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Genetic characterization of a population from Cauca Department with 15 STRs markers

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ABSTRACT

This study established allele frequencies and some parameters of forensic interest with 15 autosomal STRs markers in a sample of 172 unrelated individuals from the Department of Cauca – Colombia using the PowerPlex[®] 16 BIO System (Promega CO) and Qiagen Multiplex PCR (Qiagen) kits. All markers analyzed showed more than 61% of heterozygosity. Penta E and Penta D were the only systems that are not in Hardy Weinberg equilibrium ($p < 0.0033$) after Bonferroni correction. The probabilities of paternity (W), the power of exclusion (PE) and of discrimination (PD) accumulated for all loci analyzed were 0.9999, 0.9999 and >0.9999 , respectively. The parameters of forensic interest have values suitable for routine use in forensic genetics.

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1. Introduction

Genetic markers STR (short tandem repeat) are a widely used tool in forensic genetics and biological anthropology, with these is possible to establish the degree of structure, diversity and genetic differentiation of human populations [1]. However is evident the absence of genetic information for some regions of Colombia, so the aim of this study was to determine the genetic variability and establish a database with parameters of forensic interest for the Department of Cauca from a sample of unrelated individuals.

2. Materials and methods

Blood samples or buccal cells of 172 unrelated individuals from the Department of Cauca (87 men and 85 women) were taken. The DNA was isolated by salting-out [3] and Chelex 100[®] (Biorad) [4]. For PCR were used the 16 BIO[®] PowerPlex System (Promega CO) and Multiplex PCR (Qiagen) kits. The amplified products were separated by electrophoresis in 5% polyacrylamide gels and were

visualized with a FMBIO IIe Genetic Analyzer (HITACHI CO). The allelic assignment was performed using commercial allelic ladders. Allelic diversity and the Hardy–Weinberg equilibrium were performed using the software ARLEQUIN v3.5 [5]. The forensic parameters were calculated with the POWERSTAS software (Promega CO) v12. Bonferroni correction assumes that a 0.05 significance level used for fifteen tests (one per locus) yields an actual significance of 0.0033 [6]. The laboratory Genes Ltda, where this study took place, is accredited according to ISO/IEC 17025 and participates in the annual proficiency testing of the Spanish-Portuguese Speaking Working Group of International Society for Forensic Genetics (GHEP-ISFG).

3. Results

Table 1 shows the allelic frequencies and some parameters of forensic interest for a sample population of the Department of Cauca. Heterozygosity, assumed as a measure of population genetic variability, was higher than 61% for all loci. All systems were in Hardy–Weinberg equilibrium except Penta E and Penta D. The match probability for all systems analyzed was less than 22%. Furthermore, the cumulative probability of paternity was 0.9999, the power of discrimination and exclusion probabilities accumulated were 0.9999 and >0.9999 respectively.

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Table 1

Allele frequencies and parameters of forensic interest of 15 STR in a population sample of Cauca Department.

Allele	TH 01	TP OX	vWA	CSF 1PO	D7S 820	D5S 818	D8S 1179	D13S 317	D16S 539	D18S 51	D3S 1358	FGA	D21S 11	Penta E	Penta D
5														0.0482	
6	0.4390	0.0029													
7	0.2791	0.0029		0.0089	0.0060	0.0292		0.0029						0.0723	0.0169
8	0.0698	0.5727			0.0685	0.0058	0.0058	0.0643	0.0058					0.0151	0.0068
9	0.0581	0.0320		0.0179	0.0506	0.1053	0.0058	0.1637	0.2222						0.2601
9.3	0.1483														
10	0.0058	0.0233		0.3363	0.2798	0.0556	0.0407	0.0380	0.2251	0.0058				0.0211	0.3209
11		0.2471		0.2232	0.3006	0.4503	0.1076	0.1579	0.2515	0.0174				0.0422	0.1149
12		0.1047		0.3304	0.2143	0.2602	0.1570	0.2865	0.2193	0.0669				0.2078	0.0811
13		0.0145		0.0744	0.0714	0.0906	0.3517	0.1404	0.0643	0.0843	0.0220			0.0723	0.1520
14			0.0265	0.0089	0.0089	0.0029	0.2355	0.1404	0.0117	0.2122	0.0629			0.0753	0.0405
15			0.0824				0.0843	0.0058		0.1948	0.5031			0.1928	0.0068
16			0.4206				0.0116			0.1163	0.2610			0.0482	
17			0.2853							0.1860	0.0943	0.0057		0.0602	
18			0.1147							0.0610	0.0472	0.0230		0.0392	
19			0.0559							0.0291	0.0094	0.1092		0.0211	
20			0.0147							0.0087		0.0287		0.0512	
21										0.0087		0.0402		0.0211	
22										0.0058		0.1149		0.0090	
22.2												0.0115			
23										0.0029		0.1552		0.0030	
24												0.1552			
25												0.1552			
26												0.1264			
27												0.0345	0.0137		
28												0.0287	0.0890		
29												0.0057	0.1164		
30													0.3836		
30.2													0.0479		
31													0.0548		
31.2													0.1096		
32													0.0205		
32.2													0.0822		
33.2													0.0685		
34.2													0.0137		
45.2												0.0057			
MIN	0.0154	0.0150	0.0160	0.0164	0.0176	0.0160	0.0164	0.0171	0.0164	0.0178	0.0165	0.0341	0.0392	0.0181	0.0186
n	126	172	170	168	168	171	172	171	171	172	159	159	159	166	148
OH	0.6570	0.6163	0.7000	0.7262	0.8214	0.7076	0.7558	0.8070	0.7485	0.8547	0.6541	0.8621	0.8333	0.8374	0.7320
EH	0.7012	0.6000	0.7199	0.7241	0.7753	0.7083	0.7779	0.8235	0.7866	0.8547	0.6652	0.8865	0.8051	0.8904	0.7953
HW	0.3438	0.8201	0.6112	0.8882	0.4496	0.1715	0.8295	0.1479	0.1295	0.7415	0.1352	0.3768	0.8846	0.0030*	0.0021*
MP	0.1404	0.2114	0.1267	0.1268	0.0976	0.1372	0.0840	0.0603	0.0849	0.0408	0.1718	0.0353	0.0711	0.0298	0.0842
PD	0.8596	0.7886	0.8733	0.8732	0.9024	0.8628	0.9160	0.9397	0.9151	0.9592	0.8282	0.9647	0.9289	0.9702	0.9158
PIC	0.6524	0.5482	0.6762	0.6718	0.7379	0.6658	0.7445	0.7980	0.7491	0.8353	0.6184	0.8697	0.7693	0.8784	0.7539
PE	0.3649	0.3109	0.4283	0.4699	0.6394	0.4401	0.5198	0.6121	0.5073	0.7041	0.3609	0.7188	0.6667	0.6701	0.4757
IP	1.4576	1.3030	1.6667	1.8261	2.8000	1.7100	2.0476	2.5909	1.9884	3.4400	1.4455	3.6250	3.0417	3.0741	1.8500

MIN, minimum frequency; n, individuals; OH, observed heterozygosity; EH, expected heterozygosity; HW, Hardy–Weinberg; MP, match probability; PD, power of discrimination; PIC, polymorphic information content; PE, probability of exclusion; IP, paternity index.

* Significance value after Bonferroni correction ($p < 0.0033$).

4. Discussion and conclusions

The parameters of forensic interest, as PD, PE and probability of cumulative paternity are similar to previous reports in the literature for other populations of Colombia [2]. In conclusion, we have established a database for the Department of Cauca with 15 STR markers. The results indicate that all loci are useful to be employed in identification and paternity testing.

Conflict of interest

None.

References

- [1] J.M. Butler, C.R. Hill, Biology and genetics of new autosomal STR loci useful for forensic DNA analysis, *Forensic Science Review* 24 (2012) 15.
- [2] M.L.J. Bravo, J.J. Builes, M.M. de Pancorbo, et al., Analysis of 12 STR loci in Antioquia (Colombia) population sample, *International Congress Series* 1261 (2004) 151–153.
- [3] S.A. Miller, D.D. Dykes, H.F. Polesky, A simple salting out procedure for extracting DNA from human nucleated cells, *Nucleic Acids Research* 16 (3) (1988) 1215.
- [4] P.S. Walsh, D.A. Metzger, R. Higuchi, Chelex 100 as a medium for simple extraction of DNA for PCR-based typing from forensic material, *BioTechniques* 10 (1991) 506–513.
- [5] S. Schneider, D. Roessler, L. Excoffier, Arlequin ver. 2000: A Software for Population Genetics Data Analysis, Genetics and Biometrics Laboratory, University of Geneva, Switzerland, 2000.
- [6] B.S. Weir, Multiple tests, in: *Genetic Data Analysis II*, Sinauer Associates, USA, 1996 p. 134.