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Genetic variation of 23 STR loci in a Northeast Colombian population (department of Santander)

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ABSTRACT

The most efficient markers to solve filiation cases are the STRs, including complex cases that require the analysis of a greater number of markers. In this study samples from 123 unrelated individuals from the department of Santander (northeast Colombia) were typed for 23 autosomal STRs included in VeriFiler express kit (Thermo Fisher Scientific),and their allele frequencies and parameters of forensic relevance were determined. Results demonstrate independence within and between the loci analyzed, and the accumulate power of exclusion for the full set of markers was high (99.9996%), as well as the match probability, which was 1 in 8.77E + 29. Therefore, this northeast Colombian population database can be used in forensic to estimate the frequency of the genetic profile using of a multiple locus including in this DNA kit.

1. Introduction

Colombia is a country divided into 32 departments, one of which is Santander located on the Northeast region of the country. There are many groups in the territory, with contributions from different continents, thus being considered a multi-ethnic country. The high diversity of the Colombian populations has been confirmed by the analysis of different type of genetic markers, namely autosomal STRs [1], X-chromosomal Indels [2], Y-chromosome specific STRs, among others [3].

Some of these markers are routinely usedin kinship cases, where it is necessary to perform a statistical evaluating of the genetic evidences. For this purpose, it is necessary to establish population allele frequencies in the concerned population.

The development of new technologies prompt the need to resolve complex cases, where there are no direct relatives, using an increasing number of markers. Therefore, kits are being developed for large marker sets, which need to be evaluated and frequencies must be calculated for the new additional markers.

Therefore, the 23 autosomal STRs included in the Verifiler Express kit were genotyped in a population sample from Santander, Colombia. Based on the observed allele frequencies, forensically relevant parameters were calculated for each marker and for the complete marker set.

2. Materials and methods

A total of 123 blood samples were collected from unrelated individuals born in different places of department of Santander, under informed consent signed by the participants. DNA was extracted with Chelex ® 100 (BioRad) as described by Walsh and col. [4].

These samples were genotyped for the 23 STRs included in the PCR Amplification multiplex VeriFiler Express kit (Thermo Fisher Scientific), namely D3S1358, vWA, D16S539, CSF1PO, TPOX, Y indel, Amelogenin, D8S1179, D21S11, D18S51, Penta E, D2S441, D19S433, TH01, FGA, D22S1045, D5S818, D13S317, D7S820, D6S1043, D10S1248, D1S1656, D12S391, D2S1338 and Penta D. Amplified products were separated and detected using an ABI 3500 sequencer, and alleles were assigned with the GeneMapper IDX v.1.5. Statistical analysis included Hardy-Weinberg tests [5] and calculation of parameters of forensic relevance: observed and expected heterozygosities, mean exclusion chance, discrimination power and possible associations between loci, using the software Familias [6].

3. Results and discussion

Allelic frequencies for each marker and the statistical parameters of forensic relevance are presented in Table 1. All markers showed to be in Hardy-Weinberg equilibrium (exact p-values ≥ 0.0716). The locus Penta E presented the highest power of discrimination (PD = 0.9810),

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Table 1
Allelic frequencies of 23 autosomal STR markers and statistical parameters of forensic relevance.

Alleles	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	PentaE	D2S441	D19S433	TH01
4										0,004		
5									0,028			
6					0,012				0,004			0,394
7					0,004				0,114			0,195
8			0,004	0,008	0,467	0,004			0,020			0,061
9			0,106	0,024	0,077	0,004			0,016			0,159
9,3					0,004							0,175
10			0,195	0,260	0,024	0,057		0,012	0,028	0,382		0,016
11			0,224	0,305	0,305	0,077		0,004	0,106	0,297	0,004	
11,2											0,012	
11,3										0,061		
12			0,309	0,341	0,106	0,138		0,093	0,134	0,041	0,081	
12,2											0,012	
13	0,008	0,004	0,146	0,057		0,337		0,138	0,073	0,012	0,252	
13,2			0,004								0,106	
14	0,081	0,069	0,012			0,260		0,171	0,098	0,187	0,240	
14,2								0,004			0,020	
15	0,358	0,110		0,004		0,106		0,142	0,081	0,016	0,183	
15,2											0,033	
16	0,297	0,390				0,016		0,138	0,081		0,045	
16,2											0,004	
17	0,142	0,256						0,175	0,037		0,008	
18	0,102	0,114						0,049	0,037			
19	0,012	0,057						0,028	0,024			
20								0,028	0,065			
21								0,008	0,037			
22									0,008			
23									0,008			
24								0,004				
27							0,028	0,004				
28							0,114					
29							0,199					
30							0,313					
30,2							0,033					
31							0,065					
31,2							0,073					
32							0,016					
32,2							0,110					
33,2							0,045					
34,2							0,004					
N	246	246	246	246	246	246	246	246	246	246	246	246
Ho	0,732	0,724	0,797	0,707	0,675	0,797	0,829	0,894	0,886	0,748	0,878	0,772
He	0,750	0,752	0,787	0,722	0,673	0,782	0,827	0,872	0,922	0,728	0,827	0,750
HWE p-value	0,626	0,531	0,854	0,488	0,072	0,977	0,855	0,539	0,096	0,495	0,154	0,115
PIC	0,707	0,714	0,751	0,667	0,619	0,748	0,804	0,855	0,913	0,680	0,801	0,710
PE	0,479	0,466	0,593	0,440	0,390	0,593	0,654	0,784	0,767	0,506	0,751	0,549
PD	0,900	0,904	0,916	0,864	0,824	0,921	0,923	0,961	0,981	0,871	0,932	0,891

Alleles	**FGA**	**D22S1045**	**D5S818**	**D13S317**		**D7S820**	**D6S1043**	**D10S1248**	**D1S1656**	**D12S391**	**D2S1338**	**PentaD**
2,2												0,008
3									0,004			
7			0,053			0,012						0,004
8			0,004	0,102		0,110		0,004				0,020
9			0,053	0,126		0,065						0,199
10		0,008	0,065	0,065		0,285	0,008		0,004			0,232
11		0,033	0,390	0,240		0,289	0,159		0,045			0,199
12		0,004	0,305	0,264		0,191	0,211	0,024	0,102	0,004		0,122
13		0,004	0,106	0,130		0,045	0,102	0,224	0,093	0,004		0,130
14		0,020	0,020	0,073		0,004	0,138	0,419	0,089			0,073
14,3									0,004			
15		0,427	0,004				0,016	0,240	0,159	0,041		0,012
15,3									0,045			
16		0,419					0,004	0,081	0,126	0,041	0,012	
16,3									0,053			
17	0,004	0,077					0,037	0,004	0,069	0,085	0,211	
17,3									0,150	0,008		
18	0,008	0,008					0,085		0,008	0,224	0,049	
18,3								0,004	0,041	0,004		
19	0,077						0,114		0,004	0,236	0,146	
19,3									0,004	0,016		
20	0,069						0,041			0,138	0,150	
20,3							0,008					
21	0,114						0,016			0,073	0,049	
21,2	0,004											
21,3							0,033					

(*continued on next page*)

Table 1 (*continued*)

Alleles	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	PentaE	D2S441	D19S433	TH01
22	0,110						0,024			0,057	0,114	
22,2	0,008											
23	0,110									0,037	0,110	
24	0,142						0,004			0,016	0,073	
25	0,195									0,012	0,077	
26	0,089									0,004	0,008	
27	0,045											
28	0,008											
30	0,012											
31	0,004											
N	246	246	246	246		246	246	246	246	246	246	246
Ho	0,862	0,667	0,715	0,894		0,837	0,902	0,667	0,829	0,829	0,902	0,764
He	0,887	0,637	0,736	0,823		0,784	0,879	0,713	0,900	0,857	0,874	0,833
HWE p-value	0,170	0,953	0,448	0,519		0,249	0,490	0,168	0,218	0,446	0,735	0,302
PIC	0,872	0,566	0,694	0,796		0,748	0,863	0,662	0,887	0,839	0,856	0,807
PE	0,718	0,379	0,453	0,784		0,670	0,800	0,379	0,654	0,654	0,800	0,534
PD	0,967	0,779	0,880	0,915		0,906	0,963	0,868	0,971	0,954	0,961	0,944

N (sample size); Ho (observed heterozygosity); He (expected heterozygosity); HWE p-value (Hardy–Weinberg equilibrium); PIC (polymorphic information content); PE (probability of paternity exclusion); PD (power of discrimination).

and D2S1338 and D6S1043 loci showed the highest power of exclusion (PE = 0.8004). The accumulate power of exclusion for the full set of 23 STR marker-set was high (99.9996%), as well as the match probability, which was 1 in 8.77E + 29.

4. Conclusion

The results obtained showed that all studied markers have high values of diversity in the population of Santander, and the VeriFiler Express kit seems to be a useful tool for forensic identification and complex kinship analysis in this region.

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Declaration of Competing Interest

None.

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