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SHORT COMMUNICATION

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Turkish population data on the HLA-DQα, LDLR, GYPA, HBGG, D7S8, and GC loci

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Abstract We have determined the allele and genotype frequencies of six PCR-based genetic markers HLA-DQα, LDLR, GYPA, HBGG, D7S8 and GC in the Turkish population (n = 361 for HLA-DQα, and n = 260 for PM). All loci meet Hardy-Weinberg expectations. The frequency data can be used in forensic analyses in the Turkish population.

Key words DNA polymorphism · Turkish population · PCR · HLA-DQα · LDLR · GYPA · HBGG · D7S8 · GC

Introduction

Commercially available DNA-based kits are widely used for individual identification purposes. In this study we have determined the allele and genotype frequencies of the human leukocyte antigen DQα (HLA-DQα [1], low density lipoprotein receptor (LDLR) [2], glycophorin (GYPA) [3], hemoglobin G gammaglobin (HBGG) [4], D7S8 [5], and group specific component (GC) [6] loci in the Turkish population with the Ampli Type HLA-DQα PCR amplification and typing kit, and the Ampli Type PM PCR amplification and typing kit (Perkin Elmer).

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Material and methods

Blood samples were obtained from 361 healthy unrelated Turkish volunteers (students of Istanbul University and randomly selected disputed cases of paternity). Informed consent was obtained from the subjects. Genomic DNA was isolated according to a well established protocol [7]. The quantity and quality of DNA in each sample was estimated by UV absorbance, and agarose gel electrophoresis. For each PCR reaction, 2–40 ng of DNA was added to the PCR mix. PCR amplification, hybridization of the amplified DNA samples to probe strips and determination of the genotypes were carried out as described by the manufacturer [8].

Results and discussion

The allele frequencies of the HLA-DQα, LDLR, GYPA, HBGG, D7S8 and GC loci in the Turkish population have been determined (Table 1). All the loci conform to Hardy-Weinberg equilibrium (Table 2). Conformity to independence between GC and GYPA was tested by RxC test of independence [8] since these loci map to the same chromosome. No evidence of association was found (G = 9.06; df = 10; not significant).

The allele frequency distributions of the Turkish population and other populations [Perkin Elmer user guide and 9–11] shown in Table 1 have been compared by employing a test of homogeneity [8] (analyses are not given). No significant difference between the Turkish population and the other populations was found for the D7S8 locus. However, for the remaining loci, significant differences between the Turkish population and the other populations, except for the North Bavarian population, were observed. These differences include Swiss GYPA ($0.025 < p < 0.05$) and HBGG ($0.01 < p < 0.025$); Caucasian HLA-DQα ($0.025 < p < 0.05$) and GYPA ($0.01 < p < 0.025$); Hispanic HLA-DQα ($p < 0.001$) and GC ($0.001 < p < 0.005$); Black HLA-DQα ($0.01 < p < 0.025$), LDLR ($p < 0.001$), HBGG ($p < 0.001$) and GC ($p < 0.001$). These agree with previously reported HLA-DQα allele frequencies in the Turkish population [12]. The chi-square (χ^2) values for the goodness-of-fit between the Hardy-Weinberg expected

Table 1 Frequency of the HLA-DQα, LDLR, GYPA, HBGG, D7S8, and GC alleles in the Turkish population, and comparison with various populations

Loci			Allele frequencies							
Locus	Chr.	No. of alleles	Allele	Turkish[a] (n_1 = 361; n_2 = 260)	Turkish[b] (n = 150)	Swiss[c] (n = 200)	Norh Bavarian[d] (n = 150)	Black[e, f] (n_1 = 413; n_2 = 100)	Hispanic[e, f] (n_1 = 224; n_2 = 100)	Caucasian[e, f] (n_1 = 169; n_2 = 100)
HLA-DQα	6	6	1.1	0.149	0.190	0.148	–	0.150	0.080	0.137
			1.2	0.168	0.193	0.193	–	0.263	0.056	0.197
			1.3	0.097	0.123	0.095	–	0.045	0.012	0.085
			2	0.103	0.070	0.150	–	0.121	0.050	0.109
			3	0.129	0.157	0.145	–	0.118	0.435	0.201
			4	0.356	0.267	0.270	–	0.304	0.367	0.271
LDLR	19	2	A	0.438	–	0.435	0.377	0.250	0.480	0.430
			B	0.562	–	0.565	0.623	0.750	0.520	0.570
GYPA	4	2	A	0.618	–	0.525	0.587	0.550	0.610	0.480
			B	0.382	–	0.475	0.413	0.450	0.390	0.520
HBGG	11	3	A	0.435	–	0.475	0.500	0.420	0.390	0.530
			B	0.551	–	0.525	0.483	0.260	0.560	0.450
			C	0.014	–	0.000	0.017	0.320	0.050	0.020
D7S8	7	2	A	0.617	–	0.585	0.600	0.660	0.660	0.580
			B	0.383	–	0.415	0.400	0.340	0.340	0.420
GC	4	3	A	0.270	–	0.280	0.293	0.070	0.200	0.330
			B	0.190	–	0.175	0.157	0.740	0.360	0.150
			C	0.540	–	0.545	0.550	0.190	0.440	0.520

Chr. = Chromosome. [a] =This study; [b] = Menevşe and Ülküer [12]; [c] = Hochmeister et al. [10]; [d] = Hausmann et al. [11]; [e] = Helmuth et al. [9] (for HLADQα locus), and [f] = Perkin Elmer PM user guide (for PM loci). n = subjects examined; n_1 = HLADQα; n_2 = PM

Table 2 Chi-square (χ^2) values for the goodness-of-fit between the Hardy-Weinberg expected and observed frequencies, degrees of freedom (df), p-value, observed heterozygosity (H), allelic diversity (h), power of discrimination (PD), and power of exclusion (A) values for six loci in the Turkish population

Locus	χ^2 [8]	df [8]	*P*-value* [8]	H [13]	h [13]	PD [14]	A [15]
HLA-DQα	14.12	15	0.51	0.79	0.79	0.92	0.68
LDLR	0.07	1	0.79	0.49	0.49	0.62	0.18
GYPA	0.61	1	0.43	0.50	0.47	0.59	0.18
HBGG	2.22	3	0.52	0.63	0.51	0.55	0.19
D7S8	0.61	1	0.43	0.50	0.47	0.59	0.18
GC	1.9	3	0.59	0.50	0.60	0.77	0.19

* *p*-values were not significant (i.e. $p > 0.05$)

and observed frequencies [8], degrees of freedom (df) [8], p-value [8], observed heterozygosity [13], allelic diversity (h) [13], power of discrimination (PD) [14], and power of exclusion (A) [15] values are shown in Table 2. In conclusion, a Turkish population database has been established for six PCR-based polymorphic loci which can be used for DNA-based individual identification.

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