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Tunisian population allele frequencies for 15 PCR-based loci

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Abstract

Genotype and allele frequencies distribution for 15 PCR-based loci (D3S1358, THO1, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, VWA, D8S1179, TPOX and FGA) were determined for a Tunisian population sample. The examined population consists of a mixture of Arabic and Berber individuals coming from the three different regions of the country: North, Centre and South.

Keywords: Population genetics; STR-polymorphisms; Tunisian population

1. Introduction

Genotype and allele frequencies distribution for 15 PCR-based loci (D3S1358, THO1, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, VWA, D8S1179, TPOX and FGA) were determined for a Tunisian population sample of about 200 unrelated individuals. Conventional statistics and a between population comparison have been performed.

The present Tunisian population is relatively homogeneous and is constituted by Arabic- and Berber-speaking groups. The Berbers are considered as the oldest inhabitants in the country (since the Neolithic). Different Mediterranean people invaded the region: Phoenicians since 814 BC with the founding of Carthage, Romans since 146 BC. In 436 AC, the Vandals (German people) invaded the region until 533 with the arrival of the

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Table 1
Alleles frequency for 15 STR loci in a Tunisian population sample

Allele	Locus														
	D3S	THO1	D21	D18	Penta E	D5	D13	D7	D16	CSF1	Penta D	VWA	D8	TPOX	FGA
2.2											0.016				
5					0.028						0.003				
6		0.227												0.008	
7		0.258			0.129			0.010		0.010	0.011			0.008	
8		0.119			0.037	0.029	0.102	0.154	0.028	0.021	0.038		0.025	0.479	
9		0.216		0.006	0.014	0.043	0.043	0.121	0.121	0.010	0.168		0.008	0.139	
9.2														0.003	
9.3		0.149													
10		0.031		0.003	0.084	0.061	0.059	0.302	0.062	0.263	0.178		0.105	0.082	
10.2				0.006										0.005	
11				0.008	0.174	0.242	0.365	0.256	0.325	0.312	0.151		0.099	0.263	
12				0.136	0.211	0.413	0.298	0.136	0.294	0.130	0.135		0.085	0.013	
13	0.005			0.132	0.129	0.199	0.102	0.021	0.155	0.335	0.181		0.265		
13.2											0.005				
14	0.064			0.118	0.065	0.013	0.028		0.015	0.049	0.062	0.085	0.178		
15	0.273			0.205	0.025		0.003				0.038	0.147	0.186		
15.4					0.003										
16	0.286			0.109	0.017						0.011	0.263	0.036		
17	0.240			0.126	0.048						0.003	0.222	0.013		0.003
17.2				0.002											
18	0.117			0.059	0.011							0.201			0.005
19	0.015			0.056	0.014							0.054			0.044
19.2															0.003
20				0.021								0.028			0.113
21				0.013											0.165
22															0.173
22.2															0.005
23				0.006											0.191
23.2															0.003
24															0.159
24.2															0.005
24.3			0.005												
25															0.074
26			0.005												0.041
27			0.026												0.013
28			0.123												0.013
29			0.268												
29.2			0.002												
30			0.220												
30.2			0.016												
31			0.051												
31.2			0.074												
32			0.015												
32.2			0.102												
33.2			0.059												
34.2			0.013												
35			0.016												
36			0.005												

Table 1 (*continued*)

Allele	Locus														
	D3S	THO1	D21	D18	Penta E	D5	D13	D7	D16	CSF1	Penta D	VWA	D8	TPOX	FGA
ex/he	0.077	0.801	0.843	0.875	0.878	0.726	0.752	0.787	0.766	0.720	0.861	0.811	0.835	0.676	0.860
ob/he	0.745	0.770	0.826	0.829	0.882	0.755	0.796	0.759	0.733	0.696	0.816	0.821	0.847	0.598	0.819
DP	0.769	0.798	0.842	0.873	0.875	0.725	0.751	0.787	0.764	0.718	0.859	0.809	0.833	0.675	0.858

Byzantines. The Arabs came from the Middle East and invaded the region in the seventh, ninth and 10th centuries. In 1574, Tunisia was annexed to the Ottoman Empire. The present Tunisian population is derived from all these groups and is subdivided into two linguistic subtypes: the Arabic- (97%) and the Berber-speaking (3%) groups.

The examined population is constituted by Arabic-speaking people coming from the three different regions of the country: North, Centre and South.

2. Material and methods

2.1. Sample preparation

Blood samples from 200 unrelated individuals were deposited on FTA paper and directly amplified without quantification using the multiplex PowerPlex16 (Promega) kit instructions. Separation and detection of the alleles were carried out using capillary electrophoresis on an ABI 310 instrument.

2.2. Statistical analysis

The frequency of each allele for each locus tested was calculated from the number of observed genotypes in the sample (count method). The exact-test for within-locus (to detect deviation from Hardy–Weinberg equilibrium) and between loci testing (to detect linkage disequilibrium) was carried out according to the method of Zaykin et al. [1]. A $2 \times N$ contingency table test was used to generate a *G*-statistic with 2000 shuffling experiments to test for homogeneity between sample populations.

3. Results and discussion

The frequencies of the observed alleles are shown in Table 1.

Hardy–Weinberg equilibrium was studied by Fisher Exact test. The output indicates that CSF1PO, Penta D and TPOX loci show a significant departure from Hardy–Weinberg expectations in the examined sample population. Pairwise comparison D3S1358/D18S51, D21S11/VWA, D18S51/D5S818, D5S818/D16S539 and D16S539/CSF1PO yielded $p < 0.05$.

We also performed a pairwise comparison between the Tunisian populations and other populations coming from Egypt, Oman, Qatar, Saudi Arabia, United Arab Emirates, Yemen

and Turkey [2–7] using an $R \times C$ contingency test. No significant differences were encountered for all loci tested.

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