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Allele frequencies for STR loci in a Sicilian population: Genetic prevalence and disequilibrium

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Abstract. The aim of our work was to study the allelic frequencies and distribution within the 15 forensic STR loci in a group of 440 unrelated Sicilian subjects. Afterwards we have evaluated the genetic equilibrium among the most recurrent allele loci and have compared our data to those already published by other authors referring to different populations. © 2006 Published by Elsevier B.V.

Keywords: DNA STR typing; STR-DNA database

1. Materials and methods

1.1. PCR amplification, STR typing and allele frequencies evaluation

PCR amplification was performed using the AmpFLSTR® Identifiler™. Detection of alleles were performed using 310 AB PRISM Genetic Analyzer. The frequency of each allele for each locus was calculated from the numbers of each genotype obtained in the sample sets. Chi-square test and G-test were performed.

2. Results

Results are shown in Tables 1 and 2.

Reference

[1] M. Nei, Estimation of average heterozygosity and genetic distance from a small number of individuals, Genetics 89 (197) 583–590.

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Table 1
Partial result of allelic frequencies of the loci studied

Allele	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
5						0.1									
6						26.9						0.4			
7			3.3	0.1		14.3									
8	1.1		16.2	0.9		8.9	12.4	3.7			0.1	55.4		0.7	
9	2.0		12.2	2.3		25.4	10.1	16.7				12.4	0.2	5.1	
9.3						22.7									
10	8.5		25.3	28.5		1.7	6.0	8.5		0.2		7.5	0.8	8.6	
11	8.6		26.3	27.7			33.6	30.6		0.3	0.1	22.4	1.6	28.0	
12	10.7		14.5	32.9			26.1	24.6		11.7	0.1	1.8	15.5	36.4	0.1
12.2										1.1					
13	25.7		1.9	6.8	0.4		7.7	14.6	0.2	26.7		0.1	15.4	19.4	0.2
13.2										1.8			0.1		
14	21.4		0.3	0.6	6.6		3.9	1.3	0.1	27.6	7.8		17.9	1.6	
14.2										3.3					
14.7										0.2					
15	18.2			0.1	24.1		0.2		0.1	11.0	9.3		12.8	0.2	0.4
15.2										6.7					
16	3.6				25.5				7.0	5.2	21.9		12.9		
16.2										3.4			0.1		
17	0.2			0.1	27.7				23.1	0.4	32.9		8.6		
17.2										0.1					
18					13.8				9.7		17.9		8.2		0.9
18.2										0.3					
19					1.9				11.2		8.2		2.9		7.5
19.2															
20									16.1		1.7		1.9		10.3
20.2															
21									5.1				0.2		19.7
21.2															
22									2.3				0.1		16.5
22.2															0.9
23									10.8		0.1		0.8		14.3
23.2															
24									7.1						16.7
24.2															0.1
25									6.6						8.9

Table 2

Summary of heterozygosity statistics and Hardy-Weinberg tests

Locus	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
Observed heterozygosity	0.8364	0.8455	0.8092	0.7824	0.7368	0.7727	0.7767	0.7638	0.8825	0.7932	0.7909	0.6273	0.8644	0.7221	0.8670
Expected heterozygosity[a]	0.8283	0.8489	0.8038	0.7303	0.7772	0.7841	0.7832	0.7875	0.8702	0.8181	0.7903	0.6223	0.8719	0.7416	0.8615
Chi-square test[b]	0.886	0.908	0.129	0.000	0.073	0.131	0.189	0.039	0.269	0.103	0.708	0.849	0.043	0.540	0.464
Likelihood ratio test[b]	0.683	0.998	0.092	0.075	0.044	0.421	0.246	0.026	0.867	0.596	0.753	0.755	0.778	0.543	0.997

[a] Nei's (1973) expected heterozygosity [1].

[b] These values are probability values.