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SHORT COMMUNICATION

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Population genetic data for HumF13B, HumLPL and HumHPRTB in southeast Poland

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Abstract Allele frequencies for the three short tandem repeat systems HumF13B, HumLPL and HumHPRTB were determined in a population sample from southeast Poland. PCR products were separated by electrophoresis on denaturing polyacrylamide gels, followed by silver staining. A total of six alleles for HumF13B, seven for HumLPL and eight alleles for HumHPRTB were detected and no deviations from Hardy-Weinberg equilibrium were observed. The allele frequency data for the three systems were compared with other Caucasian populations.

Key words STRs · HumF13B · HumLPL · HumHPRTB · Poland

Introduction

The three short tandem repeat STR systems HumF13B [16], HumLPL [22] and HumHPRTB [6] are widely used in forensic casework due to their highly polymorphic nature. This paper presents allele frequency data from southeast Poland and some values for estimating the usefulness in forensic genetics and paternity testing.

Materials and methods

DNA was extracted (using standard phenol/chloroform method) from fresh blood samples of the following number of unrelated individuals: 201 (F13B), 315 (LPL), 114 females and 100 males (HPRTB), from the southeast region of Poland.

Amplification reactions were performed using the Gene Print STR systems F13B, LPL and HPRTB (Promega, Madison, Wisc.) according to the manufacturer's instructions. Separation was carried out on 4% polyacrylamide denaturing gels followed by silver staining [2].

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The statistical analysis within the examined population was performed to test for deviations from Hardy-Weinberg equilibrium using the observed and expected numbers of heterozygotes [14], the exact test [9], the likelihood ratio test [19], as well as the power of discrimination [11], polymorphism information content [3], discrimination index [21], the mean paternity exclusion probability and mean paternity index [4] and power of exclusion [20]. The heterogeneity between the examined and some other Caucasian populations was checked using the 2-way RxC contingency table according to G. Carmody (Carleton University, Ottawa, Canada).

Results and discussion

The phenotypes observed in the three STR systems were used to calculate allele frequencies (Table 1) and allele identification was performed by visual comparison with allelic ladders (Promega). In 402 meioses (HumF13B), 630 meioses (HumLPL) and 328 meioses (HumHPRTB) no mutations were observed. A total of six alleles was observed for the system HumF13B and the most frequent alleles were 10 (f = 0.448), 9 (f = 0.236) and 8 (f = 0.206). We have also observed the allele 11 (f = 0.005), which is very rare in Caucasian populations. For HumLPL seven alleles were detected and the most common were alleles

Table 1 Allele frequencies in the STR systems HumF13B, HumLPL and HumHPRTB in southeast Poland population samples

Allele	F13B (n = 201)	LPL (n = 315)	HPRTB	
			Females (n = 114)	Males (n = 100)
6	0.085			
7	0.020	0.002		
8	0.206	0.003	0.009	
9	0.236	0.048	0.017	0.010
10	0.448	0.449	0.009	
11	0.005	0.236	0.110	0.110
12		0.243	0.408	0.310
13		0.019	0.276	0.400
14			0.136	0.150
15			0.035	0.020

Table 2 The results of Hardy-Weinberg equilibrium and forensic values of the three STR systems analysed in the Polish population

	HumF13B	HumLPL	HumHPRTB (females)
Hardy-Weinberg Equilibrium:			
Homozygosity test	0.2681 d.f = 1 $P = 0.61$	2.0473 d.f = 1 $P = 0.17$	0.0204 d.f = 1 $P = 0.99$
Exact test	9.6592 d.f = 20 $P = 0.97$	17.2427 d.f = 27 $P = 0.92$	19.1393 d.f = 35 $P = 0.99$
Likelihood ratio	8.6482 d.f = 15 $P = 0.89$	13.6344 d.f = 21 $P = 0.88$	18.7312 d.f = 28 $P = 0.81$
Heterozygosity observed (expected)	0.6766 (0.6969)	0.7142 (0.6828)	0.7280 (0.7314)
Power of discrimination (PD)	0.8569	0.8388	0.8698
Polymorphism information content (PIC)	0.6446	0.6260	0.6834
Discrimination index (DI)	0.1753	0.1399	0.1277
Mean exclusion probability (MEP)	0.3930	0.4507	0.4730
Power of exclusion (PE)	0.4477	0.4240	0.4974
Mean paternity index (MPI)	1.6475	1.8205	1.8975

Table 3 Homogeneity testing for the degree of relationship between southeast Polish and other Caucasians using the test according to Carmody

Compared populations South East Poland	HumF13B		HumLPL		HumHPRTB (females)	
	χ^2	P	χ^2	P	χ^2	P
North-east Poland [10]	1.8956	0.860				
Austria [15]	2.1553	0.829				
Croatia [12]	3.5322	0.633				
Germany [1, 18]	5.1412	0.681	4.9703	0.561		
Hungary [7, 8]	10.3425	0.058	9.8407	0.175	4.4427	0.836
Italy [17]	8.7279	0.117				
Spain [13]	9.4147	0.090				
Switzerland [5]	11.5135	0.037				
Turkey [1, 18]	16.9850	0.004	24.1295	0.000		
USA (Caucasians) [*]	5.8710	0.440	12.8466	0.031	16.8983	0.034
USA (Caucasians) [6]					12.6946	0.161

10 (f = 0.449), 12 (f = 0.243) and 11 (f = 0.236) as well as two rare alleles 7 (f = 0.002) and 8 (f= 0.003). The most common alleles within HumHPRTB were 12 (f = 0.408) for females and 13 (f = 0.400) for males and two rare alleles 8 (f = 0.009) and 10 (f = 0.009) were also observed. The allele distribution for HumHPRTB (for the groups of females and males) was checked using the test by G. Carmody and homogenity of those two groups was confirmed ($\chi^2 = 7.779$, $P = 0.35$; G-test = 8.919, $P = 0.343$).

Statistical calculations for the Hardy-Weinberg analysis and other forensic values concerning these loci are presented in Table 2. No significant deviations from Hardy-Weinberg equilibrium were observed.

The allele distributions for the three loci in the Polish population are similar to most European populations as well as to American Caucasians (Table 3). The tests for heterogeneity revealed slight differences between southeast Poland and Switzerland (HumF13B $P = 0.037$) and USA Caucasians (HumLPL $P = 0.031$, HumHPRTB $P = 0.034$ population data from Promega [*]), however significant differences were observed between the Polish and Turkish populations (HumF13B $P = 0.004$, HumLPL $P = 0.000$).

The data presented in this study confirm the usefulness of the HumF13B HumLPL and HumHPRTB systems for routine forensic examinations and paternity testing, although the application of HumHPRTB is limited (especially in paternity) due to its chromosomal localisation.

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