International Congress Series 1261 (2004) 182–184

www.ics-elsevier.com

Huastecos Amerindian population (Mexico) characterised by 12 STR-PCR polymorphisms

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Abstract. The purpose of this study is to report allele frequency data of a Huastecos ethnic group population sample ($n = 89$) from La Huasteca (Hidalgo, Mexico) for 12 STR-PCR polymorphisms (HumTH01, HumvWA, D18S51, HumTPOX, D19S433, D16S539, D13S317, D8S1179, D7S820, D5S818, HumFGA and D21S11). No significant deviations from Hardy–Weinberg expectation were found for all short-tandem repeats (STR). From forensic point of view, the heterozygosity value, power of discrimination and the a priori chance exclusion value were calculated.

Keywords: Population genetics; Amerindian; STR polymorphisms; Huastecos

An Amerindian population study of 12 short-tandem repeat (STR) loci was performed on 89 unrelated Huastecos.

This ethnic group lives in ‘‘La Huasteca’’, a country northeast of Mexico. The Huasteco, or Nahualt, ethnic group is mainly concentrated in San Luis Potosí, near the Sierra Madre Oriental.

DNA was extracted from hair root samples by Chelex® method [1]. PCR were carried out in a 12-μl volume containing 0.5-ng DNA template. PCR amplifications were performed according to the recommendations for the AmpF*l*STR® Identifiler™ kit (Applied Biosystems). Genotypes from DNA amplified products were analysed in capillary gel electrophoresis using an ABI Prim™ 310 Genetic Analyzer automated laser sequencer [2].

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0531-5131/
doi:10.1016/S0531-5131(03)01497-3

Table 1
Allele frequencies distribution for D5S818, D13S317, D7S820, D16S539, HumTPOX and HumTH01 in the Nahualt population

	D5S818	D13S317	D7S820	D16S539	HumTPOX	HumTH01
6						0.4302
7	0.0787					0.4302
8		0.0225	0.0115	0.0063	0.5706	0.0058
9	0.1067	0.3764	0.0387	0.0823	0.0059	0.0058
9.3						0.1279
10	0.0337	0.1910	0.2701	0.2785	0.0353	
11	0.5843	0.1517	0.2989	0.2848	0.1765	
11.2						
12	0.1685	0.1404	0.3448	0.2785	0.2118	
12.2						
13	0.0281	0.0843	0.0402	0.0696		
13.2						
14		0.0337	0.0057			

Amplified DNA was mixed with internal fluorescent labelled size standard and external ladders were also used for adjustment.

Allele and genotype frequencies were determined. Unbiased estimates of expected heterozygosity were computed. A standard χ^2 goodness-of-fit was calculated to asses

Table 2
Allele frequencies distribution for HumvWA, D8S1179, HumFGA, D21S11, D18S51 and D19S433 in the Nahualt population

	HumvWA	D8S1179	HumFGA	D21S11	D18S51	D19S433
10		0.0674			0.0058	0.0057
11		0.0393				0.0115
11.2						0.0057
12		0.1742			0.0698	0.0172
12.2						0.0172
13		0.2584			0.0756	0.0862
13.2						0.1897
14		0.3483			0.2733	0.3046
14.2						0.0402
15	0.0337	0.1011			0.1686	0.1437
15.2						0.1322
16	0.5056	0.0112			0.0872	0.0287
16.2						0.0057
17	0.3258				0.1453	0.0057
17.2						0.0057
18	0.1011		0.0114		0.0523	
19	0.0281		0.1136		0.0523	
20	0.0056		0.0455		0.0174	
21			0.0966		0.0174	
22			0.0852		0.0291	
23			0.0568		0.0058	
23.2			0.0057			
24			0.1420			
25			0.2955			
26			0.0909	0.0056		
27			0.0511			
28			0.0057	0.0225		
29				0.1854		
29.2				0.0056		
30				0.3146		
30.2				0.0056		
31				0.1067		
31.2				0.1461		
32				0.0056		
32.2				0.1067		

Table 3
Stadistical parameters of forensic interest (*h*, heterozygosity value; PD, power discrimination; CE, chance of exclusion) and equilibrium Hardy–Weinberg (*p*)

Locus	*n*	p	*h*	PD	CE
D5S818	89	0.9064	0.607	0.809	0.299
D13S317	89	0.3039	0.236	0.908	0.534
D7S820	87	0.0800	0.264	0.851	0.486
D16S539	79	0.7540	0.316	0.901	0.403
HumvWA	89	0.8398	0.663	0.784	0.373
D8S1179	89	0.6692	0.764	0.912	0.534
HumTPOX	85	0.6417	0.632	0.777	0.331
HumFGA	88	0.9853	0.864	0.953	0.722
HumTH01	86	0.5612	0.605	0.763	0.296
D21S11	89	0.6209	0.775	0.937	0.554
D18S51	86	0.3253	0.756	0.951	0.520
D19S433	87	0.1583	0.799	0.942	0.586

Hardy–Weinberg expectations. From forensic point of view, the power discrimination, heterozygosity value and the "a priori" chance exclusion value were calculated.

The allele frequencies observed in each system in the Nahualt Amerindian population are shown in Tables 1 and 2. In Table 3, we were resumed the forensic parameters (*h*, heterozygosity index, CE chance exclusion and PD power discrimination) [3] and the equilibrium Hardy–Weinberg (p) [4].

The allele frequency data reported were preliminary results of a further study of Amerindian genetic map of Mesoamerica (or Central America).

We are thankful to the Huastecos population for its generous collaboration in the present study.

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