TECHNICAL NOTE

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Data on the PCR Turkish Population Based Loci: LDLR, GYPA, HBGG, D7S8, and Gc

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ABSTRACT: Allele and genotype frequencies for the five PCR-based loci were analyzed in 157 unrelated Turkish individuals. The five PCR-based loci included LDLR, GYPA, HBGG, D7S8, and Gc. The results of the chi-square and exact tests showed that the genotype distribution at the LDLR, GYPA, D7S8, and Gc loci did not significantly differ from the Hardy-Weinberg Expectation (HWE). However, the genotype distribution at the HBGG locus did not conform to HWE. Moreover, the genotype frequencies calculated in this study were compared with the published genotype frequencies of US African American and US Caucasian populations. The Turkish population was significantly different at the HBGG locus from the US Caucasian population. However, there were highly significant differences at the LDLR, HBGG, and Gc loci between the Turkish and African American populations.

KEYWORDS: forensic science, DNA typing, Turkey, population genetics, Hardy-Weinberg, polymerase chain reaction, LDLR, GYPA, HBGG, D78S, Gc

The polymerase chain reaction (PCR) (1) and subsequent typing of the amplified products have become useful techniques to characterize forensic biological samples genetically in recent years. PCR analysis can be used to amplify regions containing specific sequence differences, such as HLA-DQA1 (2) and PolyMarker (PM) loci (3). The PM loci are LDLR, GYPA, HBGG, D7S8, and Gc. The collection of allele/genotype frequency data at these loci enables forensic scientists to estimate the rarity of a genetic profile (4,5,6).

This paper presents the report of the allele/genotype frequency data for LDLR, GYPA, HBGG, D7S8, and Gc loci in the Turkish population. Also, the observed genotype frequencies in the Turkish population were compared with the previously published data in US African American and US Caucasian populations (7).

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Materials and Methods

Samples

The samples were collected from 157 unrelated Turkish individuals randomly selected from criminal cases. The DNA was extracted from fresh blood leucocytes, bloodstains, tissues, and single hairs following the published methods (8,9).

Typing

The extracted DNA was amplified and typed for the PM loci using AmpliType PM PCR Amplification and Typing Kit according to the manufacturer's protocol. Amplification was carried out in a Perkin Elmer DNA Thermal Cycler 480 (Perkin Elmer Corporation, Norwalk, CT).

Statistical Analysis

The frequency of each of 5 loci was calculated from the numbers of each genotype in the sample. Unbiased estimates of expected heterozygosity were computed as described by Edwards, et al. (10). The hypothesis that the genotype frequency distribution for each of the five loci conform to the HWE was tested using the chi-square and exact tests (11). Moreover, the observed genotype frequencies in the Turkish population were compared with the published genotype frequencies of the US African American and US Caucasian populations (7).

Results and Discussion

The allele frequencies calculated from the numbers of each genotype in the sample are given in Table 1. To control the hypothesis that the genotype frequencies for the five PM loci conform to the HWE, the expected genotype frequencies were calculated from the allele frequencies (Table 1) assuming the HWE. The observed and expected genotype frequencies are given in Table 2. The expected genotype frequencies were compared with the observed frequencies using the chi-square and exact tests (Table 2).

The results showed that the Turkish population did not significantly deviate from the HWE, except for the HBGG locus. The fact that many people have migrated to Turkey from abroad in recent years was regarded as the reason for the deviation of the HBGG locus from the HWE. However, when the origin of the data was in-

vestigated, there were no migrated people in the sample. Therefore, more data are going to be collected and examined to find out why there is a statistically significant deviation from the HWE for HBGG locus. As seen in Table 2, the most common genotype at the LDLR, HBGG, and D7S8 loci was "AB" having the highest observed genotype frequency. However, the "CC" was the most common genotype at the Gc locus.

The results obtained in this study support that the genotypes frequencies at the loci LDLR, GYPA, D7S8, and Gc can be estimated from allele frequencies. The observed genotype frequencies in the Turkish population were also separately compared with those in the US African American and US Caucasian populations using the chi-square test. The results of these analyses are presented in Table 3.

The result of the comparison for the Turkish population vs. US Caucasian population at the LDLR, GYPA, D7S8, and Gc loci showed no statistically significant differences (Table 3). In the comparison of the Turkish population vs. US Caucasian population at the HBGG locus, the genotypes AA, AB, and BB were taken into account because the genotypes BC and CC were not observed in the Turkish population while there were no genotypes AC and BC in the US Caucasian population. As given in Table 3, the chi-square test confirmed that there was a statistically significant difference at the HBGG locus between the Turkish and US Caucasian populations. Highly significant deviations exist between the Turkish population and the US African American population at the LDLR, HBGG, and Gc loci.

TABLE 1—*The allele frequencies for the five PM loci in 157 unrelated Turkish population.*

Allele	Frequency
LDLR A	0.378
LDLR B	0.622
GYPA A	0.566
GYPA B	0.434
HBGG A	0.405
HBGG B	0.592
HBGG C	0.003
D7S8 A	0.643
D7S8 B	0.357
Gc A	0.259
Gc B	0.166
Gc C	0.575

TABLE 2—*The observed and expected genotype frequencies in the Turkish population.*

	Observed		Expected			
Genotype	n	freq.	n	freq.	χ^2	Exact
LDLR						
AA	20	0.127	22.45	0.143	0.2674	
AB	79	0.503	73.79	0.470	0.3679	
BB	58	0.370	60.76	0.387	0.1254	
			df=1	χ^2	0.7607	p=0.492
				p=0.383		
GYPA						
AA	48	0.306	50.24	0.320	0.0999	
AB	82	0.522	77.09	0.491	0.3127	
BB	27	0.172	29.67	0.189	0.2403	
			df=1	χ^2	0.6529	p=0.418
				p=0.419		
HBGG						
AA	18	0.115	25.75	0.164	2.3325	
AB	90	0.573	75.36	0.480	2.8441	
BB	48	0.306	55.26	0.352	0.9538	
AC	1	0.006	0.157	0.001	4.5264	
BC	0	0.000	0.471	0.003	0.4710	
CC	0	0.000	$1.4\ 10^{-3}$	9.10^{-6}	$1.4\ 10^{-3}$	
			df=3	χ^2	11.1292	p=0.012
				p=0.011		
D7S8						
AA	60	0.382	64.84	0.413	0.3613	
AB	82	0.522	72.06	0.459	1.3711	
BB	15	0.096	20.10	0.128	1.2940	
			df=1	χ^2	3.0264	p=0.116
				p=0.082		
Gc						
AA	10	0.064	10.52	0.067	0.0257	
AB	13	0.083	13.50	0.086	0.0185	
BB	7	0.045	4.24	0.027	1.7966	
AC	48	0.306	46.79	0.298	0.0313	
BC	25	0.159	29.99	0.191	0.8303	
CC	54	0.343	51.97	0.331	0.0793	
			df=3	χ^2	2.7817	
				p=0.427		

TABLE 3—*The results of the comparison of Turkish population vs. US African American and Caucasian populations.*

Turkish Population vs.	Locus	χ^2	df	*p*
US Caucasian	LDLR	3.882	2	0.144
US Caucasian	GYPA	1.015	2	0.602
US Caucasian	HBGG	6.474*	2	0.039
US Caucasian	D7S8	0.867	2	0.648
US Caucasian	Gc	3.163	5	0.678
US Af. American	LDLR	17.641†	2	0.0001
US Af. American	GYPA	5.013	2	0.082
US Af. American	HBGG	140.396†	5	$p<0.0001$
US Af. American	D7S8	0.691	2	0.708
US Af. American	Gc	133.530†	5	$p<0.0001$

* $p<0.05$.
† $p<0.01$.

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