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Y-chromosomal polymorphic loci DYS19, DYS389 I/II, DYS390, DYS391, DYS392 and DYS393 in a population sample from southwestern Poland

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Abstract

The aim of this study was to present the allelic frequencies of DYS19, DYS389 I/II, DYS390, DYS391, DYS392 and DYS393 systems in a southwest Poland population sample. The results were compared to the other available data from Poland and some European populations. We have observed significant differences between some allele frequencies in the analysed population samples. Differences between Slavonic and German populations are particularly noticeable in the case of DYS19 and DYS390 systems.

Keywords: Short tandem repeats; Y chromosome; Population analysis

1. Introduction

During the last few years, the interest in STR systems on the Y chromosome has continuously increased. These systems are reproducible, sensitive and can be used for forensic applications like stain analyses (especially male identification in sexual assault cases) and paternity testing of male offspring. All statistic calculations require knowledge of the allele frequencies. The main purpose of this study was to present allele frequencies of DYS19, DYS389 I/II, DYS390, DYS391, DYS392 and DYS393 systems in a southwest Poland population sample.

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2. Material and methods

2.1. Population sample

Blood samples were collected from 110 and 165 unrelated males. DNA was extracted using standard phenol–chloroform or Chelex procedures.

2.2. Amplification conditions

Amplifications were performed in the Perkin Elmer 2400 thermocycler using fluorescent dye labeled primers. The primers for DYS390, DYS391 and DYS393 were labeled with FAM and for DYS19, DYS389 I/II and DYS392 were labeled with NED. PCR reactions were carried out in 12 μl consisting of 1 U thermostable DNA polymerase (Perkin Elmer), 12 μM each dNTP, 10× concentrated PCR buffer, 0.1–0.2 μM of each primer. PCR conditions were as follows: 95 °C/11 min initial denaturation, 94 °C/1 min, 56–62 °C /1 min, 72 °C/2 min for 31 cycles, 60 °C/45 min final extension. PCR

Table 1
Population data of analysed STR systems in southwestern Poland

Alleles	Frequencies					
	DYS19 (*n*=155)	DYS389 I/II (*n*=139)	DYS390 (*n*=165)	DYS391 (*n*=124)	DYS392 (*n*=125)	DYS393 (*n*=110)
8				0.01		
9		0.09		0.02	0.02	
10		0.63		0.64	0.02	
11		0.26		0.32	0.73	
12		0.02		0.01	0.04	0.10
13	0.02				0.12	0.77
14	0.15				0.07	0.10
15	0.21					0.03
16	0.40					
17	0.20					
18	0.02					
19						
20						
21			0.01			
22			0.07			
23			0.14			
24			0.34			
25		0.01	0.38			
26		0.09	0.06			
27		0.33				
28		0.37				
29		0.16				
30		0.03				
31		0.01				
Discrimination index	0.733	0.246	0.712	0.487	0.445	0.386

conditions essentially were according to Kayser et al. [2]. Primer sequences have been previously described [2].

2.3. Electrophoresis

The PCR products were analysed in the ABI PRISM 310 Applied Biosystems Genetic Analyser using 310 GeneScane 2.1 program.

3. Results and discussion

The population data of the Y-chromosome STR systems analysed in southwest Poland are shown in Table 1. We have observed statistically significant differences between some allele frequencies in the analysed population samples. Differences between Slavonic and German populations are particularly noticeable in the case of DYS19 [1–6] and DYS390 systems [1,3–6]. The allele frequencies of DYS391 [1–5] in the analysed population sample from Poland are especially interesting. Although the DYS391 gene frequencies from southern Poland are similar to the population from Ukraine, in the sample from southwestern Poland, we have noted a distribution of allele frequencies similar to that observed in German populations.

References

[1] S. Degenhartt, K. Leim, S. Clerici, W. Reichert, R. Mattern, Studies on 7 autosomal and 5 Y-chromosomal STR loci in a South-West German population, Prog. Forensic Genet. 7 (1998) 527–530.
[2] M. Kayser, A. Caglia, D. Corach, N. Feretwell, C. Gehrig, G. Graziosi, F. Heidorn, S. Herrmann, B. Herzog, M. Hidding, K. Honda, M. Jobling, M. Krawczak, K. Leim, S. Meuser, E. Meyer, W. Oesterreich, A. Pandya, W. Parson, G. Penciano, A. Perez-Lezaun, A. Piccinini, M. Prinz, C. Schmitt, P.M. Schneider, R. Szibor, J. Teifel-Grendig, G. Weichhold, P. de Knijff, L. Roewer, Evaluation of Y chromosomal STRs: a multicenter study, Int. J. Leg. Med. 110 (1997) 125–133, 141–149.
[3] P. de Knijf, M. Kayser, A. Caglia, D. Corach, N. Feretwell, C. Gehrig, G. Graziosi, F. Heidorn, S. Herrmann, B. Herzog, M. Hidding, K. Honda, M. Jobling, M. Krawczak, K. Leim, S. Meuser, E. Meyer, W. Oesterreich, A. Pandya, W. Parson, G. Penciano, A. Perez-Lezaun, A. Piccinini, M. Prinz, C. Schmitt, P.M. Schneider, R. Szibor, J. Teifel-Grendig, G. Weichhold, L. Roewer, Chromosome Y microsatelites: population genetic and evolutionary aspects, Int. J. Leg. Med. 110 (1997) 134–140, 134–149.
[4] S. Kravchenko, L. Livshits, Analysis of human Y-microsatellite haplotypes in Ukraine, Eur. J. Hum. Genet. 9 (Suppl. 1) (2001) 291.
[5] T. Kupiec, W. Branicki, C. van Mersbergen, G. van Hemert, A. Kloosterman, Population genetic study of Y chromosome specific STR loci in a population sample from Southern Poland, Prog. Forensic Genet. 8 (2000) 312–314.
[6] R. Pawowski, W. Branicki, T. Kupiec, Y-Chromosomal polymorphic loci DYS19, DYS390, DYS393 in a population sample from Northern Poland, Electrophoresis 20 (1999) 1702–1706.