

## For the Record

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# Distribution of HLA-DQA1 and AmpliType PM Locus Alleles in a Turkish Population Sample

**Population:** Central Anatolia Region, Turkey

**Keywords:** forensic science, DNA typing, population genetics, polymerase chain reaction, DQA1, LDLR, GYPA, HBGG, D7S8, GC, Central Anatolia 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 quantity of DNA was determined (2) by using the Quantiblot<sup>®</sup> Human DNA Quantitation Kit (Perkin Elmer, Norwalk, CT).

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The samples were typed for HLA-DQA1/PM loci by using the AmpliType PM and DQA1 kit as per the manufacturer's instructions (3).

Exact tests were performed by using the computer program GDA (Genetic Data Analysis, Lewis PO, and Zaykin D) for checking the Hardy-Weinberg expectations. Data were analyzed by The Promega Software, POWERSTATS.

The dataset can be accessed at <http://w3.gazi.edu.tr/~leyacik>

## References

- Walsh PS, Metzger DA, Higuchi R. Chelex 100 as a medium for the simple extraction of DNA for PCR-based typing from forensic materials. *BioTechniques* 1991;10(4):506-13.
- Waye JS, Presley LA, Budowle B, Shutler GG, Fourney RM. A simple and sensitive method for quantifying human genomic DNA in forensic specimen extracts. *BioTechniques* 1989;7(8):852-55.
- Perkin-Elmer Corp., Foster City, CA.

TABLE 1—Distribution of HLA-DQA1 and AmpliType PM locus alleles.

N = 104	HLA-DQA1	
	Allele	Frequency
	1.1	0.106
	1.2	0.125
	1.3	0.135
	2	0.192
	3	0.178
	4	0.264
	Ho	0.808
	He	0.823
	P*	0.606
	P†	0.188
	PD	0.933
	PEP	0.613
	MP	0.067
	PIC	0.79
	TPI	2.60

  

N = 129	LDLR		GYPA		HBGG			D7S8		GC								
	Allele	Frequency	A	B	A	B	C	A	B	A	B	C						
		0.295		0.705		0.682	0.318		0.488	0.508	0.004		0.601	0.399		0.333	0.143	0.523
	Ho	0.357		0.450		0.450	0.550		0.566				0.566			0.628		
	He	0.420		0.416		0.416	0.506		0.481				0.481			0.598		
	P*	0.069		0.854		0.854	0.349		0.066				0.066			0.491		
	P†	0.133		0.840		0.840	0.344		0.068				0.068			0.199		
	PD	0.581		0.580		0.580	0.604		0.565				0.565			0.736		
	PEP	0.090		0.147		0.147	0.236		0.252				0.252			0.326		
	MP	0.416		0.418		0.418	0.394		0.429				0.429			0.267		
	PIC	0.33		0.34		0.34	0.38		0.36				0.36			0.52		
	TPI	0.78		0.91		0.91	1.11		1.13				1.13			1.37		

Ho: observed heterozygosity, He: expected heterozygosity, P\*: heterozygosity, P†: exact test, PD: power of discrimination, PEP: excluding probability of paternity, PIC: polymorphism information content, MP: matching probability, TPI: typical paternity index.

\* $\chi^2$  test based on unbiased estimate with 3200 shufflings.

† based on 3200 shufflings.