

FOR THE RECORD

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Distribution of HLA-DQA1 and Amplitype PM Locus Alleles in Aegean Region of Turkey

POPULATION: Unrelated individuals from Aegean Region of Turkey.

KEYWORDS: forensic science, DNA typing, population genetics, polymerase chain reaction, DQA1, LDLR, GYPA, HBGG, D7S8, GC, Aegean Region, Turkey

The samples were collected from unrelated individuals randomly selected from criminal cases. The DNA was extracted from fresh blood leucocytes, bloodstains, and single hairs by Chelex 100 method (1).

The extracted DNA was quantitated according to the quantification procedure (2). Slot-blot hybridization was done using the Quantiblot[®] Human DNA Quantitation Kit (Perkin Elmer, Norwalk, CT).

The samples (2 ng targeted DNA) were typed for HLA-DQA1/PM loci by using the Amplitype PM and DQA1 kit as per the manufacturer's instructions (3). The samples were amplified us-

ing GeneAmp PCR System 9700 (PE Biosystems, Foster City, CA).

Exact tests were performed by using the computer program GDA for checking the Hardy-Weinberg expectations (4). Data were analyzed by PowerStats (5).

The dataset can be accessed at <http://hadicakir.medyatext.gen.tr>.

References

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2. Waye JS, Presley LA, Budowle B, Shutler GG, Fournay RM. A simple and sensitive method for quantifying human genomic DNA in forensic specimen extracts. *BioTechniques* 1989;7(8):852-55.
3. Perkin-Elmer Corp., Foster City, CA, USA.
4. Lewis PO, Zaykin D. Genetic data analysis, computer program for the analysis: of allelic data, Version 1.0 (d16c), 2001.
5. Tereba A. Tools for analysis of population statistics. *Promega Corporation. Profiles in DNA* 1999;(2):14-16.

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TABLE 1—Observed alleles frequencies for HLA-DQA1/PM loci in Aegean Region of Turkey.

		HLA-DQA1											
		N = 147											
		Allele		Frequency									
		1.1		0.085									
		1.2		0.119									
		1.3		0.102									
		2		0.095									
		3		0.228									
		4		0.371									
		Ho		0.789									
		He		0.772									
		P*		0.664									
		P**		0.067									
		PD		0.910									
		PEP		0.579									
		PIC		0.74									
		TPI		2.37									
N = 131		LDLR		GYPA		HBGG			D7S8		GC		
Allele		A	B	A	B	A	B	C	A	B	A	B	C
Frequency		0.401	0.599	0.603	0.397	0.469	0.519	0.012	0.615	0.385	0.267	0.195	0.538
Ho		0.481		0.458		0.580			0.481		0.664		
He		0.482		0.481		0.512			0.476		0.603		
P*		0.843		0.471		0.121			0.949		0.119		
P**		1.000		0.723		0.248			1.000		0.219		
PD		0.614		0.622		0.600			0.608		0.759		
PEP		0.171		0.153		0.268			0.171		0.375		
PIC		0.36		0.36		0.39			0.36		0.53		
TPI		0.96		0.92		1.19			0.96		1.49		
Combined PE						0.7808							
Combined PD						0.9995							
PI _{tot}						1/2016							

Ho: (observed heterozygosity), He: (expected heterozygosity), P*: Heterozygosity; χ^2 |_{df} based on unbiased estimate with 3200 shufflings), P**: exact test; based on 3200 shufflings), PD: (power of discrimination), PEP: (excluding probability of paternity), PIC: (polymorphism information content), PI: (Probability of identity).