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Validation of five X-chromosomal STRs DXS6800, DXS6807, DXS6798, DXS8377 and DXS7423 in an Antioquian population sample

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Abstract. The X linked short tandem repeat (STR) markers have proven to be very useful tools for paternity testing when the disputed child is female. This paper aims to describe the polymorphism of five X-chromosomal STR loci (DXS6800, DXS6807, DXS6798, DXS8377 and DXS7423) in an Antioquian (Colombian) population sample, and evaluate their efficiency in forensic practice and paternity testing. The comparisons of the allele frequency distributions for Antioquian population are similar to European populations. The forensic efficiency values demonstrate that especially DXS8377 and DXS6798 are highly informative markers for kinship analysis and deficiency cases.

Keywords: X-chromosome; Antioquia; Colombia; DXS6800; DXS6807; DXS6798; DXS8377; DXS7423

1. Introduction

The advantage of non-autosomal testing is that males transmit an X-chromosome to all their daughters and a Y-chromosome to all of their sons, thus, father and daughters should share at least one allele at every X-linked locus. X-linked STRs are powerful auxiliary system to autosomal STR, for human identification, kinship and paternity testing [1,2] mainly in deficiency paternity cases when the disputed child is a female, in these cases,

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Table 1
Allelic frequencies and forensic interest parameters of DXS6798, DXS6807, DXS7423, DXS6800 and DXS8377 loci in 300 male Antioquian (Colombian) population

Allele	DXS6798	DXS6807	DXS7423	DXS6800	DXS8377
1					
2	0.003				
3					
4	0.013				
5	0.020				
6	0.033				
7	0.050				
8	0.060				
9	0.113				
9.2	0.003				
10	0.383				
11	0.213	0.437			
12	0.083	0.023			
13	0.017	0.137	0.030		
14	0.017	0.237	0.343		
15		0.147	0.397		
16		0.013	0.120	0.513	
17		0.007	0.110	0.013	
18				0.113	
19				0.263	
20				0.010	
21				0.077	
22				0.010	
40					0.007
41					0.010
42					0.027
43					0.057
44					0.087
45					0.100
46					0.163
47					0.080
48					0.123
49					0.073
50					0.100
51					0.087
52					0.047
53					0.020
54					0.020
MEC_1	0.7323	0.6300	0.6065	0.5299	0.8951
MEC_2	0.6282	0.5260	0.5007	0.4523	0.8193
PD_1	0.9522	0.9182	0.9092	0.8813	0.9908
PD_2	0.7802	0.7117	0.6973	0.6486	0.9043

MEC_1: mean exclusion chance in trios involving daughters.

MEC_2: mean exclusion chance in father/daughter duos lacking maternal genotype information.

PD_1: power of discrimination in females.

PD_2: power of discrimination in males.

investigations of X-chromosome markers may yield the desired information, which is even higher than that of autosomal markers with comparable polymorphism information content (PIC) values [3].

The aim of this study was to describe the polymorphism of five X-chromosome STR loci (DXS6800, DXS6807, DXS6798, DXS8377 and DXS7423) in Antioquian population (Colombian) and add those markers to the panel of paternity testing and forensically used markers.

2. Materials and methods

DNA samples were obtained from 300 unrelated healthy donors who were born in Antioquia (Colombia) and collected from the DNA bank from the paternity testing from Genes Ltda Laboratory.

The primer sequences of loci and cycling conditions were as recommended [4–6]. Thermal cycling was conducted using PTC 100 (MJ Research Inc). Alleles were identified based on the number of variable repeats and their attribution was made by comparison with an in-house constructed allelic ladder and following the published nomenclature and ISFG guidelines for STR analysis [7].

Power of discrimination in females (PD1) and males (PD2) and mean exclusion chance in trios involving daughters (MEC1) and in father/daughter duos lacking maternal genotype information (MEC2) were determined as proposed by Desmarais et al. [8].

3. Results and discussion

Table 1 shows the allele frequencies and parameters of interest for five STR loci DXS6807, DXS7423, DXS6798, DXS8377 and DXS6800 in an Antioquian population. 269 different haplotypes were found. Comparison of our allele frequencies with some few existing population data for these STRs resulted a significant difference with Corea and China Populations [9,10]. Allele frequency distribution of DXS6807 in Antioquia is similar to German population [11] and different from those from Corea [10] and China [9]. Allele frequency distribution of DXS7423 in Antioquia is similar to Spain population [12] and different from those from Germany [11], Corea [10] and China [9].

Power of discrimination (PD) in males and females and mean exclusion chance (MEC) for five X-linked STRs are shown in Table 1. DXS8377 has been proven to be the most informative marker for Antioquia population, with PD of 0.9908 and 0.9043 for males and females respectively and MEC of 0.8951 and 0.8153 in trios involving daughters and in father/daughter duos lacking maternal genotype information respectively.

Analysis of DXS6807, DXS7423, DXS6798, DXS8377 and DXS6800 loci in Antioquia population contribute to establish X-chromosome haplotyping procedure as a powerful tool in human identification, complicated kinship testing and paternity testing, specially in deficiency cases where alleged child is a female.

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