J Forensic Sci, May 2004, Vol. 49, No. 3
Paper ID JFS2003395
Published 7 April 2004
Available online at: www.astm.org

FOR THE RECORD

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Autosomic STR Loci (HUMTPOX, HUMTH01, HUMVWA, D18S535, D1S1656 and D12S391) in San Salvador (El Salvador, Central America)

POPULATION: This study involved the analysis of six STR in 120 male individuals from San Salvador which is the capital city of El Salvador (Central America). They represent a prominent population of the country: Mestizos who are descendents of Spanish and Amerindian people. The data can be used for forensic and paternity analyses where this population may be relevant.

KEYWORDS: forensic science, DNA typing, microsatellites, short tandem repeats, population genetics, San Salvador, Central America, Amerindian, Mestizos

Blood samples were taken from 120 healthy unrelated Mestizo individuals born and living in San Salvador (El Salvador, Central America). DNA was isolated from the samples using the standard phenol-chloroform extraction method. The loci HUMTPOX, HUMTH01, HUMVWA, D18S535, D1S1656 and D12S391 were amplified by PCR individually using previously described conditions (1,2). Detection of the amplified products was carried out using a monochromatic (Automatic Laser Fluorescent DNA sequencer, Pharmacia Biotech). The recommendations of the International Society for Forensic Genetic were followed for typing and interpretation (3). Statistical analyses were performed as described previously (see Ref 4 for details).

Table 1 summarizes the distributions of observed allele frequencies for the 6 autosomal STR loci in the population from San Salvador, the results of the different test procedures for testing the correspondence of the genotype frequencies with Hardy-Weinberg expectations and the forensic value of the analyzed systems expressed as various statistical parameters (see Table 1). In all cases, the data were shuffled 5000 times. These parameters reveal the high forensic efficiency of all the STR loci analyzed. Cumulative power of discrimination (cum PD) was 0.9999998 and cumulative mean exclusion chance (cum MEC) was 0.9958356.

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The complete dataset is available to any interested researcher upon request from the corresponding author.

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TABLE 1—*Allele frequencies of 6-STR loci in a Mestizo population sample from San Salvador.*

Allele *n* =	TH01 120	TPOX 120	vWA 120	D18S535 120	D1S1656 120	D12S391 120
5						
	0.0040					
6						
	0.4290	0.0130				
7						
	0.2670	0.0130				
8						
	0.0880	0.4570		0.0170		
9						
	0.0710	0.1000				
9.3		–		–		
	0.1250					
10						
	0.0130	0.0710		0.0000	0.0080	
11						
	0.0040	0.1830		0.0130	0.0000	
12						
		0.1500	0.0080	0.0420	0.0670	
13						
		0.0130	0.0040	0.1460	0.1540	
14						
			0.0790	0.4280	0.1000	
15						
			0.0880	0.2380	0.1210	0.0080
15.3						
			–	–	0.1000	–
16						
			0.3170	0.1080	0.0670	0.0380
17						
			0.2630	0.0080	0.1710	0.1170
17.3						
			–		0.1500	–
18					–	
			0.1500			0.2210
18.3					0.0540	
			–			–
19					–	
			0.0750			0.2540
19.3					0.0080	
			–			–
20						
			0.0040			0.1580
21						
			0.0130			0.1000
22						
						0.0420
23						
						0.0330
24						
						0.0040
25						
						0.0210
26						
						0.0040
P min	0.0220	0.0230	0.0230	0.0220	0.0240	0.0230
X^{2*}	0.4100	0.0590	0.4940	0.1190	0.7810	0.4920
G test*	0.1580	0.0150	0.5250	0.1240	0.8290	0.2950
Exact Test*	0.1430	0.0200	0.4450	0.9340	0.6560	0.1660
Obs H	0.6670	0.7420	0.7670	0.7080	0.8000	0.7750
MEC	0.4890	0.5060	0.5940	0.5020	0.7520	0.6710
PIC	0.6740	0.6850	0.7590	0.6860	0.8650	0.8130
PM	0.1180	0.1230	0.0780	0.1200	0.0300	0.0520
PD	0.8820	0.8770	0.9220	0.8800	0.9700	0.9480

* Tests for Hardy-Weinberg equilibrium. P min: minimum allele frequency, Obs H: observed heterozygosity, Mec: mean exclusion chance, MEP: mean exclusion probability, PIC: polymorphism information content, PM: probability of match, PD: power of discrimination.