Genetic diversity of 15 autosomal STR loci in a Moroccan population

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Abstract- Allelic distribution of 15 STR loci (D3S1358, D5S818, D7S820, D13S317, vWA, FGA, TH01, TPOX, CSF1PO, D16S539, D8S1179, D21S11, D18S51, D19S433, and D2S1338) were analyzed in 80 unrelated Moroccan men from two regions using *AmpF/STR Identifiler* kit. The combined power of exclusion (PE) was 0.999993525 and the combined power of discrimination (PD) was >0.999999999. Comparisons with other published population data are also presented.

Index Terms: Allelic frequencies, STRs, Forensic parameters, Moroccan population, Arabic speakers.

I. Introduction

STRs markers have a high mutation rates, which make them the most widely polymorphic markers applied in Forensic DNA analyses and population genetic studies. In this study, we designed an analysis of 80 Moroccan men speaking Arabic language as first dialect, aiming to estimate the allelic frequencies and forensic parameters of 15 autosomal STRs, included in *AmpFlSTR Identifiler* kit (Applied Biosystems). Samples-Blood of individuals participating in this study were collected from two different regions: North-Central and West-Central Morocco. Pairwise comparisons were performed between the allelic distributions of the 15 STRs obtained for our population samples and other world population distributions.

II. Material and Methods

Population: 80 unrelated men from two different regions of Morocco, N=35 were from West-Central region (Doukkala) and N=45 from North-Central region (Jbala land). Informed consents were obtained from all participants. All them have ancestors born in the same region on at least three generations and their first spoken dialects belong to the Arabic language.
Extraction: DNA was extracted from peripheral blood using the organic Phenol-chloroform method.
PCR: Simultaneously amplification of a set of 15 autosomal STR loci (D19S433, FGA, TPOX, D18S51, D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D5S818, and vWA) was performed using *AmpFlSTR Identifiler* kit (Applied Biosystems) according to the manufacturer's instructions.
Typing: Separation of Multiplex PCR products was carried out on capillary electrophoresis *ABI PRISM 3130 Genetic Analyzer* (Applied Biosystems). Genotypic analysis was performed with Gene Mapper software Version 7.3 (Applied Biosystems).
Quality control: Laboratory internal controls and *AmpFSTR Identifiler* kit controls.
Analysis of genotypic data: we used Power Marker software version 3.25 and Genetix software version 4.05.2 [1] to calculate allelic frequencies, expected, and observed heterozygosities for the 15 STRs genotyped. Hardy–Weinberg equilibrium (HWE) was performed by Guo and Thompson's exact test [2], integrated in the Power Marker software version 3.25 [3]. Pairwise comparisons of the 15 loci available in the bibliography performed by an exact test of differentiation [4], included in the Arlequin Software Version 3.1 [5].

III. Results and Discussion

Distributions of the allelic frequencies for the 15 STR loci, at the global Moroccan sample (table 1), show only one significant deviation from the Hardy–Weinberg equilibrium at the CSF1PO locus (*P value = 0.0129*), which becomes no significant after the Bonferroni correction (*P value = 0.0119 > 0.0033*). Considered separately, our regional samples shows one deviation for the West-Central group at D21S11 locus (0.017) and no significant deviation for the North-Central group. Several Possible reasons could explain these observed deviations, like molecular properties of each locus that can be effectively neutral or under selection, population size, inbreeding or population substructure.

The power of discrimination (PD) varies between 0.8594 (CSF1PO) and 0.9575 (D18S51), the probability of exclusion (PE) varies between 0.3552 (TPOX) and 0.7196 (D2S1338).

The combined power of discrimination (PD) and the combined power of exclusion (PE) for the 15 studied loci were 0.999999999 and 0.999993525, respectively.

Table 1: Allelic frequencies and forensic parameters of 15 STRs loci (*AmpFLSTR Identifiler*) in a Moroccan population.

Allele	CSF1PO	D13S317	D16S539	D18S51	D19S433	D21S11	D2S1338	D3S1358	D5S818	D7S820	D8S1179	FGA	TH01	TPOX	vWA
6													0.1750	0.0250	
7	0.0063									0.0063			0.2313	0.0063	
8	0.0188	0.0688	0.0250						0.0500	0.1250			0.1125	0.3875	
9	0.0188	0.0813	0.0938						0.0438	0.1188			0.3750	0.1625	
9.3													0.0813		
10	0.3563	0.0250	0.0938						0.0438	0.3813	0.0688		0.0250	0.0938	
11	0.3000	0.3125	0.2313	0.0063	0.0125				0.2438	0.2063	0.1438			0.2938	
12	0.2250	0.3563	0.3125	0.1125	0.1000			0.0063	0.4188	0.1500	0.1438			0.0313	
12.2					0.0125										
13	0.0688	0.1375	0.2125	0.1188	0.2375				0.1625	0.0125	0.2188				
13.2					0.0250										
14	0.0063	0.0188	0.0313	0.1375	0.3438			0.1000	0.0313		0.2125				0.0813
14.2					0.0688										
15				0.1438	0.1250			0.2813	0.0063		0.1813				0.1813
15.2					0.0438										
16				0.1938	0.0250		0.0313	0.2688			0.0313				0.2750
16.2					0.0063										
17				0.1500			0.2750	0.1688							0.2500
18				0.0313			0.1188	0.1500				0.0125			0.1188
19				0.0375			0.1125	0.0250				0.0500			0.0750
20				0.0188			0.1375					0.1000			0.0063
21				0.0375			0.0813					0.1875			0.0125
22							0.0750					0.1813			
23							0.0750					0.2563			
24				0.0125			0.0563					0.0875			
25							0.0250					0.0688			
26							0.0063					0.0188			
27						0.0188	0.0063					0.0125			
28						0.0938						0.0125			
29						0.2000									
29.2						0.0063									
30						0.2625						0.0063			
30.2						0.0250									
31						0.0813						0.0063			
31.2						0.0875									
32						0.0125									
32.2						0.1813									
33.2						0.0188									
34.2						0.0063									
35						0.0063									
	CSF1PO	D13S317	D16S539	D18S51	D19S433	D21S11	D2S1338	D3S1358	D5S818	D7S820	D8S1179	FGA	TH01	TPOX	vWA
MP	0.1406	0.1066	0.0834	0.0425	0.0750	0.0588	0.0447	0.0888	0.1044	0.0941	0.0591	0.0528	0.1009	0.1191	0.0728
PD	0.8594	0.8934	0.9166	0.9575	0.9250	0.9413	0.9553	0.9113	0.8956	0.9059	0.9409	0.9472	0.8991	0.8809	0.9272
PIC	0.6792	0.7049	0.7527	0.8553	0.7656	0.8135	0.8418	0.7546	0.6944	0.7258	0.8035	0.8219	0.7193	0.6828	0.7745
PE	0.5098	0.3907	0.5535	0.6704	0.4886	0.6224	0.7196	0.6224	0.3727	0.4680	0.5761	0.6704	0.5314	0.3552	0.4886
TPI	2.0000	1.5385	2.2222	3.0769	1.9048	2.6667	3.6364	2.6667	1.4815	1.8182	2.3529	3.0769	2.1053	1.4286	1.9048
H_O	0.7500	0.6750	0.7750	0.8375	0.7375	0.8125	0.8625	0.8125	0.6625	0.7250	0.7875	0.8375	0.7625	0.6500	0.7375
H_E	0.7270	0.7442	0.7845	0.8693	0.7916	0.8336	0.8560	0.7870	0.7315	0.7597	0.8271	0.8405	0.7554	0.7267	0.8025
PHW	**0.0129**	0.2573	0.1766	0.1470	0.2260	0.2105	0.3631	0.4269	0.5958	0.4391	0.5131	0.3775	0.1092	0.3226	0.7432

H_O: Observed Heterozygosity; H_E: Expected Heterozygosity; PIC: Polymorphism Information Content; PD: Power of Discrimination; PE: Power of Exclusion; TPI Typical Pattern Index; PHW: P values of the exact test for Hardy–Weinberg equilibrium (significance level <0.05).

The pairwise comparisons (table 2) reveals no significant difference between our Moroccan population and two other North African populations (Egypt and Libya), and also with two Iberian populations (Portugal and Andalusia), except only one significant P value observed at TH01 with Portugal. The other comparisons resulted in one significant P value observed at TH01 locus with the Sudanese population, two significant differences with Iraq at D13S3317 and D16S539 loci and two other significant differences with Lebanon at D2S1338 and D5818 loci (both last populations are from Middle East).

Table 2: Population differentiation test between Moroccan and other published populations based on 15 STRs tested.

	Egypt [6]	Libya [7]	Sudan [8]	Iraq [9]	Lebanon [10]	Portugal [11]	Andalusia [12]
CSF1PO	0,5141	0,9240	0,5368	0,5491	0,5718	0,7399	0,8423
D2S11	0,6632	0,5593	0,0938	0,5212	0,1902	0,4741	0,2973
D2S1338	0,9950	0,8886	0,1325	0,5808	**0,0000**	0,5974	0,8025
D3S1358	0,9497	0,8147	0,1972	0,7361	0,9623	0,7449	0,8320
D8S1179	0,9695	0,9988	0,0836	0,7511	0,9991	0,5059	0,7399
D7S820	0,9497	0,8147	0,1972	0,7361	0,9623	0,7449	0,8320
D13S3317	0,4658	0,7731	0,9387	**0,0006**	0,2818	0,4961	0,0622
D16S539	0,6462	0,7432	0,0430	**0,0342**	0,1307	0,6645	0,6738
D18S51	0,7423	0,6457	0,2349	0,2646	0,3863	0,4990	0,1876
D19S433	0,7454	0,8675	0,6709	0,0878	0,4817	0,7132	0,6364
D5818	0,1633	0,4595	0,2343	0,0999	**0,0343**	0,2962	0,1112
FGA	0,7374	0,6488	0,2317	0,2885	0,3651	0,4932	0,1616
THO	0,9859	0,5855	**0,0007**	0,0571	0,1835	**0,0002**	0,0718
TPOX	0,2380	0,9666	0,0546	0,0707	0,2900	0,0709	0,2911
VWA	0,4841	0,7929	0,6863	0,0635	0,0804	0,2884	0,5389

IV. CONCLUSION

The autosomal STRs data and the values of indices calculated demonstrate that these markers represent a powerful and usefulness tool in forensic and paternity studies of Moroccan population. They also demonstrate their usefulness in other genetic population studies of the Moroccan population.

The comparison analysis performed with seven populations included in our database revealed that our Moroccan population is close to other North African ones and probably more genetically differentiated from Middle Eastern than other neighboring populations, with whom they had contact during their common history.

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