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

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Abstract. We studied and established a data base 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 of 173 unrelated males of Cartagena (Colombia) and some parameters of forensic importance were calculated. The haplotype diversity was 1.000 ± 0.0006. This approach represents a very powerful tool for individual identification and paternity testing in forensic medicine. © 2005 Published by Elsevier B.V.

Keywords: Cartagena; Y-chromosome; STR; Population; Colombia

1. Introduction

The Y-chromosome non-recombinant portion represents a paternally inherited haploid transmission pattern [1]. Because of that 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.

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

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Table 1
Gene frequencies and diversities of the 16 Y-chromosonal STR in Cartagena ($n=173$) population; NA: Allele number; GD: Gene diversity

Allele	DYS19	DYS389I	DYS 389II	DYS 390	DYS 391	DYS 392	DYS 393	Allelic class DYS 385				DYS635	DYS438	DYS437	DYS461	GATAH4	DYS439	GATAA10	DYS460
7													0.006						
9					0.029			10/14	0.040	13/18	0.006		0.110						0.052
10		0.012			0.520			11/11	0.017	13/19	0.006		0.249		0.017		0.017		0.295
11		0.012			0.416	0.416		11/12	0.006	14/14	0.017		0.162		0.185		0.064		0.509
12	0.006	0.185			0.035	0.040	0.168	11/13	0.040	14/15	0.012		0.468		0.555		0.312		0.139
13	0.104	0.613				0.474	0.671	11/14	0.306	14/16	0.012		0.006		0.225		0.491	0.052	0.006
14	0.526	0.173				0.069	0.116	11/15	0.046	14/17	0.017			0.422	0.006		0.110	0.295	
15	0.231	0.006					0.046	12/12	0.017	14/18	0.006			0.491	0.006			0.509	
16	0.104							12/13	0.023	15/15	0.029			0.081				0.139	
17	0.029							12/14	0.040	15/16	0.012	0.006		0.006				0.006	
18															0.006				
19												0.012							
20												0.046							
21				0.110				12/15	0.023	15/17	0.035	0.208							
22				0.075				12/16	0.012	15/18	0.035	0.121							
23				0.249				12/17	0.029	16/16	0.023	0.497							
24				0.497				13.2/15	0.006	16/17	0.035	0.092							
25				0.058				13/13	0.012	16/18	0.006	0.017							
26			0.012	0.006				13/14	0.017	16/19	0.006					0.006			
27			0.006	0.006				13/15	0.023	17/17	0.006					0.410			
28			0.127					13/16	0.029	18/18	0.006					0.532			
29			0.416					13/17	0.046							0.052			
30			0.329																
31			0.075																
32			0.035																
NA	6	6	7	7	4	4	4	35				8	6	4	7	4	6	5	5
GD	0.651	0.563	0.700	0.674	0.558	0.599	0.509	0.891				0.688	0.685	0.578	0.610	0.549	0.649	0.636	0.574

2. Materials and methods

Samples of 173 unrelated males were obtained from healthy individuals from Cartagena (Colombia). Genomic DNA was extracted by 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 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 Table 1. The highest diversity value in this study was found at the locus DYS385 (0.891), followed by the DYS635 (0.688). 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 1.0000.

By combining the allelic states of the 16 Y-chromosomal STR we could construct highly informative haplotypes that allowed the discrimination of 100% (173 out of 173) 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].

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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