RESEARCH NOTE

Short tandem repeat (STR) polymorphisms in Turkish population

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Introduction

In recent years, short tandem repeat (STR) systems have gained importance in forensic analysis of biological specimens as well as in paternity testing, as an alternative to the use of restriction fragment length polymorphism (RFLP) analysis (Edwards *et al.* 1991; Hammond *et al.* 1994; Nakamura *et al.* 1987). The analysis of STR polymorphisms by PCR-based method offers certain advantages over RFLP typing: (1) STR loci can be typed with a high degree of specificity and sensitivity in a short time period, (2) these loci can be succesfully amplified from a limited amount of DNA even if it is degraded, and (3) typing of multiple loci can be accomplished in a single multiplex reaction (Hochmeister *et al.* 1991; Lins *et al.* 1996). In this study, allele frequencies for the nine STR loci—D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317 and D7S820—were analyzed in 200 unrelated Turkish individuals. All loci, except for the FGA locus, were in Hardy-Weinberg equilibrium. The observed heterozygosity (H_o), expected heterozygosity (H_e), power of discrimination (PD), probability of exclusion (PE) and polymorphism information content (PIC) were calculated for the nine loci. The combined power of discrimination and combined probability of exclusion were 0.999999 and 0.999909 over the nine STR loci, respectively. These results suggest that these nine STR loci are a useful marker for forensic identification and paternity analysis.

Materials and methods

Sample preparation

This study was carried out on Turkish individuals living in Turkey, and randomly chosen from criminal cases. The samples were collected from 200 unrelated Turkish individuals. Genomic DNA was extracted from blood by the Chelex method (Walsh *et al.* 1991). The results obtained have previously been used for forensic purposes.

STR amplification and typing

1-5 ng of template DNA was used in each PCR reaction. Amplification of the STR loci were done using the AmpF*l* STR™ Profiler Plus Kit (Applied Biosystems, Foster City, CA, USA). AmpF*l*STR Profiler Plus PCR products were analyzed on ABI Prism™ 377 DNA sequencer. The GeneScan-500 (ROX) internal lane size standard was used.

Statistical analysis

The exact test was used to verify whether the genotypic distribution at each locus was in conformity with Hardy-Weinberg equilibrium (Guo *et al.* 1992). The power of discrimination (PD), probability of paternity exclusion (PE), polymorphism information content (PIC), expected heterozygosity (H_e) and observed heterozygosity (H_o) were also calculated (Fisher *et al.* 1951; Nei 1978; Botstein *et al.* 1980; Chakravarti *et al.* 1983).

Results and discussion

The observed allele frequencies of the nine STR loci are shown in table 1. The exact test was applied to these frequencies to test whether these loci taken into consideration were in Hardy-Weinberg equilibrium. The results indicated that the loci were in Hardy-Weinberg equilibrium, except for the FGA locus ($p = 0.027$), a deviation that may perhaps be due to migration. The expected (H_e) and observed (H_o) heterozygosity, PD, PE, and PIC values are presented in table 2. The heterozygosity of the nine STR loci screened in this study ranged from 0.735 to 0.860 (table 2), indicating that these loci could be used in determination of identity because of the high heterozygosity. These loci can also

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Table 1. Allele frequencies at nine STR loci in Turkish population.

Allele	D3S1358	vWA	FGA	D8S1179	21S11	D18S51	D5S818	D13S317	D7S820
7							0.002		0.005
8				0.015			0.007	0.130	0.162
9				0.015		0.002	0.052	0.070	0.090
10				0.062		0.007	0.107	0.082	0.250
11				0.050		0.020	0.340	0.305	0.257
12	0.005			0.110		0.097	0.320	0.275	0.162
13	0.002	0.002		0.280		0.147	0.162	0.100	0.050
13.2						0.020			
14	0.072	0.072		0.222		0.137	0.007	0.035	0.017
14.2						0.027			
15	0.250	0.122		0.147		0.125		0.002	0.005
16	0.337	0.195		0.072		0.157			
17	0.180	0.302		0.020		0.090			
18	0.137	0.202	0.005	0.005		0.065			
19	0.015	0.087	0.040			0.047			
20		0.015	0.090			0.030			
21			0.190			0.015			
22			0.140			0.010			
23			0.205						
24			0.170						
25			0.110						
26			0.040		0.002				
26.2									
27			0.007		0.015				
28			0.002		0.127				
29					0.222				
29.2					0.002				
30					0.235				
30.2					0.022				
31					0.055				
31.2					0.132				
32					0.012				
32.2					0.110				
33					0.002				
33.2					0.045				
34					0.002				
34.2					0.010				
35					0.002				

accurately distinguish between two unrelated people since the discrimination power of these loci was very high (combined PD = 0.999999; combined PE = 0.999909). As seen in table 2, the PE and PIC of the D18S51 locus (PE = 0.782; PIC = 0.880) were higher than the others, whereas the PE value of the D5S818 locus was the lowest (PE = 0.512; PIC = 0.699).

The combined PD, PE and PIC values of nine loci in Turkish population were also compared with those from Japanese, Spanish, French-Canadian Caucasian and Greek populations. The combined PE value (0.9999) of Turks was slightly higher than that of Japanese (0.9991), African-American 0.9996) and U.S. Caucasian (0.9994), Spanish population (0.9998) and French-Canadian Caucasian population (0.9874) (data for the non-Turkish populations are from Yamamoto *et al.* 1999; Arce *et al.* 2001; Busque *et al.* 1997). The combined PD value in the Turkish population (0.999999) also seems to be a little higher than that of French-Canadian Caucasian population (0.999998) (Busque *et al.* 1997). However, the combined PD value of the Turkish population was similar to Japanese (0.999999), African-American (0.999999) and U.S. Caucasian (0.999999), Spanish population (0.999999) (Yamamoto *et al.* 1999; Arce *et al.* 2001). The H_e, H_o, PE, PD and PIC values calculated in this study were compared with those reported for a Greek population (Skitsa *et al.* 2003) and were found to be generally similar, although slight differences were observed at some loci for H_o and PE values. It can be concluded that the nine STR loci studied here appear to be informative genetic markers for identity and paternity testing in the Turkish population.

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Table 2. Result of exact test for Hardy-Weinberg equilibrium, and statistical properties of nine STR loci in Turkish population.

Locus	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
p	0.200	0.374	0.027*	0.194	0.079	0.094	0.141	0.583	0.065
H_e	0.769	0.803	0.852	0.828	0.845	0.894	0.743	0.793	0.809
H_o	0.805	0.770	0.800	0.790	0.820	0.860	0.735	0.805	0.770
PD	0.909	0.932	0.959	0.948	0.957	0.979	0.891	0.928	0.935
PE	0.55	0.612	0.698	0.659	0.689	0.782	0.512	0.599	0.619
PIC	0.731	0.774	0.832	0.804	0.825	0.880	0.699	0.763	0.780

P , exact test *P*-values; * $P < 0.05$; H_e expected heterozygosity; H_o observed heterozygosity; PD power of discrimination; PE probability of exclusion; PIC polymorphism information content.

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