Population genetic data for 13 STR loci in a northeast Colombian (department of Santander) population

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Abstract

Before a new marker system can be introduced into forensic casework, a database for the relevant population must be established for statistical evaluation of the evidence. Therefore, this report presents allele frequency data in a northeast Colombian (department of Santander) population sample (n=103–399) for the loci TH01, TPOX, CSF1PO, D3S1358, FGA, VWA, D5S818, D13S317, D7S820, D8S1179, D21S11, D18S51 and D16S539. The combined power of exclusion is estimated as 99.9988% and the combined power of discrimination is >99.99999%. These 13 STR systems have been shown to be a useful tool for personal identification. The allele frequency data can be used for deriving estimates of multiple locus profile frequencies for identity testing purposes using the product rule.
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1. Materials and methods

Genomic DNA was extracted by the salting out extraction procedure. PCR amplification was performed according to the manufacturer's recommendations using AmpFlSTR Profiler Plus and Cofiler Amplification kits. Samples were denatured for 3 min at 95 °C and loaded onto an ABI 310 sequencer. Allele designations were made according to

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Table 1
Observed allele frequency for STR loci

	D3S1358 (N=399)	VWA (N=399)	FGA (N=399)	TH01 (N=395)	TPOX (N=395)	CSF1PO (N=395)	D5S818 (N=399)	D13S317 (N=399)	D7S820 (N=399)	D8S1179 (N=103)	D21S11 (N=103)	D18S51 (N=103)	D16S539 (N=132)
6				0.3873	0.0063								
7				0.2266		0.0013	0.0526		0.0075				
8				0.0544	0.4823	0.0063	0.0088	0.1040	0.0890	0.0049			0.0152
9				0.1354	0.0785	0.0215	0.0714	0.1617	0.0852	0.0049			0.1212
9.3				0.1861									
10				0.0101	0.0570	0.2253	0.0652	0.0689	0.3008	0.0534		0.0194	0.1553
11		0.0013			0.2873	0.2924	0.3496	0.2118	0.2757	0.0825		0.0146	0.2727
12					0.0823	0.3810	0.3170	0.2794	0.2080	0.1214		0.1165	0.2689
13	0.0050	0.0025			0.0063	0.0620	0.1228	0.1028	0.0251	0.3398		0.1117	0.1553
14	0.0777	0.0827				0.0089	0.0125		0.0702	0.2330		0.1699	0.0114
15	0.4048	0.0727				0.0013		0.0013	0.0013	0.1456		0.1311	
16	0.2644	0.3045								0.0146		0.1262	
17	0.1353	0.2970										0.1602	
18	0.1053	0.1742	0.0163									0.0631	
19	0.0075	0.0614	0.0614									0.0291	
20		0.0025	0.0890									0.0291	
21		0.0013	0.1165									0.0194	
22			0.1266									0.0097	
23			0.1353										
24			0.1729										

24.2			0.0025										
25			0.1441										
26			0.0940										
27			0.0363								0.0194		
28			0.0050								0.1019		
29											0.1602		
30											0.3398		
30.2											0.0291		
31											0.0680		
31.2											0.0922		
32											0.0291		
32.2											0.1117		
33											0.0049		
33.2											0.0340		
34.2											0.0049		
36											0.0049		
Minimum frequency	0.0072	0.0074	0.0079	0.0072	0.0069	0.0072	0.0073	0.0075	0.0075	0.0273	0.0282	0.0304	0.0221
χ^2 test	0.6205	0.3770	0.5660	0.4070	0.0330	0.5005	0.2120	0.2965	0.3460	0.3940	0.6760	0.1145	0.9715
Exact test	0.4910	0.2805	0.4620	0.4020	0.0970	0.4490	0.1630	0.3260	0.3675	0.5080	0.6910	0.0510	0.9305
H observed	0.7318	0.7694	0.8496	0.7139	0.6582	0.7190	0.7619	0.7870	0.7970	0.7864	0.8252	0.9029	0.8182
H expected	0.7317	0.7738	0.8804	0.7435	0.6694	0.7150	0.7508	0.8209	0.7753	0.7882	0.8236	0.8839	0.7930
MEC	0.4792	0.5436	0.6941	0.4501	0.3666	0.4582	0.5304	0.5751	0.5935	0.5741	0.6467	0.8014	0.6332
DP	0.8847	0.9122	0.9724	0.8956	0.8383	0.8681	0.9027	0.9441	0.9091	0.9192	0.9439	0.9614	0.9175

recommendations of the DNA Commission of the International Society for Forensic Genetics [1].

Statistical evaluations were performed using the computer program Genetic Data Analysis (GDA) as previously described [2]. Analyses included the possible divergence from Hardy–Weinberg expectations and other parameters of forensic importance: observed and expected heterozygosities, mean exclusion chance (MEC), discrimination power (DP) and the possible associations between loci.

2. Results and discussion

The observed allele frequencies and the results of the different test procedures for testing the correspondence of the genotype frequencies with their HWE proportions for the 13 STR loci are shown in Table 1. The genotype frequency distributions for most of the loci do not deviate from HWE expectations based on the χ^2 test and the exact test (in all cases, the data were shuffled 2000 times). Minimum allele frequencies for PCR-based loci, based on statistical and population genetics theory [3], were determined. Thus, a greater confidence of the DNA profile frequency estimates can be attained with current size databases. Table 1 shows several statistical parameters of forensic importance, such as expected and observed heterozygosities, mean exclusion chance (MEC) and discrimination power (DP). An interclass correlation test analysis demonstrated that there is no evidence for correlation between the alleles at any of the pairs of loci (data not shown).

In conclusion, a Colombian population database (department of Santander) has been established for the analysed systems. The combined power of exclusion is estimated as 99.9988% and the combined power of discrimination is >99.99999%.. The allele frequency data can be used for deriving estimates of multiple locus profile frequencies for identity testing purposes using the product rule.

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