FOR THE RECORD

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Genetic Data Analysis of Nine STRs in Two Caribbean Colombian Populations: César and Guajira

POPULATION: We have analyzed the distribution of the allele frequencies and parameters of forensic interest at nine short tandem repeat (STR) loci (CSF1PO, D3S1358, D5S818, D7S820, D13S317, FGA, TH01, TPOX, and vWA) in a sample population of 165 unrelated individuals from César and Guajira, Caribbean populations of Colombia.

KEYWORDS: forensic science, DNA typing, population genetics, STR, CSF1PO, D3S1358, D5S818, D7S820, D13S317, FGA, TH01, TPOX, vWA, César, Guajira, Colombia

Blood samples from 165 unrelated individuals from César and Guajira (Colombia) were collected. DNA was extracted from 200 μL of peripheral blood by the salting-out procedure (1).

PCR amplification was performed according to the manufacturer's instructions (AmpF'STR Profiler PCR amplification kit, AB Applied Biosystems). PCR products were separated in an ABI 310 and reference sequenced ladders provided with the kit were used (AmpF'STR Profiler PCR amplification kit, AB Applied Biosystems). Correct allele calling was additionally assured by successful participation in the Proficiency testing of the GEP-ISFG Working Group (http://www.gep-isfg.org).

The frequency of each allele for each locus tested was calculated from the number of observed genotypes in the sample using GENEPOP software Ver. 3.2a (2). Expected and observed heterozygosity values and Hardy–Weinberg equilibrium test were carried out using the Arlequin Software version 2.000 (3). Bonferroni correction assumes that a 0.05 significance level used for nine tests (one per locus) yields an actual significance of 0.0056 (4). Statistical parameters for forensic and paternity testing, power of discrimination (PD) and a priori exclusion chance (CE), were calculated with Powerstats version 1.2 (Promega Corp.) (5). Complete data are available at the e-mail address of the corresponding author upon request (Table 1).

References

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TABLE 1—*Allele frequencies and statistical parameter for nine STR loci in César and Guajira populations (n = 165).*

Alleles	CSF1PO	D13S317	D5S818	D7S820	TH01	TPOX	vWA	FGA	D3S1358
5					0.0273				
6					0.3333	0.0212			
7	0.0091		0.0576	0.0242	0.2212	0.0212			
8	0.0394	0.0970	0.0303	0.1242	0.1242	0.4061			
9	0.0242	0.1242	0.0879	0.0879	0.1758	0.1273			
9.3					0.0909				
10	0.2818	0.0394	0.0758	0.2909	0.0273	0.0879			
11	0.2848	0.2455	0.3061	0.2818		0.2394			
12	0.2818	0.2909	0.3152	0.1667		0.0848	0.0030		
13	0.0636	0.1303	0.1212	0.0242		0.0121	0.0121		0.0061
14	0.0152	0.0667	0.0061				0.0455		0.1182
15		0.0061					0.1727		0.3212
16							0.3212		0.2970
17							0.2727	0.0030	0.1727
18							0.1212	0.0212	0.0788
19							0.0485	0.0667	0.0061
20							0.0030	0.1000	
21								0.1303	
22								0.1364	
23								0.1455	
24								0.1788	
25								0.1091	
26								0.0667	
27								0.0273	
28								0.0152	
Minimum	0.0175	0.0177	0.0170	0.0174	0.0176	0.0171	0.017	0.0191	0.0169
n	330	330	330	330	330	330	330	330	330
Parameters									
Ho	0.7879	0.8061	0.7515	0.7818	0.8000	0.7576	0.7697	0.8848	0.7394
He	0.7558	0.8097	0.7769	0.7862	0.7863	0.7479	0.7757	0.8818	0.7609
HWE-HE	0.7645	0.0394*	0.0057*	0.1746	0.0178*	0.4645	0.1177	0.0400*	0.2756
PD	0.8906	0.9251	0.9012	0.9176	0.9103	0.8909	0.9073	0.9673	0.8963
PE	0.5767	0.6103	0.5124	0.5657	0.5990	0.5228	0.5441	0.7646	0.4918
MP	0.1094	0.0749	0.0988	0.0824	0.0897	0.1091	0.0927	0.0327	0.1037
PIC	0.7120	0.7816	0.7427	0.7517	0.7532	0.7118	0.7392	0.8668	0.7198
TPI	2.3571	2.5781	2.0122	2.2917	2.5000	2.0625	2.1711	4.3421	1.9186

n, allele number; Ho, observed heterozygosity; He, expected heterozygosity; PD, power of discrimination; PE, power of exclusion; MP, matching probability; PIC, polymorphism information content; TPI, typical paternity index; P: Hardy–Weinberg equilibrium, exact test based on more than 2000 shufflings, for standard error <0.01. Bonferroni correction (0.05/9 = 0.0056).