

A. Arnaiz-Villena  
M. Karin  
N. Bendikuze  
E. Gomez-Casado  
J. Moscoso  
C. Silvera  
F.S. Oguz  
A. Sarper Diler  
A. de Pacho  
L. Allende  
J. Guillen  
J. Martinez Laso

# HLA alleles and haplotypes in the Turkish population: relatedness to Kurds, Armenians and other Mediterraneans

## Key words:

HLA; Turks; Kurds; Armenians; Jews; Cretans; Iberians; Lebanese; Egyptians; Greeks; Berbers; Algerians; Iranians

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## Abstract:

Turkish and Kurdish HLA profiles are studied for the first time. The comparative study of their allele frequencies, characteristic haplotypes, genetic distances with other Mediterraneans is complemented by neighbor-joining dendrograms and correspondence analyses. Turks, Kurds, Armenians, Iranians, Jews, Lebanese and other (Eastern and Western) Mediterranean groups seem to share a common ancestry: the older "Mediterranean" substratum. No sign of the postulated Indo-European (Aryan) invasion (1200 B.C.) is detected by our genetic analysis. It is concluded that this invasion, if occurred, had a relatively few invaders in comparison to the already settled populations, i.e. Anatolian Hittite and Hurrian groups (older than 2000 B.C.). These may have given rise to present-day Kurdish, Armenian and Turkish populations.

Present-day Turks number about 62 million. Turk tribes started moving towards Azerbaijan, Iran and Anatolia from the Altai Mountains and Lake Aral areas around the 10th century A.D. (1). They spoke an Altaic language (Altai Mountains, in Siberia, North Mongolia). Turks came into Iran and Anatolia, took power in what is now Iran/Iraq and quickly advanced towards the West threatening both Byzantium (Roman Empire) and Muslim conquests in Anatolia and the Middle East (1). First, Selyuk and in a second place Ottoman Turks conquered part of Roman areas and Constantinople (Istanbul, 1453 A.D.) respectively. By 1800 A.D., Turks still held power in Algeria, Libya, Tunisia, Egypt, Saudi Arabia, Yemen, Palestine, Syria, Lebanon, Iraq, all Balkan countries and neighboring southern Russia, Hungary, Anatolia and southern Caucasus (Georgia, Armenia) (1). Confrontation with Mediterraneans and Russians started and many countries obtained independence (Greece, Egypt, Bulgaria, Rumania, Serbia, etc.). After World War I (1918), the former Turkish Empire was split and seized by France, Great Britain, Italy and Greece. Mustafa Kemal (Ataturk) declared the Turkish Republic in 1922 (1) and Turks thus started living within

## Authors' affiliations:

A. Arnaiz-Villena<sup>1\*</sup>,  
M. Karin<sup>2\*</sup>,  
N. Bendikuze<sup>3</sup>,  
E. Gomez-Casado<sup>1</sup>,  
J. Moscoso<sup>1</sup>,  
C. Silvera<sup>1</sup>,  
F.S. Oguz<sup>2</sup>,  
A. Sarper Diler<sup>2</sup>,  
A. de Pacho<sup>1</sup>,  
L. Allende<sup>1</sup>,  
J. Guillen<sup>1</sup>,  
J. Martinez Laso<sup>1</sup>

<sup>1</sup>Department of Immunology and Molecular Biology, H. 12 de Octubre, Universidad Complutense, Madrid, Spain,

<sup>2</sup>Dept. Medical Biology, University of Istanbul, Istanbul, Turkey,

<sup>3</sup>Institute for Clinical and Experimental Medicine, Prague, Czechoslovakia

\* The contribution by Antonio Arnaiz-Villena and Mahmut Karin is equal and the order of authorship is arbitrary

## Correspondence to:

Antonio Arnaiz-Villena  
Departamento de  
Inmunología y Biología  
Molecular  
H. 12 de Octubre  
Universidad Complutense  
Carretera Andalucía  
28041 Madrid  
e-mail:  
arnaiz@eucmax.sim.ucm.es.  
http:  
//chopo.pntic.mec.es/biolumol

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the limits of what is present-day Turkey. On the other hand, Kurds are about 30 million people and are distributed in Turkey (11.4 million), Iran (6.6 million), Iraq (3.9 million), Armenia and Azerbaijan (0.9 million) (1). Their Diaspora throughout other countries accounts for another 5.5 million. They speak an Iranian language with a strong Caucasian influence (Ergative composition, toponyms, 2); there are Kurd communities also in the West of South Caucasus republics including Georgia (in its capital, Tblisi, 1).

In the present work, it is intended to obtain for the first time the Turkish HLA gene profile and the characteristic haplotypes, studying the relative contribution of ancient Mediterraneans to the genetic pool of present day Turkish people. A Kurd group is also analyzed and both ethnic groups will be compared with the HLA genetic structure of neighboring Armenians and other Mediterraneans. For these purposes, both the HLA class I and class II genes have been studied since the HLA system has been shown to be very polymorphic, able to be compared among ethnic groups and useful to distinguish and/or relate populations (3, 4).

## Material and methods

### Population samples

Two hundred and twenty-eight unrelated Turkish individuals were used for HLA typing and phylogenetic calculations. The samples were taken from volunteers among unrelated blood donors from the

Medical Biology Department of Istanbul University and they include representatives from all over Anatolia, including the Easternmost parts (but excluding Kurdish speaking people). Kurd samples were collected in Tblisi (Georgia) from thirty healthy unrelated blood donors belonging to the Kurdish community living in Tblisi (Georgia). The origin of all other populations used for comparisons are detailed in Table 1 (see also Fig. 1).

### HLA typing and statistics

Generic HLA class I (A and B) and class II (DR and DQ) typing for the Turkish sample was done by a standard microlymphocytotoxicity technique as previously described (5); in addition the Kurdish sample class I and II alleles were typed by amplification refractory mutation system-polymerase chain reaction (ARMS-PCR) (6). Statistical analysis was performed with Arlequin v1.1 software kindly provided by Excoffier and Slatkin (7). In summary, this program calculated HLA-A, -B, -DR and -DQ allele frequencies, the linkage disequilibrium between two alleles at two different loci, their level of significance ( $P$ ) for  $2 \times 2$  comparisons and also their relative linkage disequilibrium (RLD; 8) and tested the Hardy-Weinberg equilibrium. In addition, the most frequent complete haplotypes were deduced from: (a) the 2, 3, and 4 HLA loci haplotype frequencies (9); (b) the previously described haplotypes in other populations (10); and (c) haplotypes if they appeared in two or more individuals and the alternative haplotype was well defined (10). In order to compare phenotype and haplotype HLA frequencies with other populations,



**Fig. 1. Map of the area referred in the text.**  
1.- Inset square represents localization of map within the Mediterranean area; 2.- White characters: countries names. **ABCD**: Location of classic populations. Green dots area: Kurds distribution; small dots: high density, big dots: low density. Anatolian Peninsula is named in large white letters (Refs. 2, 34, 39).

**Populations used for the present work**

Figs. 3 and 4  
Identification  
numbers

Region and population	n	Reference(s)
Turks	228	Present study
Spaniards	176	20
Basques (from Spain)	80	20
Portuguese	228	9
French	179	10
Italians	284	10
Sardinians	91	10
Moroccans (El Jadida)	98	18
Berbers (Souss)	98	32
Algerians (Algiers)	102	4
Jews (Morocco)	94	45
Jews (Ashkenazi)	80	21
Jews (non-Ashkenazi)	80	21
Cretans	135	17
Greeks (Attica)	96	11
Lebanese (NS)	59	11
Lebanese (KZ)	93	11
Iranians	100	11
Egyptians (Siwa)	101	11
Armenians	141	10
Kurds	30	Present study
Japanese	493	10
San (Bushmen)	77	10

n=number of individuals analysed for each population.

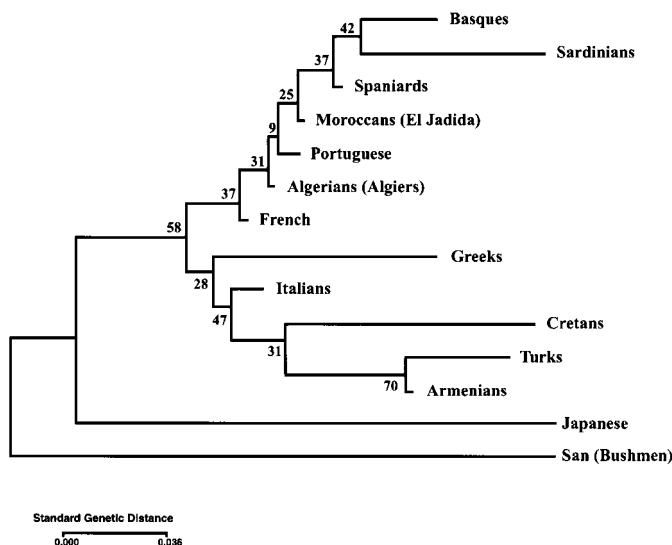
**Table 1**

the reference tables of the 11th and 12th International HLA Workshops were used (10, 11) (see also Table 1). Phylogenetic trees (dendrograms) were constructed from the allele frequencies by using the Neighbor-Joining (NJ) method (12) with the standard genetic distances (SGD, 13), by using DISPAN software containing the programs GNKDST and TREEVIEW (14, 15). Correspondence analysis in three dimensions and its bidimensional representation was carried out by using the VISTA v5.02 computer program (16, <http://forrest.psych.unc.edu>). Correspondence analysis consists of a geometric technique that may be used for displaying a global view of the relationships among populations according to HLA (or other) allele frequencies. This methodology is based on the allele frequency variance among populations (similarly to the classical components methodology) and on the display of a statistical visualization of the differences.

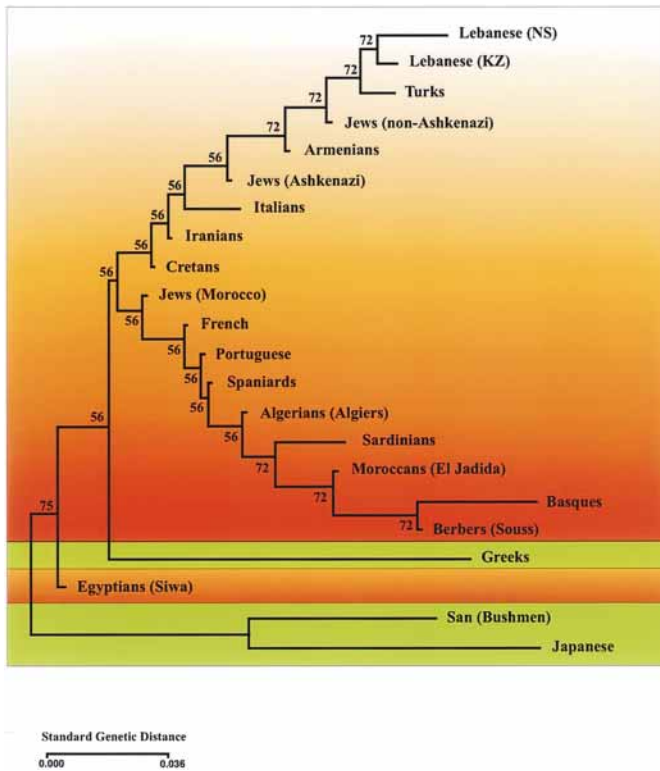
**Results**

**Characteristic HLA allele frequencies and correspondence analysis of the Turkish and Kurdish populations compared to other Mediterraneans (Table 2 and Figs. 2, 3 and 4)**

The observed gene frequency values for the HLA-A, -B, -DR and -DQ loci in the Turkish population are given in Table 2. The genotype frequencies are in Hardy-Weinberg equilibrium. Table 2 shows the HLA allele frequencies found in the Turkish population. The Kurdish allele frequencies are not listed in the table because they belong to only 30 unrelated individuals and will be analyzed separately due to the difference to other populations' sample size except for the correspondence analysis. Differences in samples size do not greatly distort the correspondence graphic representation. The Kurdish allele frequencies are in Hardy-Weinberg equilibrium and are as follows: A\*01 (8.6%), A\*02 (15.5%), A\*03 (17.2%), A\*11 (10.3%), A\*23 (5.2%), A\*24 (8.7%), A\*26 (8.6%), A\*29 (5.3%), A\*30 (3.4%), A\*31 (1.7%), A\*32 (6.9%), A\*68 (8.6%), B\*05 (1.8%), B\*07 (8.9%), B\*08 (3.6%), B\*13 (7.1%), B\*15 (1.8%), B\*18 (5.4%), B\*27 (5.4%), B\*35 (10.7%), B\*38 (1.8%), B\*44 (14.2%), B\*47 (1.8%), B\*48 (1.8%), B\*49 (1.8%), B\*50 (3.6%), B\*51 (14.1%), B\*52 (3.6%), B\*53 (1.8%), B\*55 (3.6%), B\*56 (3.6%), B\*57 (1.8%), B\*59 (1.8%); DRB1\*01 (3.3%), DRB1\*03 (13.3%), DRB1\*04 (18.3%), DRB1\*07 (6.7%), DRB1\*10 (6.7%), DRB1\*11 (16.7%), DRB1\*13 (6.7%), DRB1\*14 (8.3%), DRB1\*15 (18.3%), DRB1\*16 (1.7%); DQB1\*02



**Fig. 2. Neighbor-joining dendrogram showing relatedness between Turkish and other populations.** Standard genetic distances (SGD) were calculated by using generic HLA-A, -B, -DR and -DQ allele frequency data. Data from other populations were from references in Table 1. Bootstrap values from 1,000 replicates are shown.

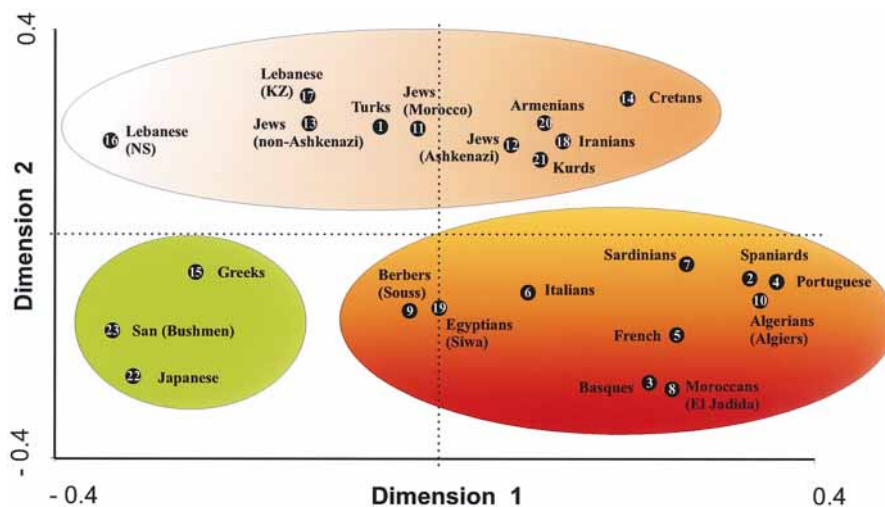


**Fig. 3. Neighbor-joining dendrogram showing relatedness between Turkish and other populations.** Standard genetic distances (SGD) were calculated by using generic HLA-DR, -DQ allele frequency data. Data from other populations were from references in Table 1. Bootstrap values from 1,000 replicates are shown.

(18.3%), DQB1\*03 (1.7%), DQB1\*0301 (21.6%), DQB1\*0302 (13.3%), DQB1\*03032 (1.7%), DQB1\*0501 (10.0%), DQB1\*0502 (1.7%), DQB1\*05031 (10.0%), DQB1\*06 (1.7%), DQB1\*0601 (16.7%), DQB1\*0603 (3.3%). Two types of analysis were carried out

to compare Turkish HLA frequencies with other populations' frequencies: in the first place, with pooled class I (A and B) and class II (DR and DQ) data (Fig. 2) and, in the second place, with only class II (DR and DQ) data (Fig. 3). Both types of analyses were also performed because some of the populations used for comparisons lacked HLA-A and -B data [Lebanese (NS and KZ), Jews (Ashkenazi, non-Ashkenazi and Moroccans), Iranians, Egyptians (Siwa oasis) and Berbers (Souss, Agadir area), see Table 1]. These partially HLA-typed populations should have been ignored, but they could be analyzed jointly taking into account only their DR and DQ frequencies (Table 3, Fig. 3). Results obtained by mixing class I and II data differ slightly from the results obtained by using only class II data (17, 18). In fact, the neighbor-joining tree constructed with both class I (A and B) and class II (DR and DQ) allele frequencies (Fig. 2) yield lower confidence limits (bootstrap values). This is most likely due to: (a) the lower class I allelism makes the comparisons more homogeneous, diminishing the class II discriminating ability and, (b) the fact that the number of compared populations with pooled class I and II data is lower than with only class II data.

The topology of HLA class II neighbor-joining tree shows a specific distribution of populations with a Mediterranean West to East gradient (Fig. 3). Populations are grouped in two main branches that are inter-related. At one side western Mediterraneans (both Europeans and North Africans) are placed and at the other one, eastern Mediterraneans, including Turks, Cretans, Jews, Lebanese, Armenians and Iranians among others are observed (Fig. 2). The Turkish population shows the closest genetic distances with eastern Mediterraneans: Non Ashkenazi Jews, Armenians, Lebanese (KZ), Iranians, Ashkenazi Jews, Italians, Cretans, Lebanese (NS) and Kurds (Table 3). After Turks-Kurds pairwise distance ( $5.90 \times 10^{-2}$ ), a discontinuity can be observed with the next closest value corre-



**Fig. 4. Correspondence analysis showing a global view of the relationship between Turkish and other populations according to HLA-DR and -DQ allele frequencies in three dimensions (bi-dimensional representation).**

**Frequencies of HLA-A, -B, -DR and DQ alleles in the Turkish population**

Alleles	Allele Frequencies (%)	Alleles	Allele Frequencies (%)
<b>HLA-A</b>		<b>HLA-B</b>	
A1	6.6	B7	3.9
A2	21.9	B8	3.5
A3	10.9	B13	4.4
A11	6.1	B18	3.1
A23	5.3	B27	2.8
A24	21.3	B35	14.0
A25	1.3	B37	0.4
A26	13.5	B38	3.3
A28	3.5	B39	1.1
A29	1.5	B40	0.4
A30	1.3	B41	1.5
A31	2.9	B44	13.4
A32	2.8	B45	0.4
A33	1.1	B49	6.6
A34	0.4	B50	5.0
A blank	0.2	B51	15.8
		B52	1.7
		B55	7.1
		B56	0.2
		B57	1.3
<b>HLA-DR</b>		B58	0.8
DR1	3.6	B60	3.5
DR2	0.2	B62	2.4
DR3	9.6	B63	1.1
DR4	13.1	B61	1.9
DR7	11.7	B blank	0.4
DR8	0.2		
DR9	6.8		
DR10	0.6		
DR11	35.4		
DR12	0.4		
DR13	6.2		
DR14	4.3		
DR15	5.2		
DR16	2.7		
DR blank	0.0		
<b>HLA-DQ</b>			
DQ1	27.3		
DQ2	23.8		
DQ3	48.2		
DQ4	0.7		
DQ blank	0.0		

**Table 2**

**Standard genetic distances (SGD) between Turkish and other populations ( $\times 10^2$ ) obtained by using HLA-DR,-DQ allele frequencies (see Table 1 for identification of populations)**

DR-DQ	Genetic distances ( $\times 10^2$ )
Non-Ashkenazi Jews	0.15
Armenians	0.78
Lebanese (KZ)	1.52
Iranians	2.80
Ashkenazi Jews	3.05
Italians	3.27
Cretans	3.85
Lebanese (NS)	4.55
Kurds	5.90
<b>DISCONTINUITY</b>	
Jews (Moroccans)	10.56
Portuguese	11.00
French	12.39
Algerians	13.27
Egyptians (Siwa)	13.66
Sardinians	14.04
Moroccans (El Jadida)	14.31
Spaniards	14.98
Berbers (Souss)	15.98
<b>DISCONTINUITY</b>	
Greeks	19.42
San (Bushmen)	20.56
Basques	28.85
Japanese	30.25

**Table 3**

sponding to Turks-Jews (Morocco) ( $10.56 \times 10^{-2}$ ). The genetic distances show another discontinuity between Berbers (Souss) and Greeks ( $15.98 \times 10^{-2}$  vs.  $19.42 \times 10^{-2}$ ) further supporting that the latter have a distant relationship with Mediterranean populations, as previously described (17, 18), and cluster together with San and Japanese as outliers. In fact, Greeks have been shown to have a substantial sub-Saharan admixture (19). The Basques although close to Iberians and North Africans (9) are distant to Turks, probably because Basques represent a relatively homogeneous genetic isolate in comparison to the diverse Turks. Also, Egyptians are not clustered together with either western or eastern Mediterraneans in the tree (Fig. 3); however, the genetic distance data include this population as a western Mediterranean group (Table 3). Probably, the Egyptian sample from Siwa Oasis is closer to North African Berbers than to Middle East people. These data and previously re-

ported analyses show that Greeks do not relate to other Mediterraneans (17); neighbor-joining and genetic distances data indicate that Greeks are not related to Turks. The HLA-DR-DQ correspondence analyses (Fig. 4) correlate with those obtained with genetic distances and neighbor-joining trees: Turks cluster within the eastern Mediterraneans, including Kurds and Armenians, linked to western Mediterraneans while Greeks, San and Japanese form an outgroup. Taking all our different types of data analyses together, Turks, other Anatolians (like Kurds and Armenians) and Iranians appear as belonging to the older Mediterranean substratum, included within the eastern Mediterranean group. Kurds' genetic distance to Turks is  $5.90 \times 10^{-2}$ ; this together with their correspondence analysis (Fig. 4) suggests that Kurds are also integrated within the older Mediterranean substratum (see below, haplotypes). More Kurds should be analyzed in the future.

#### HLA-A, -B, -DR and -DQ linkage disequilibria in Turks and Kurds (Tables 4 and 5)

HLA Turkish haplotypes have been defined for the first time and allow us to compare them with those previously reported in other populations (Tables 4 and 5). HLA-DR-DQ and A-B two-loci linkage disequilibrium data (Table 4) show that two specific combinations

(A24-B44 and DR11-DQ7) have the highest frequency (more than three times) compared to the other two-loci combinations, possibly reflecting an ancient founder effect. These A-B associations are mainly present in Mediterraneans and the other ones found at lower frequency, like A26-B38, A11-B52 and A25-B18, are also present all over the Mediterranean area (4, 10, 20, 21).

The HLA-A-B-DR-DQ extended haplotypes found in the Turkish population (Table 5) reflect a basic Mediterranean background (see Table 5 and footnote). The most frequent haplotypes are: A24-B51-DR11-DQ7 also found in Italians (10); A23-B49-DR11-DQ7 is mainly present in Mediterraneans (10), A2-B50-DR7-DQ2 is also found in Mediterraneans (11, 22); A2-B8-DR3-DQ2 is also present in Mongolians and Central Europe (10); A2-B18-DR11-DQ7 is a characteristic Mediterranean haplotype (10, 20). Other low-frequency haplotypes present in Turks are also shared with Mediterraneans (10), like A1-B35-DR11-DQ7, A1-B44-DR11-DQ7, A2-B51-DR3-DQ2, A26-B38-DR4-DQ3 and A26-B38-DR11-DQ7; the last two are characteristic of Jewish populations (23).

Kurds show mostly Mediterranean haplotypes. A3-B35-DR4 (3.6%) found in Armenians (3%) (10); A2-B51-DR11 (3.6%) found in Armenians (2.1%) (10); B52-DR15 (3.6%) found in Iberians and North Africans (4, 20) and B7-DR10 (3.6%) found also in Algerians (0.9%) (4). Other lower frequency Kurd haplotypes are A26-B38 also

**HLA-A-B, B-DR and DR-DQ two-loci haplotypes with significant linkage disequilibrium ( $P < 0.05$  in all cases) in the Turkish population**

*Table 4*

Haplotype	HF	LD	RLD	Haplotype	HF	LD	RLD
<b>A-B</b>				<b>DR-DQ</b>			
A24-B44	19.5	8.21	0.46	DR11-DQ7	30.0	14.0	0.75
A23-B49	3.0	2.45	0.65	DR3-DQ2	9.2	7.0	0.97
A26-B38	1.5	1.01	0.40	DR4-DQ3	8.9	3.0	0.43
A30-B13	1.1	0.92	0.83	DR7-DQ2	8.9	6.0	0.72
A11-B13	0.9	0.58	0.12	DR13-DQ6	6.1	5.0	1.00
A1-B57	0.6	0.51	0.47	DR15-DQ6	4.8	4.0	0.95
A11-B52	0.6	0.49	0.34	DR14-DQ5	4.4	4.0	1.00
A25-B18	0.6	0.55	0.49	DR1-DQ5	3.3	3.0	0.87
				DR16-DQ5	2.4	2.0	0.95
<b>B-DR</b>							
B51-DR11	7.4	2.00	0.21				
B50-DR7	2.0	1.00	0.29				
B49-DR14	1.3	1.00	0.25				
B27-DR9	1.1	1.00	0.34				
B60-DR13	1.1	1.00	0.27				
B13-DR14	0.9	1.00	0.16				

HF, haplotype frequency ( $\times 100$ ); LD, linkage disequilibrium ( $\times 100$ ); RLD, relative linkage disequilibrium.

**Most frequent HLA-A, -B, -DR, -DQ extended haplotypes in the Turkish populations. HF: Haplotype frequency**

Haplotype (A-B-DR-DQ)	HF (%)	Possible origin
A24-B51-DR11-DQ7 <sup>1</sup>	5.3	Mediterranean
A23-B49-DR11-DQ7 <sup>2</sup>	2.6	Mediterranean
A2-B50-DR7-DQ2 <sup>3</sup>	1.3	Euroasiatic
A24-B35-DR3-DQ2 <sup>4</sup>	1.3	Mediterranean
A2-B8-DR3-DQ2 <sup>5</sup>	1.1	Euroasiatic
A2-B18-DR11-DQ7 <sup>6</sup>	1.1	Mediterranean
A1-B35-DR11-DQ7 <sup>7</sup>	0.9	Mediterranean/Central Europe
A26-B38-DR4-DQ3 <sup>8</sup>	0.9	Jewish

<sup>1</sup> This haplotype has been found in Italians (HF: 0.5) (10).

<sup>2</sup> Only found in Italians (HF: 0.4); the partial haplotype B49-DR11-DQ7 is present in Armenians (HF: 3.5), Albanians (HF: 1.7) and Germans (HF: 1.0) (10).

<sup>3</sup> Present in Mongolians (HF: 3.2), Manchu (HF: 2.2), Spaniards (HF: 1.2) and Italians (HF: 0.5) (10).

<sup>4</sup> Found as B35-DR3-DQ2 in Uralics (HF: 3.1), Sardinians (HF: 2.8), Greeks (HF: 1.9), French (HF: 0.9) and North American Negroids (HF: 0.7) (10).

<sup>5</sup> Haplotype found in Mongolians (HF: 2.8), Austrians (HF: 2.2), German (HF: 1.2), Greeks (HF: 1.2), and Italians (HF: 0.7) (10).

<sup>6</sup> Found in Greeks (HF: 4.0), Albanians (HF: 3.9), Yugoslavians (HF: 3.5), Romanians (HF: 2.4) and Spaniards (HF: 1.9) (10).

<sup>7</sup> The partial haplotype B35-DR11-DQ7 is present in South African Negroid (HF: 2.1), Albanians (HF: 3.3), Armenians (HF: 5.0), Austrians (HF: 4.0), French (HF: 1.1), Germans (HF: 3.4), Greeks (HF: 2.6), Italians (HF: 6.8), Spaniards (HF: 1.3), Hungarians (HF: 3.9), Indians (HF: 3.1), Timorese (HF: 2.1) and Caucasoid Australians (HF: 3.7) (10).

<sup>8</sup> Found in Jews and Portuguese as one of the most frequent (9, 23).

**Table 5**

found in Jews (23) and Turks (present paper); A30-B13 also found all over the Mediterranean area (10); A2-B8-DR3 found also in Turks (present paper); A26-B44-DR5 found also in Algerians (4) and A24-B44-DR7 also found in Basques (10).

**Discussion**

Close cultural and circum-Mediterranean contacts have been frequent during the last 10,000 years (24–33). The best documented long-distance travelers (i.e. Cretans, Mycenaean, Phoenicians, Greeks and Romans), who set up colonies all over the Mediterranean Sea coast probably did not mix extensively with autochthonous populations, because they were mostly dedicated to trading and war.

**Turks HLA profile reflects that of ancient Anatolians**

Anatolian development was quite distinct to Egypt and Mesopotamia. By 5400 B.C., Hacilar culture flourished in the South-eastern Anatolian Lake District. Fortified citadels were common in central and western Anatolia and also in Mycenae (nowadays Greece) by 3000

B.C. Probably, local developments (and not invasions) led to the Hittite Empire flourishing in the central Anatolian part and to the Arzawa Kingdom at the Aegean coast (1400 B.C.); others put Hittite origins (as autochthonous) back to the 3rd millennium B.C. (34). Still more scholars identify Hittites with Indo-European invaders who spoke a different language (1400–1200 B.C.). The “Sea People” led to the fall of both Hittite and Arzawa cultures after 1200 B.C. Later, Neo-Hittites (in northern Syria), Assyrians and Arameans held power through different times and parts of Anatolia. By 800 B.C., a new Kingdom appeared: Urartu, in the Armenian mountains. Urartu rule was destroyed by Assyrians; also, Cimmerians from southern Russia broke through the Caucasus and descended on Urartu (714 B.C.), but were withheld by an Assyrian-Anatolian coalition. Medes (from Iran) and Babylonians invaded Anatolia in the 6th century B.C.; the former entered the Armenian mountains (northwards) while the latter confronted with central Anatolian people (Lydians). Peace followed and Persians led by Cyrus defeated the Medes and overran Anatolia bringing to an end the Neo-Hittite and other so-called pre-Indo-European speaking people rule (5th century B.C.) (34). Alexander the Great expelled the Persians from Anatolia (4th century B.C.) and after his death it was inherited by his general Selyuk. Romans and to a lesser degree Muslims took over Anatolia until the Turks, coming from central Asia (Altai mountains), invaded Anatolia in 1055 A.D. and finally took Istanbul in 1453 A.D.

In spite of all these varied invasions, present day Turkish HLA profiles reflect an old Mediterranean substratum, not very different from Jewish or Lebanese (see Fig. 3, Table 3). It seems that the genetic input coming from the Altai mountains regions was comparatively low. Other genetic studies using classical allozyme markers also support that Anatolians belong to the older Mediterranean substratum (35). Our results cast doubts on the “out of Anatolia” origin for the Hittites and related people who are considered by some on a linguistic basis as Indo-Europeans immigrants. Most of the Anatolian invasions detailed above may have been accomplished by a so-called “elite” dominance process (36–38).

**Kurds are also a part of the older Mediterranean stock**

HLA genetic distances and haplotypes observed in Kurds place them among the Middle East-Mediterranean stock; present-day Turkish and Kurdish people seem originally to belong to a similar ethnic group. The lack of any other genetic data about Kurds makes it necessary to perform further studies. However, their characteristic Mediterranean HLA haplotypes make any other origin for the Kurds unlikely. Kurdish tribes have traditionally lived in the mountains. The Halaf culture “autochthonous” people (6000 B.C.) (Tell Halaf, Southern Diyarbakir, Turkish Kurdistan (39–41) (see Fig. 1)

and the Hurrians (2000 B.C.), who spoke a Caucasian (non-Indo-European) language may be the present-day Kurds more ancient substratum (39). Urartu, Mushku, Urkish, Subara, Bani, Guti and Manna city states evolved from the Hurrian society. Mittani political power appeared by 1500 B.C. around nowadays Diyarbakir (Turkish-Kurdistan); it is not clear whether it was or it was not an autochthonous development. By 1200 B.C. Medes and other political powers invaded Hurrian cities (and the entire Mittani) and by 850 B.C. the old language (probably from the Dene Caucasian group, 37, 38) had changed to a so called Indo-European one throughout the mountains, giving rise to the present day Kurdish language. Kurdish historians consider themselves as coming from Medes (42) and the first recorded name of Kurds (Kurti) was given around 1000 B.C. by Assyrians to people living in Mt. Azu or Hizan (near Lake Van, easternmost Turkey). "Kurts" are also mentioned by early classical historians like Polybios (133 B.C.) and Strabo (48 A.D.). Kurds remained as "the Mountains People" through Persian, Greek and Roman Anatolian rule.

Our present Kurdish genetic HLA analysis show that Kurds' genetic distances (Table 3), haplotype (see Results section) and correspondence analyses (Fig. 4) place Kurds among eastern Mediterraneans, suggesting that they belong, like Turks, to a very old Anatolian substratum. These data are also supported by the above-detailed historical data.

## Armenians

Armenians believe that they come from the old Urartians (see Fig. 1), who are one of the groups of Hurrian tradition (see above; 39) that achieved maximum regional power by 900 B.C. Assyrians first (from the West) and Scythians from southern Russia conquered Urartu by 600 B.C. Present day Armenians have their own alphabet and speak an Indo-European language probably imposed by the Medes (whose language is completely unknown). Persian was followed by Roman rule (Alexander the Great did not invade Armenia). The Armenian people has remained Christian ever since. Armenians were attacked and deported (2) between 900 and 1400 A.D. by Byzantium Romans, Turks, and Muslims. An Armenian King-

dom was founded by displaced Armenians in the Mediterranean coast between what is now Turkey and Syria. Later, Armenian people come back to the southern Caucasus pushed by Turks (2). Meanwhile, the Armenian Diaspora had led many Armenians to Istanbul, Macedonia, Bulgaria, Poland, Italy and France.

At the beginning of the 19th century 3 million Armenians were living either in the Turkish or the Persian Empire (15% lived outside the Armenian region). They were mixed with Kurds, Georgians, Turks and Azeris from Diyarbakir/Erzurum (West) to Ganya (East); also, Mediterranean coastal Armenian people remained. Mostly, Christianity and its language (with its own alphabet from 400 A.D.) maintained Armenian identity. Russia helped Armenians to return to the present day Armenia after war with Turks and Kurds (1915 A.D.). High Karabaj region was included in Azerbaijan in spite of its 80% Armenian population (2) and remains still a disputed land.

The haplotypes A33-B14, B35-DR11 and B49-DR11 show that Armenians belong to the older Mediterranean substratum. Also, their genetic distances are very close to Turks (Table 3) and also to Kurds. HLA dendrograms (Figs 2 and 3) and correspondence analysis (Fig. 4) show how close Armenians are genetically to Turks, and also to Kurds. The Armenian Diaspora may have displaced a common Armenian haplotype A33-B14 to all over the Mediterranean, including to the westernmost part (Iberian, Morocco and Algeria) (4, 18, 20).

In summary, it seems than Turks, Kurds and Armenians are very close genetically and all of them seem to have been living in the area for many millennia, because typical Asian HLA genes are not found (39, 42–44). Probably, small different "elite" invaders imposed different languages on these three different groups who originally spoke a similar pre-Indo-European language (36). Armenians (Urartu 900 B.C.) and Kurds ("Kurti") probably were initially splits of Hurrian groups (2nd millennium – 1st millennium B.C.), the Kurds remaining mainly at the mountains. Thus, the postulated Asian invasion (1200 B.C.) is not noticed on our HLA genetic studies. Finally, the cause that Greeks are genetically different from other Mediterraneans (Figs. 3 and 4) is that a part of their genetic pool comes from sub-Saharan Africa. Greeks are related to Anharic, Oromo and Fulani groups from Ethiopia and Burkina-Faso (19).



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