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SHORT COMMUNICATION

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Hungarian population data on six STR loci – HUMVWFA31, HUMTH01, HUMCSF1PO, HUMFES/FPS, HUMTPOX, and HUMHPRTB – derived using multiplex PCR amplification and manual typing

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Abstract We present a Hungarian population study for six tetrameric short tandem repeat (STR) loci employing multiplex PCR amplification, electrophoresis of the PCR products in DNA sequencing gels and subsequent detection of allelic fragments by silver staining. The loci were HUMVWFA31, HUMTH01, HUMCSF1PO, HUMFES/FPS, HUMTPOX, and HUMHPRTB. All loci met Hardy-Weinberg expectations in the examined Hungarian Caucasian population sample (N = 223 individuals). In addition, there was no evidence for association of alleles among the five autosomal loci HUMVWFA31, HUMTH01, HUMCSF1PO, HUMFES/FPS, and HUMTPOX.

Key words Short tandem repeats (STR) · DNA typing · Multiplex PCR · Population genetics · Hungary

Introduction

Short tandem repeat (STR) loci are widely used polymorphic markers for forensic personal identification and paternity testing [1, 2]. In this study allele frequency data in a Hungarian population sample are presented for five autosomal loci (HUMVWFA31, HUMTH01, HUMCSF1PO, HUMFES/FPS, HUMTPOX, and one X-linked STR locus (HUMHPRTB).

Materials and methods

EDTA-blood samples were collected from 223 unrelated healthy Hungarian Caucasian individuals (102 females and 121 males) residing in the Budapest area (Central Hungary). DNA was extracted as previously described [3]. DNA samples (2–5 ng) were amplified in two different PCR triplexes using reagents provided in the GenePrint STR multiplex system CSF1PO-TPOX-TH01 and the GenePrint STR multiplex system HPRTB-FESFPS-vWF (Promega, Madison, Wis.) according to the manufacturer's instructions. Denaturing gel electrophoresis and typing of PCR products were performed as described previously [1].

Possible divergence from Hardy-Weinberg expectations (HWE) was determined by the exact test [4]. An interclass correlation criterion [5] was used for detecting disequilibrium between autosomal STR loci. Population homogeneity was tested using a computer programme (R × C contingency table; G-statistic) kindly provided by G. Carmody (Carleton University, Ottawa, Canada).

Results and discussion

The distributions of observed allele frequencies and homozygosities for the six STR loci in the Hungarian population sample are shown in Table 1. At the HUMHPRTB locus two variant alleles were observed and temporarily designated as 10 M and 11 M. Further sequencing analysis is needed to exactly characterize these variant alleles. By computing the G-statistic of an R × C contingency table we found that the HUMHPRTB allele frequency distribution in the female population set was similar to males ($P = 0.95$). The genotype frequency distributions for all STR loci showed no significant deviations from HWE based on the exact test (Table 1). An interclass correlation analysis demonstrated that there was no evidence for correlation between the alleles at any of the pairs of autosomal loci (two-sided $P \geq 0.17$). Furthermore, there was no evidence of association for the five autosomal loci using the the s_k^2 criterion [6] ($s_k^2 = 0.784$, 95% confidence interval of variance is 0.768–1.099).

Pair-wise testing for population homogeneity revealed no significant differences for all five autosomal STR loci between the Hungarians and Spanish Caucasians [1] ($P \geq 0.08$). The typing results obtained in this survey for HUMVWFA31 and HUMTH01 also showed no significant differences (VWA: $P = 0.95$; TH01: $P = 0.66$) in comparison with the corresponding allele frequency data observed in another Hungarian population sample analysed previously [7]. Additionally, in the present study an HUMVWFA31

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Table 1 Observed allele freqencies, homozygosities, and exact test for six STR loci

Allele	VWA ($n = 446$)	TH01 ($n = 446$)	CSF1PO ($n = 446$)	FES/FPS ($n = 446$)	TPOX ($n = 446$)	HPRTB[a] ($n = 204$)	HPRTB[b] ($n = 121$)
5		0.002					
6		0.220					
7		0.159					
8		0.114	0.002	0.018	0.596	0.005	
9		0.209	0.038		0.099	0.020	0.033
9.3		0.283					
10		0.013	0.307	0.247	0.074	0.005	
10M						0.005	
11			0.262	0.448	0.204	0.132	0.116
11M							0.008
12			0.318	0.224	0.027	0.353	0.364
13	0.002		0.063	0.061		0.284	0.298
14	0.108		0.009	0.002		0.137	0.149
15	0.114					0.054	0.033
16	0.206					0.005	
17	0.307						
18	0.173						
19	0.072						
20	0.016						
21	0.002						
Observed homozygosity	17.0%	17.5%	28.3%	29.2%	39.5%	31.4%	
Exact test[c]	0.082	0.283	0.938	0.062	0.828	0.390	

n = number of alleles

[a] For females

[b] For males

[c] These values are probability values

allele 13 was found, which has not yet been observed in the Hungarian population.

References

1. Martin P, Alonso A, Budowle B, Albarrán C, García O, Sancho M (1995) Spanish population data on 7 tetrameric short tandem repeat loci. Int J Legal Med 108:145–149
2. Sprecher CJ, Puers C, Lins AM, Schumm JW (1996) General approach to analysis of polymorphic short tandem repeat loci. Biotechniques 20:266–276
3. Kanter E, Baird M, Shaler R, Balazs I (1986) Analysis of restriction fragment length polymorphisms in deoxyribonucleic acid (DNA) recovered from dried bloodstains. J Forensic Sci 31: 403–408
4. Guo SW, Thompson EA (1992) Performing the exact test of Hardy-Weinberg proportion for multiple alleles. Biometrics 48: 361–372
5. Karlin S, Cameron EC, Williams PT (1981) Sibling and parent-offspring correlation estimation with variable family size. Proc Natl Acad Sci USA 78:2664–2668
6. Chakraborty R (1984) Detection of nonrandom association of alleles from the distribution of the number of heterozygous loci in a sample. Genetics 108:719–731
7. Furedi S, Woller J, Padar Z (1995) Hungarian population data for the STR systems TH01 and VWA. Int J Legal Med 108:48–49