

Table 3

Comparison between the Moroccan and Syrian populations^a

	D3S1358	TH01	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	vWA	D8S1179	TPOX	FGA
<i>P</i>	< 10 ⁻⁶	< 10 ⁻⁶	< 10 ⁻⁶	< 10 ⁻⁶	< 10 ⁻⁶	0.0225	< 10 ⁻⁶	< 10 ⁻⁶	< 10 ⁻⁶	< 10 ⁻⁶	< 10 ⁻⁶	< 10 ⁻⁶	< 10 ⁻⁶	< 10 ⁻⁶	< 10 ⁻⁶

^a Probability values were calculated with the program R × C (M.P. Miller, <http://bioweb.usu.edu/mpmbio>).

Table 4
Interpopulation comparison between Syria, Morocco and Egypt^a

	Moroccan-Egyptian	Syrian-Egyptian
D3S1358	0.00014	0.03338
D21S11	$< 10^{-6}$	$< 10^{-6}$
D18S51	$< 10^{-6}$	$< 10^{-6}$
D5S818	$< 10^{-6}$	$< 10^{-6}$
D13S317	$< 10^{-6}$	$< 10^{-6}$
D7S820	$< 10^{-6}$	0.00552
vWA	$< 10^{-6}$	$< 10^{-6}$
D8S1179	$< 10^{-6}$	$< 10^{-6}$
FGA	$< 10^{-6}$	$< 10^{-6}$

^a *P* values were calculated with the program $R \times C$. Egypt data from Ref. [7].

other forensic statistical parameters was done with the computer programs TFPGA (M.P. Miller) and PowerStats (Promega), respectively. The frequency profile comparisons between the Arabian populations were carried out using the program $R \times C$, that performed Fisher's Exact test on contingency tables through the use of Metropolis algorithm (M.P. Miller, <http://bioweb.usu.edu/mpmbio>).

3. Results and discussion

No deviation from Hardy–Weinberg equilibrium could be observed except for vWA in the Moroccan population (Tables 1 and 2). The most informative loci were D18S51, Penta E and FGA in both populations. The combined PD and PE values of all 15 loci in the Moroccan population were 0.99999999999999928 and 0.9999983, respectively, and those in the Syrian population were 0.99999999999999962 and 0.9999973, respectively.

The interpopulation comparisons between Morocco and Syria revealed significant differences in all 15 loci (Table 3). Thus, a common STR database for the two Arabian populations could not be established. Therefore, we have compared our data with the Egyptian

population [7], that is geographically located in between. Significant differences were observed at all nine loci that could be analyzed (Table 4).

According to the statistical parameters the combined analysis of these 15 STR loci is a powerful tool for forensic identification and paternity testing in the Arabian populations.

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