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SHORT COMMUNICATION

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Frequency data on four tetrameric STR loci D18S1270, D14S608, D16S3253 and D21S1437 in a Korean population

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Abstract We present the results of a population study in Korea for four new tetrameric short tandem repeat (STR) loci employing multiplex PCR amplification, polyacrylamide gel electrophoresis of the PCR products and silver staining, which allow single base pair resolution and rapid typing. The loci tested were D18S1270, D14S608, D16S3253 and D21S1437 and all loci showed no significant deviations from Hardy-Weinberg equilibrium in more than 100 unrelated Koreans. This allelic frequency data can be used in forensic analyses and paternity tests to estimate the frequency of a multiplex PCR based DNA profile in the Korean population.

Key words Quadruplex · Short tandem repeat · DNA typing · Korean population

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Introduction

The short sequences and high degree of polymorphism make the STR loci attractive for forensic and paternity analyses and amenable to amplification by the PCR (Edwards et al. 1991; Jeffreys et al. 1992; Lygo et al. 1994). In this paper, we report the allele frequency data and suitability for forensic markers for the four autosomal loci D18S1270, D14S608, D16S3235 and D21S1437 in a Korean population sample using a multiplex PCR technique.

Materials and methods

DNA preparation and amplification were performed as described previously (Park et al. 1997; Lee et al. 1998). The primer concentrations for each locus were 2.15 μM for D18S1270, 0.3 μM for D14S608, 0.3 μM for D16S3235, and 0.25 μM for D21S1437 (Table 1). The construction of allelic ladders, separation of amplified products and statistical calculations were performed as described previously (Park et al. 1997; Lee et al. 1998).

Results and discussion

All 106 unrelated Korean blood samples were typed successfully for the four STR loci D18S1270 (GenBank

Table 1 Characteristics of STR markers used in this study

Locus	Chromosome location	Repeat sequence	Number of alleles[a]	Fragment [a] length (bp)	Sequence of primers
D18S1270	18q21	TCTA	8	268–296	U:5′ - TTCACCATTGTCAATTATAAAACA - 3′ L:5′ - TCCAGACTGCCTTCAGACTC - 3′
D14S608	14q11.2	TCTA	8	200–228	U:5′ - TAAAGGTTTATCCATGCTGTAGC - 3′ L:5′ - ACGTGGTACAGGTAGATAAATGG - 3′
D16S3253	16q11.2	TAGA	8	167–195	U:5′ - GTTCAAGCATGGGTGGATAG - 3′ L:5′ - TTGTGTGGGAATATAGTGATGC - 3′
D21S1437	21q11.1	GGAA	8	115–143	U:5′ - ATGTACATGTGTCTGGGAAGG - 3′ L:5′ - TTCTCTACATATTTACTGCCAACA - 3′

[a] Our study in a Korean population

Table 2 Allele frequencies (%) of the four STR loci in a Korean population sample. Allelic designation refers to the number of repeats of the core sequence motif indicated in the locus column, *n* to the number of individuals sampled

Allele	D18S1270 (*n* = 106)	D14S608 (*n* = 106)	D16S3253 (*n* = 106)	D21S1437 (*n* = 106)
6			11.79	
7			0.94	
8	0.47	6.60	14.15	
9	4.72	15.57	5.66	
10	5.66	2.83	30.66	12.74
11	16.04	10.38	31.13	14.62
12	31.13	23.11	3.30	1.42
13	18.40	27.36	2.36	8.49
14	22.17	10.38		44.81
15	1.42	3.77		12.74
16				4.25
17				0.94

Table 3 Forensic values for the four STR loci under study (PIC polymorphism information content, PD power of discrimination)

Locus	Observed heterozygosity (%)	χ^2 test p value	PIC	PD
D18S1270	84.91	0.796	0.955	0.924
D14S608	82.08	0.718	0.967	0.944
D16S3253	77.36	0.243	0.947	0.913
D21S1437	72.64	0.922	0.930	0.902

G07989), D14S608 (GenBank # G09052), D16S3253 (GenBank # G07926) and D21S1437 (GenBank # G08082). All four loci showed 8 different alleles in Korean population (Table 2), and showed no significant deviations from Hardy-Weinberg equilibrium based on χ^2 test (Table 3). In conclusion, the data in this study demonstrate that the four loci have enough usefulness for use as forensic markers in Korean population.

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