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Analysis of 16 Y-chromosomal STRs in a Córdoba (Colombia) population sample

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Abstract. We studied and established a database of 16 Y-STR (DYS19, DYS385, DYS389I/II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439, DYS460, DYS461, GATA-A10, GATA-H4 and DYS635) in a population sample of 123 unrelated males of Córdoba (Colombia) and some parameters of forensic importance were calculated. The haplotype diversity was 0.9987. This approach represents a very powerful tool for individual identification and paternity testing in forensic medicine. © 2006 Published by Elsevier B.V.

1. Introduction

The Y-chromosome non-recombinant portion represents a paternally inherited haploid transmission pattern [1]. Because Y-STRs can be employed to construct highly discriminative Y haplotypes, they are useful in stain analysis [2], paternity testing (lineage cases with male offspring) [1–3] and forensic genetics because of their male-specificity [4] and in the population genetic studies.

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Here we report gene frequencies, gene and haplotype diversity for 16 Y-STR loci in the Córdoba (Colombia) population. These will increase the database and the knowledge of polymorphisms on Colombian populations.

2. Materials and methods

Samples of 123 unrelated males were obtained from healthy individuals from Córdoba (Colombia). Genomic DNA was extracted by a salting-out [5]. DNA Amplification and detection of the amplicons were performed according to Builes et al. [6,7]. 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 recommendations on Y chromosome STR analysis [8]. The AMOVA, gene frequencies and gene/haplotype diversity values were calculated using the software ARLEQUIN version 2000 [9] and Nei formulation [10].

3. Results and discussion

Allele frequencies of the systems and gene diversity values are shown in Tables 1 and 2. The highest diversity value in this study was found at the locus DYS385 (0.9045), followed by the DYS389 II (0.7389). The haplotype diversity has the same value as the power of discrimination (PD) [11] and chance of exclusion (CE) [12]. The 16 STRs described in this study result in informative Y-haplotypes with CE and PD values of 0.9987.

Table 1
Gene frequencies and diversities of the Minimum Haplotype systems in Valle (*n* = 150) population

Allele	DYS19	DYS389I	DYS 389II	DYS 390	DYS 391	DYS 392	DYS 393	Allelic class	DYS 385	Allelic class	DYS 385
9					0.0406			10/14	0.0163	13/17	0.0325
10					0.5284			10/15	0.0081	13/19	0.0244
11		0.0162			0.4065	0.4227	0.0244	11/11	0.0244	14/14	0.0732
12	0.0081	0.2276			0.0244	0.0813	0.1545	11/12	0.0163	14/15	0.0325
13	0.1626	0.5447				0.3984	0.6504	11/13	0.0488	14/16	0.0488
14	0.5366	0.2114				0.0732	0.1382	11/14	0.2927	14/17	0.0244
15	0.1870					0.0244	0.0325	11/15	0.0163	15/15	0.0244
16	0.0732							11/18	0.0081	15/16	0.0163
17	0.0325							12/12	0.0081	15/17	0.0163
20				0.0081				12/14	0.0244	15/19	0.0325
21				0.0894				12/15	0.0081	16/17	0.0081
22				0.1219				12/17	0.0163	16/18	0.0081
23				0.2358				12/18	0.0163	17/17	0.0325
24				0.4227				13/14	0.0081	17/18	0.0325
25				0.1057				13/14.2	0.0081	17/19	0.0081
26				0.0081				13/15	0.0081	18/18	0.0163
27			0.0406	0.0081				13/16	0.0406		
28			0.1220								
29			0.3984								
30			0.2601								
31			0.1463								
32			0.0325								
NA	6	4	6	8	4	5	5		33		
GD	0.6490	0.6100	0.7389	0.7358	0.5565	0.6598	0.5354		0.9045		

NA: Allele number; GD: Gene diversity.

Table 2
Gene frequencies and diversities of the GEPY systems in Valle ($n = 150$) population

Allele	DYS635	DYS438	DYS437	DYS461	GATAH4	DYS439	GATAA10	DYS460
7		0.0081						
8		0.1219						
9		0.4065		0.0081				0.0244
10		0.1219		0.0163		0.0325		0.3577
11		0.3089		0.2114		0.3821	0.0081	0.5772
12		0.0325		0.5854		0.4309	0.0976	0.0406
13		0.0081		0.1545		0.1301	0.3090	
14			0.4959	0.0244		0.0244	0.5122	
15			0.3496				0.0650	
16			0.1301				0.0081	
17	0.0081		0.0163				0.0081	
18	0.0162		0.0081					
19	0.0732							
20	0.2601							
21	0.1463							
22	0.4146							
23	0.0732							
24	0.0081							
25	0.0081							
26					0.0081			
27					0.0163			
28					0.2114			
29					0.5854			
NA	9	7	5	6	4	5	7	4
GD	0.7376	0.7136	0.6182	0.5919	0.6528	0.6535	0.6363	0.5397

NA: Allele number; GD: Gene diversity.

By combining the allelic states of the 16 Y-chromosomal STR we could construct highly informative haplotypes that allowed the discrimination of 91.87% (113 out of 123) of the samples tested. The AMOVA results show that the percentage of variation is mainly within populations (99.95%) in agreement with previous results in European populations [13]. Thirty-six percent of this haplotypes do not match any sample in the Y-STR Haplotype Reference Database which assigned specific region characteristic to these population samples.

Development of Y-chromosome specific polymorphisms will be of great benefit in analyzing mixed DNA samples, in investigating sexual assaults as well as in paternity testing where the alleged father is not available but other patrilineal relatives are.

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