Int J Legal Med (1997) 110 : 107–108

SHORT COMMUNICATION

S. Füredi · J. Woller · Z. Pádár

A population study of the STR loci HUMLPL, HUMF13B, and HUMF13A01 in Hungary

Received: 19 October 1996 / Received in revised form: 6 January 1997

Abstract Allele frequencies of the three STR systems HUMLPL, HUMF13B, and HUMF13A01 were determined in a Hungarian population sample of 223 unrelated Caucasian individuals. All loci met Hardy-Weinberg expectations and there was no evidence for association of alleles among the three STR loci. In addition, little evidence was found for departures from expectations of independence between any of the three STR and other previously investigated microsatellite polymorphisms.

Key words Short tandem repeat (STR) · HUMLPL · HUMF13B · HUMF13A01 · Population genetics

Introduction

Genetic typing of short tandem repeat loci (STRs) is a powerful means of forensic identification and paternity testing. In spite of the increasing number of Hungarian population databases [1–3], there are many forensically interesting STR polymorphisms which have not yet been surveyed in Hungary. This paper presents allele frequency distributions and locus independence data for the three STR loci HUMLPL, HUMF13B, and HUMF13A01 [4] in a Hungarian population sample.

Materials and methods

Blood samples were collected from 223 unrelated healthy Hungarian Caucasian individuals residing in the Budapest area (Central Hungary). DNA was extracted as previously described [5]. DNA samples (2–4 ng) were amplified using reagents provided in the GenePrint Fluorescent Quadruplex STR System F13A01-FESFPS-F13B-LPL (Promega, Madison, Wis.) according to the manufacturer's instructions. The PCR products were analyzed on an A.L.F. DNA sequencer (Pharmacia) according to the A.L.F. protocol.

Possible divergence from Hardy-Weinberg expectations was determined by the exact test [6]. An interclass correlation criterion [7] was used for testing disequilibrium between loci.

Results and discussion

The distributions of observed allele frequencies and homozygosities for the three STR loci in the Hungarian population sample are shown in Table 1. There was no evidence to suggest departures from independence either within or between the STR loci based on the exact test (Table 1) and the interclass correlation test ($P \geq 0.067$).

Table 1 Observed allele frequencies, homozygosities, and statistical data for the three STR loci in 223 unrelated Hungarian Caucasians (PD discrimination power, MEC mean exclusion chance)

Allele	LPL	F13B	F13A01
3.2			0.061
4			0.034
5			0.191
6		0.092	0.327
7		0.004	0.312
8		0.278	0.004
9	0.040	0.217	
10	0.408	0.401	
11	0.267	0.007	
12	0.249		0.002
13	0.029		0.013
14	0.007		0.013
15			0.029
16			0.009
17			0.002
18			0.002
Observed homozygosity	34.5%	27.8%	25.1%
Exact test[a]	0.070	0.846	0.067
PD	0.857	0.858	0.899
MEC	0.441	0.452	0.535

[a] These values are probability values

S. Füredi (✉) · J. Woller · Z. Pádár
Department of Biology, Institute for Forensic Sciences,
PO Box 314/4, H-1903 Budapest, Hungary

Furthermore, using the s_k^2 criterion [8] there was no evidence for allelic association among the three STR loci ($s_k^2 = 0.651$, 95% confidence interval of variance is 0.512–0.717). Additionally, based on the interclass correlation test no evidence was found for departures from the expectation of independence between any of the three STR and other previously reported [3] microsatellite polymorphisms (HUMVWFA31, HUMFES/FPS, HUMTH01, HUMTPOX, HUMCSF1PO; $P \geq 0.137$). The forensic efficiency data (Table 1) suggest that the three STR loci investigated are very discriminating in the Hungarian population (combined discrimination power = 0.998, combined mean exclusion chance = 0.858)

Acknowledgements Computer programs were kindly provided by B. Budowle (Forensic Science Research and Training Center, FBI Academy, Quantico, USA).

References

1. Furedi S, Woller J, Padar Z (1995) Hungarian population data for the STR systems TH01 and VWA. Int J Legal Med 108: 48–49
2. Csete K, Schürenkamp M, Varga T (1996) The STR sustems HumVWA and HumACTB2 in a Hungarian population. Int J Legal Med 108:316–317
3. Füredi S, Budowle B, Woller J, Pádár Z (1996) Hungarian population data on six STR loci – HUMVWFA31, HUMTH01, HUMCSF1PO, HUMFES/FPS, HUMTPOX, and HUMHPRTB – derived using multiplex PCR amplification and manual typing. Int J Legal Med 109:100–101
4. Sprecher CJ, Puers C, Lins AM, Schumm JW (1996) General approach to analysis of polymorphic short tandem repeat loci. Biotechniques 20:266–276
5. 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
6. Guo SW, Thompson EA (1992) Performing the exact test of Hardy-Weinberg proportion for multiple alleles. Biometrics 48:361–372
7. 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
8. 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