

Analysis of 16 Y-chromosomal STRs in a Valle (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 150 unrelated males of Valle (Colombia) and some parameters of forensic importance were calculated. One hundred forty-six different haplotypes were found, 142 haplotypes of them were found to be unique and the others were shared by two persons. The haplotype diversity was 0.9996. The AMOVA results show that the percentage of variation is mainly within populations (99.95%) in agreement with previous results in European populations. By combining the allelic states of the 16 Y-chromosomal STRs, we could construct highly informative haplotypes that allowed the discrimination of 97.3% (146 out of 150) of the samples tested. This approach represents a very powerful tool for individual identification and paternity testing in forensic medicine. © 2006 Published by Elsevier B.V.

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

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

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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 Valle (Colombia) population. These will increase the database and the knowledge of polymorphisms on Colombian populations.

2. Materials and methods

Samples of 150 unrelated males were obtained from healthy individuals from Valle (Colombia). Genomic DNA was extracted by a salting-out [5]. The primer sequences of loci and cycling conditions to GEPY systems were as recommended [6–8] and described in [9] and to Minimum Haplotype systems were as recommended [10–12] and described in [13]. PCR products were separated by electrophoresis in denaturing polyacrylamide gels silver stained. Allele designation was performed according to ISFG recommendations on forensic analysis using Y-chromosome STRs [14] using an allelic ladder constructed in-house. The AMOVA, gene frequencies and gene/haplotype diversity values were calculated using the software ARLEQUIN version 2000 [15] and Nei formulation [16].

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 (0.842), followed by the DYS389 II (0.774). The haplotype diversity has the same value as the power of discrimination (PD) [17] and chance of exclusion (CE) [18]. The 16 STRs described in this study result in informative Y-haplotypes with CE and PD values of 0.9996.

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

Allele	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	Allelic class	DYS385	Allelic class	DYS385
8					0.0067			9/14	0.0067	14/14	0.0467
9					0.0333			10/14	0.0133	14/15	0.0333
10					0.5533			10.2/12	0.0067	14/17	0.0267
11					0.3933	0.3867	0.0067	11/13	0.0200	14/18	0.0133
12		0.1733			0.0133	0.0467	0.0933	11/14	0.3933	15/15	0.0067
13	0.1733	0.5933				0.4467	0.7333	11/15	0.0267	15/16	0.0267
14	0.4867	0.2200				0.0933	0.1067	12/12	0.0067	15/17	0.0200
15	0.2067	0.0133				0.0267	0.0600	12/13	0.0133	15/18	0.0200
15/16	0.0800							12/14	0.0200	15/19	0.0133
16	0.0067							12/15	0.0200	16/17	0.0467
17	0.0467							12/16	0.0067	16/18	0.0267
21				0.1133				12/18	0.0067	16/19	0.0133
22				0.0600				13/14	0.0267	17/17	0.0333
23				0.2200				13/16	0.0133	17/18	0.0267
24				0.4467				13/17	0.0133	17/19	0.0200
25				0.1400				13/18	0.0133	19/19	0.0067
26				0.0200				13/21	0.0067		
27			0.0267								
28			0.1333								
29			0.3067								
30			0.2733								
31			0.2000								
32			0.0600								
NA	6	4	6	6	5	5	5	33			
GD	0.6879	0.5726	0.7736	0.7198	0.5410	0.6525	0.4410	0.8422			

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
8		0.0333						0.0067
9		0.0733				0.0067		0.0533
10		0.2000		0.0133		0.0400		0.4000
11		0.2067		0.1933		0.3067		0.4800
12		0.4800		0.6067		0.4800		0.0533
13		0.0067	0.0133	0.1667		0.1533	0.1067	0.0067
14			0.4867	0.0200		0.0133	0.3333	
15			0.4200				0.4733	
16			0.0800				0.0733	
17							0.0133	
20	0.0333							
21	0.0200							
22	0.1933							
23	0.1267							
24	0.5000							
25	0.0867							
26	0.0267				0.04			
27	0.0067				0.34			
28					0.56			
29					0.06			
NA	8	6	4	5	4	6	4	6
GD	0.6916	0.6844	0.5835	0.5695	0.5725	0.6540	0.6519	0.6073

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 97.3% (146 out of 150) 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 [19]. Twenty-seven 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 unavailable but other patrilineal relatives are.

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