International Congress Series 1288 (2006) 216–218

www.ics-elsevier.com

Peruvian population study with 16 Y-STR loci

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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 of 77 unrelated males of Perú. Seventy-six different haplotypes were found, seventy-five haplotypes of them were found to be unique and only one was detected in two men. The haplotype diversity was 0.9997 ± 0.0022. By combining the allelic states of the 16 Y-chromosomal STRs, we could construct highly informative haplotypes that allowed the discrimination of 97.4% (76 out of 77) 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: Y-chromosome; STR; Population; Perú

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 that 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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0531-5131/ © 2006 Published by Elsevier B.V.
doi:10.1016/j.ics.2005.09.086

Table 1
Gene frequencies and diversities of the minimum haplotype systems in Perú ($n=77$) population

Allele	DYS19	DYS389I	DYS 389II	DYS 390	DYS 391	DYS 392	DYS 393	Allelic class	DYS 385	Allelic class	DYS 385
9					0.076			10/12	0.013	14/14	0.013
10					0.620	0.013		10/13	0.013	14/15	0.013
11	0.013				0.304	0.152		10/14	0.025	14/16	0.089
12	0.013	0.089				0.051	0.063	11/13	0.038	14/17	0.139
13	0.468	0.582				0.241	0.759	11/14	0.190	14/18	0.038
14	0.367	0.316				0.430	0.177	11/17	0.025	14/19	0.013
15	0.101	0.013				0.076		12/12	0.013	14/20	0.013
16	0.013					0.025		12/14	0.051	15/15	0.013
17	0.025					0.013		12/15	0.013	15/16	0.013
21				0.076				13/13	0.013	15/17	0.051
22				0.051				13/15	0.038	15/18	0.013
23				0.278				13/16	0.013	15/19	0.013
24				0.443				13/17	0.013	16/16	0.013
25				0.127				13/18	0.038	18/20	0.013
26				0.025				13/19	0.038	19/21	0.013
27			0.025					14/13	0.013		
28			0.089								
29			0.241								
30			0.342								
31			0.278								
32			0.025								
NA	7	4	6	6	3	8	3	31			
GD	0.643	0.560	0.748	0.710	0.524	0.734	0.394	0.932			

NA: allele number; GD: gene diversity.

Here, we report gene diversity and gene frequencies for 16 Y-STR loci in the Perú population. These will increase the database and the knowledge of polymorphisms on Latin American populations.

2. Materials and methods

Samples of 77 unrelated males were obtained from healthy individuals from Perú. 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. Gene frequencies and gene 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 (0.932), followed by the DYS389 II (0.748). 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 0.9997.

Table 2
Gene frequencies and diversities of the GEPY systems in Perú ($n=77$) population

Allele	DYS635	DYS438	DYS437	DYS461	GATAH4	DYS439	GATAA10	DYS460
7								0.011
8								0.023
9								0.506
10		0.115				0.034		0.402
11		0.494		0.069		0.241		0.057
12		0.379		0.713		0.540	0.011	
13		0.011	0.011	0.172		0.161	0.057	
14			0.667	0.046		0.011	0.195	
15			0.276			0.011	0.506	
16			0.046				0.172	
17							0.046	
18							0.011	
20	0.023							
21	0.080							
22	0.471							
23	0.345							
24	0.069							
25	0.011				0.011			
26					0.034			
27					0.333			
28					0.586			
29					0.034			
NA	6	4	4	4	5	6	7	5
GD	0.6556	0.6067	0.483	0.4610	0.5502	0.631	0.6793	0.5859

By combining the allelic states of the 16 Y-chromosomal STR, we could construct highly informative haplotypes that allowed the discrimination of 98.7% (76 out of 77) of the samples tested.

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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