Research Report

The Northern Migrations from a drying Sahara (6,000 years BP): cultural and genetic influence in Greeks, Iberians and other Mediterraneans

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(Received 24 April 2021; Accepted 10 May 2021; Published 20 May 2021)

Abstract - Greeks have a Sub-Saharan gene input according to HLA and other autosomic markers. Iberians, Canarians, and North Africans show a close genetic relatedness. This is concordant with a drying humid Sahara Desert, which may have occurred about 6,000 years BC, and the subsequent northwards emigration of Saharan people may have also happened in Pharaonic times. Present study confirms this African gene input in Greeks according to 12th HLA International Workshop data, which was studied some years before by us. This genetic input into Atlantic and Mediterranean Europe/Africa is also supported with Lineal Megalithic Scripts in Canary Islands (as well as in Iberia) together with simple Iberian semi-syllabary rock inscriptions both at Canary Islands and Ti-m Missaou (Algeria, Central southern Sahara). Lineal African/European scripts are found in some language scripts like Berber/Tuareg, Iberian, Runes, Etruscan, Bulgarian (Sitovo and Gradeshnitza, 6,000 years BP), Italian Old Scripts (Lepontic, Venetic, Raetic), Minoan Lineal A, and other Aegean scripts. The possibility that Megalithic Lineal Scripts have given rise to these languages lineal writing is feasible because admixture of languages rock scripts and Megalithic Lineal Scripts may be found. Thus, resistance of Canarian aborigines (Guanches) to Cartago, Rome and Arabs left a bulk of Canarian-Saharan information which is used to study both Saharan and Canarian Prehistory, and also Atlantic and Mediterranean beginning of European and other civilizations: this preserved prehistoric inheritance may be named the "Saharo-Canarian Circle" of prehistoric knowledge. Also, linguisticsepigraphy, physical anthropology ,archaeology and domesticated cattle shows a close North Africa-Iberia Mesolithic/Neolithic relationship and demonstrates that the demic diffusion model does not exist in Iberia. Also, Tassili Sahara paintings of domesticated cattle appear 1,000 years before that agricultural practices started at Middle East.

Keywords: Greeks, Macedonians, Sahara, Africa, Iberia, HLA, Genetics, Spaniards, Portuguese, Berbers, Algerians, demic, diffusion, Canary Islands, Lanzarote, Malta, Cart-ruts, Quesera, Cheesboard, Iberian, language, Guanche, Usko-Mediterranean, Phoenicians

Introduction

Jean Dausset at 5th HLA Anthropology Workshop (Evian, France 1972) showed that HLA was useful as a very polymorphic autosomic marker for studying origin, relatedness and unrelatedness of human populations (Degos & Dausset 1974). In a systematic study of Mediterranean populations with HLA-DRB1 alleles, we unexpectedly found that Greek populations behaved as outgroups with respect to other Mediterraneans (Arnaiz-Villena et al. 2001a). Further looking into these results, we found that some Greek HLA-DRB1 alleles were shared with Sub-Saharan populations and not with other Mediterraneans. Greek HLA typing had been done by Greek laboratories in the context of 12th HLA Workshop (Bodmer et al. 1997; Clayton & Lonjou 1997; Hammond et al. 1997). These published Workshop results were controversial when further analysed (Arnaiz-Villena et al. 2001a; 2002) in spite that other autosomic markers were found to support that Greek gene pool have more in common with Sub-Sahara Africans than other Mediterraneans (Dörk et al. 1998; Padoa et al. 1999). In addition, other independent authors also found that HLA genes in Greeks were shared with Sub-Saharans (Hajjej et al. 2006) and behaved as outgroups of the Mediterranean populations cluster. Finally, these results have lately been ignored in scientific literature and another single publication from a Greek group established that apparently Greek HLA-DRB1 genes were not shared with Sub-Saharans (Papassavas et al. 2000). We have now decided to put up and repeat all analyses and data sources in order to fix the question whether Greeks share or not HLA-DRB1 genes with Sub-Saharan Africans and whether they behave as an outgroup of other Mediterranean populations or not according to the double-blinded results given by Greek laboratories and their double blinded HLA-DRB1 typing assigned by the Central Analysis laboratories of 12th HLA Workshop (Rennes and Oxford) (Bodmer et al. 1997; Clayton & Lonjou 1997; Hammond et al. 1997).

In the present paper, we aim to: 1) further analyse the contradictory Greek genetic results in order to definitive clarify the origin of Greek HLA-DRB1 alleles genetic and cultural bases in comparison with Mediterranean and African populations, and 2) summarize ours and others findings that show African genetic relatedness with Iberians since Prehistory, demonstrating that a gene flow existed from Africa to southern Europe

at different times and that this gene flow could also be bidirectional, i. e.: also from Europe to Africa (Arnaiz-Villena *et al.* 1999a, 1999b; 2001a, 2001b; 2002).

Material and Methods

- Sampling

A) Specific HLA-DRB1 allele frequencies of Greeks and Sub-Saharan populations obtained from 12th International Histocompatibility Workshop data (Bodmer *et al.* 1997; Clayton & Lonjou 1997; Hammond *et al.* 1997) were used for our study (Arnaiz-Villena *et al.* 2001a). Origin of these and other populations is shown in Table **1**. Greek samples came from Attika (Bodmer *et al.* 1997, pages 275, 676, 677, 678; Stavropoulos-Giokas *et al.* 1997, page 325), Cyprus (Bodmer *et al.* 1997, pages 275, 676, 677, 678; Stavropoulos-Giokas *et al.* 1997, page 325), and Aegean Islands (Bodmer *et al.* 1997, pages 275, 676, 677, 678; Stavropoulos-Giokas *et al.* 1997, page 325). Total number of Greek individuals was 295 (Attika Greeks: 96; Aegean Greeks: 98; Cypriot Greeks: 101). 12th Workshop Thrace Greeks (Pomaki) were left out from our study (Stavropoulos-Giokas *et al.* 1997, page 325) because a possible mixed origin. Also, Pontii Greeks (individuals from North Anatolia, Turkey, Greek speakers) were left out because of their uncertain origin.

B) Other HLA-DRB1 Greek allele frequencieswere obtained and published by (Papassavas *et al.* 2000) from an undetermined Greek origin (see Table **4** and Typing section below). **Total number of Greek individuals was 246.**

C) Other populations were either HLA-DRB1 typed in our laboratory or taken from other authors publications in order to perform relatedness analyses (Table 1).

- Typing

A) Populations included in the 12th International Histocompatibility Workshop were **double-blinded** typed in different laboratories and most assigned typing was decided at the Central Workshop Laboratory (Rennes, France). Some participant labs had sampling facilities but not typing facilities, and other ones vice versa; 58 laboratories offered samples to other laboratories for typing and 50 laboratories asked for samples to test (see Appendix I, page 31). These 12th HLA Workshop Greek typings were the ones used by us for the present and previous papers (Arnaiz-Villena *et al.* 2001a); Sub-Saharan HLA typing were also taken from 12th HLA Workshop data (Table 1). Method of HLA Class II typing was SSO-PCR (Stavropoulos-Giokas *et al.* 1997, page 325).

- B) Greek individuals sample from (Papassavas *et al.* 2000), HLA class II typing was carried out as follows (literally taken from this reference; Material and Methods section): "Two hundred forty-six unrelated random healthy individuals originated from different parts of Greece entered the study. The age ranged between 20 and 59 years. The population consisted of 114 and 132 females. Peripheral blood was drawn after informed consent. All individuals were of Greek origin and their parents and grandparents were born in Greece". HLA high resolution typing was performed by PCR-reverse dot blot method.
- C) Other populations analysed in our own laboratory and in others are included in the comparison. Some of them have been re-typed for DRB1 alleles following a PCR-SSOP-Luminex method for the present study. Other laboratory typing protocols have been used in different laboratories (Table 1).

- Statistical analyses

Phylogenetic trees (dendrograms) were constructed with the allelic frequencies by applying the Neighbour-Joining (NJ) method (Saitou & Nei 1987), with the genetic distances between populations (Nei 1972) and using DISPAN software containing the programs GNKDST and TREEVIEW (Nei 1973; Nei *et al.* 1983). A two-dimensional representation was carried out using the VISTA v5.02 computer program (Young & Bann 1996). Correspondence analysis comprises 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 allelic frequency

variance among populations (similarly to classical principal components methodology) and on the display of a statistical projection of the differences.

	Region and population	n	Reference
1	Macedonians	172	Arnaiz-Villena et al. 2001a
2	Moroccans	98	Gomez-Casado et al. 2000
3	Berbers (Souss)	98	Izaabel et al. 1998
4	Moroccan Jews	94	Roitberg-Tambur et al. 1995
5	Spaniards	176	Martinez-Laso et al. 1995
6	Spanish Basques	80	Martinez-Laso et al. 1995
7	French	179	Imanishi et al. 1992
8	Algerians	102	Arnaiz-Villena et al. 1995
9	Sardinians	91	Imanishi et al. 1992
10	Italians	184	Imanishi et al. 1992
11	Jews Ashkenazi	80	Martinez-Laso et al. 1996
12	Jews Non-Ashkenazi	80	Martinez-Laso et al. 1996
13	Cretans	135	Arnaiz-Villena et al. 1999a
14	Greeks (Attika)	96	Clayton & Lonjou 1997 (12 th HLA Workshop)
15	Greeks (Aegean)	98	Clayton & Lonjou 1997 (12 th HLA Workshop)
16	Greeks (Cyprus)	101	Clayton & Lonjou 1997 (12 th HLA Workshop)
17	Lebanese (NS)	59	Clayton & Lonjou 1997 (12 th HLA Workshop)
18	Lebanese (KZ)	93	Clayton & Lonjou 1997 (12 th HLA Workshop)
19	Oromo	83	Clayton & Lonjou 1997 (12 th HLA Workshop)
20	Amhara	98	Clayton & Lonjou 1997 (12 th HLA Workshop)
21	Fulani	38	Clayton & Lonjou 1997 (12 th HLA Workshop)
22	Rimaibe	39	Clayton & Lonjou 1997 (12 th HLA Workshop)
23	Mossi	42	Clayton & Lonjou 1997 (12 th HLA Workshop)
24	San (Bushmen)	77	Imanishi <i>et al</i> . 1992
25	Senegalese	192	Imanishi et al. 1992

Table 1. Populations used for comparisons performed in the present work.N = number of individuals analysed for each population. See the references Bodmer et al. 1997; Clayton
& Lonjou 1997; Hammond et al. 1997.

Results

Greeks and presently Sub-Saharan African genes

In order to clarify the possible origin of the 12th HLA Workshop Greek populations, which appeared as outgroups in both Neighbour-Joining and correspondence analysis, (results not shown; see Arnaiz-Villena *et al.* 1999a; Gomez-Casado *et al.* 2000), HLA-DRB1 alleles were only studied in Greeks and also searched for in other nearby populations including. Some of these alleles were found mostly in Sub-Saharan populations and sporadically in non-Mediterranean populations around the world (Dos Santos *et al.* 2016). The populations in which the highest frequencies of these alleles have been found are mostly from Ethiopia (Amhara and Oromo) and West Africa (Mossi, Fulani and Rimaibe) (see Discussion, Table 2). Then, they were included in the Mediterranean relatedness analysis: Greeks still behave as an out-group and cluster with the above mentioned Sub-Saharan groups (**Figs. 1** and **2**).

The Neighbour-Joining phylogenetic tree generated, as well as the correspondence analysis performed support this genetic relationship (**Figs. 1** and **2**). These groupings are observed between all the Greek populations included in our study with the 12th International Workshop data and the Sub-Saharans (data taken from the same 12th HLA Workshop, see Table **1**). Other Mediterranean populations, geographically close to Greece, are genetically placed more distant (**Figs. 1** and **2**). There is no close relationship between the Greeks and the Senegalese/South African blacks or the Bushmen (San) (**Fig. 2**) (Bantu expansion, McEvedy & Jones 1978). Close long tree branches do not mean relatedness between branches but that they are very different to each other and are outgroups far from other dendrogram populations (**Fig. 1**); Figure **2** places Senegalese and San-Bushmen as out-groups.

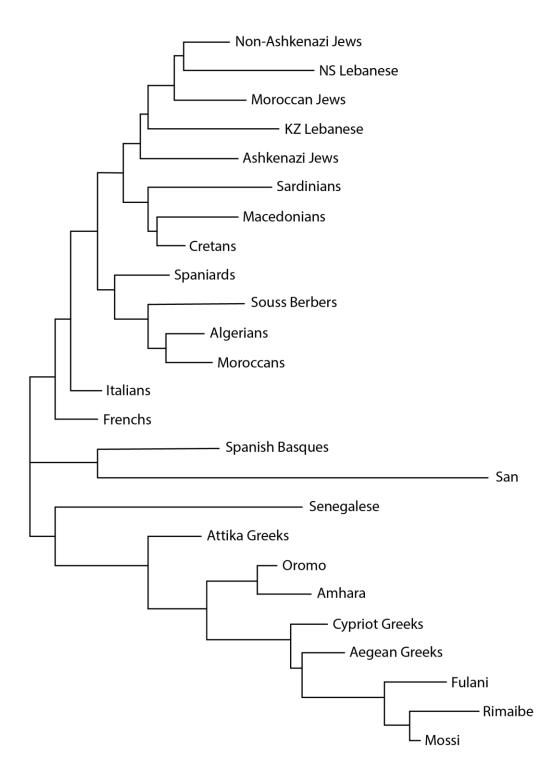


Fig. 1 Dendrogram performed with Neighbour-Joining method showing genetic relatedness between Attika, Aegean and Cyprus Greeks and other Mediterranean and Sub-Saharan populations.

Genetic distances between populations were calculated with GNKDST software using high-resolution HLA-DRB1 frequencies (Bodmer *et al.*, 1997, pages 676, 677, 678; Clayton & Lonjou 1997; Hammond *et al.* 1997; Bootstrap test showed values of 100 in all of the nodes after 1000 replicates.

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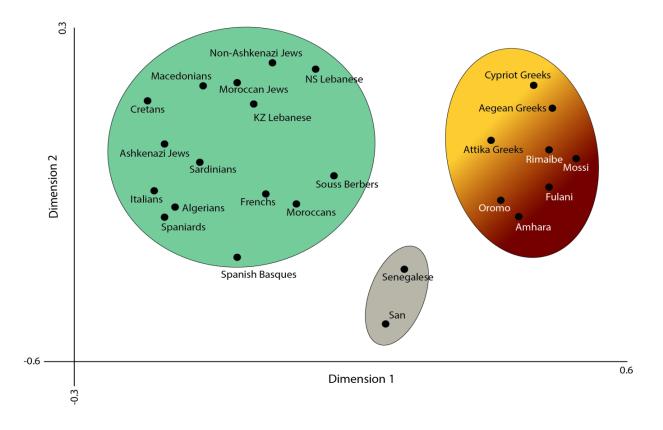


Fig. 2. Correspondence analysis showing a global view of the relationship between Greeks and other Mediterranean and Sub-Saharan populations. The analysis was performed using HLA-DRB1 high-resolution frequencies.

Discussion

There is no doubt that North Africa and Southern Europe gene flow has occurred since Prehistory, probably in both directions. However, Sahara extreme changes to desert, which started about 6,000 years BC, suggest that South to North gene (people) flow was more important. This has brought cultural and anthropological consequences. Genetically, a Iberians and Maghreb inhabitants close relationship is found by several different groups with different methodology (Arnaiz-Villena et al. 1999a; 1999b; 2002; Currat et al. 2010; Botigue et al. 2013; González-Fortes et al. 2019). Genetic differences between Western Mediterraneans and North West Africans and Canary Islanders are very scanty (Arnaiz-Villena et al. 2015; 2017; Hajjej et al. 2018); these latter groups of people belong to a very related cultural, genetic and geographic population (Arnaiz-Villena et al. 2001b; 2001c; 2001d; 2002; 2015; 2017; 2019a; Medina & Arnaiz-Villena 2018a; 2018b). In addition, a strong very old (probably Megalithic) culture and thus genetic Atlantic relationships are established among Western Africa, Europe and Canary Islands (Arnaiz-Villena et al. 2018; 2019a; Medina & Arnaiz-Villena 2018a; 2018b). In contrast, Eastern-North Africa, Saharan migrations and European relationships are less studied (Arnaiz-Villena et al. 1999b; 2001a; 2002) but they obviously existed. In that context, Greek and Sub-Saharan populations genetic relationships must be interpreted. Europe and Greece immigration from Africa has occurred since Prehistory (see above), but also during Egyptian pharaonic times a Black dynasty with their followers were expelled ad established in Greece. Indeed, ancient Greeks believed that their religion and culture came from Egypt (Bernal 1987; Herodotus 1989). Also, Herodotus (Herodotus 1989) states that the daughters of Danaus (who were black) came from Egypt in great numbers to settle in Greece.

Western Europe and North Africans: Genetics, Archaeology and physical Anthropology

Several studies (Degos & Dausset 1974; Cambon-Mouzon *et al.* 1982) and our own previous research (Rodríguez-Córdoba *et al.* 1981; Arnaiz-Villena *et al.* 1981; Regueiro & Arnaiz-Villena 1988) have pointed out that the HLA-A30-B18-DR3-BF*F,1 haplotype was a marker for Basques, Sardinians and Spaniards. Its frequency in other

populations was significantly lower, except for Mediterranean North Africans; this suggested a paleo-North African/Iberian origin for part of the Basque gene pool (Arnaiz-Villena *et al.* 1981). Also, complete HLA data on Basques and Spaniards (Martínez-Laso *et al.* 1995) have been analysed by DNA indirect sequencing and compared with data from North African populations (Algerians) with at least 70% Berber component (Julien 1951; Benmamar *et al.* 1993; Rachid 1994; Arnaiz-Villena *et al.* 1995).

Skeletal studies from Mesolithic and Neolithic Iberian samples have been extensively carried out by Meiklejohn et al. (1984), Lubell et al. (1994), Lalueza-Fox (1996), and Jackes et al. (1997a). Jackes et al. (1997a) analysed the agricultural transition by using dental and skeletal variables obtained from partial data. They performed an exhaustive analysis of their own and other data on Mesolithic and Neolithic Iberian skeletal parameters. A scatter plot of 8 craniometric variables from 20 skeletons from Iberia (Spain: Majorca, Tarragona, Basque Country, Catalonia, Cantabria, Barcelona, Burgos, Castilla, Andalusia, Granada; Portugal: Eira, Pedrinha, Escoural, Melides, Cabezo da Aruda, Moita de Sehastiago) showed that there was no significant change in the studied variables between Neolithic and Mesolithic samples. Both, Lalueza-Fox (1996) and Jackes et al. (1997a, 1997b) agreed that stature is similar in Neolithic and Mesolithic Iberian skeletons. Dental caries rates do not show a discontinuity either, and the observed reduction rate in the Neolithic shows complex dietary changes that started during the Mesolithic and continued into the Neolithic (Lubell et al. 1994). Thus, the demic diffusion model put forward by Cavalli-Sforza et al. 1994, which implies an important (or complete) replacement of the population, is not sustainable for Iberia, where no revolutionary way of life changes or physical anthropometry and diet differences were found.

In conclusion, the demic diffusion model hypothesizes that Neolithic farmers who were coming from the Middle East were slowly reaching Mesolithic Western Europe **DOES NOT HOLD** (Cavalli-Sforza 1996). First, there is no evidence of Neolithic replacement of people on the Iberian Peninsula. On the contrary, the suggested conformity of Iberian craniometric data to a demic diffusion model simply does not exist (Cavalli-Sforza 1976); Mesolithic and Neolithic bones show clear continuity (Jackes et al 1997b). Second, genetic data in North Africans, Spaniards, Basques, Portuguese and Cretans (Arnaiz-Villena *et al.* 1981; 1997; 1999b; Corte-Real *et al.* 1996; Izaabel *et al.* 1998) support substantial gene flow from paleo-North African

populations to Iberia. Also, common extended HLA haplotypes between present day North African and Iberian populations, including Basques, exist (Arnaiz-Villena et al. 1997; Izaabel et al. 1998). Third, archaeological studies at the mouth of the Guadalquivir River (La Marismilla, Sevilla) (Escacena-Carrasco 1996) showed that domesticated bovines and cats came with people from Africa about 5,000 years ago; in addition, the predynastic Egyptian El-Badari culture (4,500 years ago) is similar to many southern Iberian Neolithic settlements in pottery and animal domestication (Escacena-Carrasco 1996). Cardial impressed pottery is common and contemporary in Western Europe and North African coasts. The coastal distribution of cardial impressed pottery in Western Mediterranean Europe (Lewthwaite 1986) and across the Maghreb (Gilman 1992; Lubell et al. 1992) provides good evidence of circum-Mediterranean contacts by sea. Both El-Badari and Iberian Neolithic people probably came from the drying Sahara area, forced to migrate since about 6,000 years BC (McCauley et al. 1982; Chandan & Peltier 2020). Indeed, Tassili cave paintings in the Middle of the Sahara Desert (south-eastern Algeria) show domesticated bovine about 1,000 years before documented Neolithic agricultural practices starting in the Middle East (Cavalli-Sforza 1996), and Sahara also contains Iberian lineal semi-sillabary writing lineal characters (Arnaiz-Villena et al. 2021). Fourth, the Iberian language has been transcripted and translation proposals put forward and have been found to be similar to Etruscan and Minoan Linear A (Arnaiz-Villena & Alonso García 1998; 1999; 2008; 2009). Basque (and its Spanish translation) has been the Rosseta stone. In fact, Basque and Old Iberian language numerals are almost identical (Orduña-Aznar 2005; 2013; Ferrer i Jane 2009). The Basque language had also been related to North Caucasian and to Etruscan languages (Bengston 1991; Ruhlen 1991; Cavalli-Sforza et al. 1994; Arnaiz-Villena & Alonso-Garcia 2008; Arnaiz-Villena & Alonso-García 2009). Thus, the question that Jared Diamond posed to Terrell et al. 1998 - Do Terrell et al. believe all Europeans spoke a single tongue, Basque, until a few thousand years ago? – can be answered. The answer is: it is possible. Caucasians, Etruscans, and the first Minoans from Crete spoke a language similar to Basque and Berber; probably, the origin of this language came from the Saharan people who were forced to migrate northward in pre-Neolithic times when desiccation started (McCauley et al. 1982). Finally, it is noteworthy that Canary Islands aborigines or Guanches long survived invasions from Cartago, Rome and Arabs before Europeans defeated them (Arnaiz-Villena & Alonso-García 2001).

Allele	Greeks AF (%)		West Africans AF (%)			Ethiopia AF (%)		
DRB1	Attika	AegeanIslands	Cyprus	Mossi	Fulani	Rimaibe	Amhara	Oromo
03:05		2.5		0.8	0.2	0.8		
03:07		2.2	3.2	0.8	0.2	0.8	2.1	
04:11			0.4		0.6			
04:13	0.5	0.6	0.9				0.6	0.6
04:16		0.6	0.9				0.6	0.6
04:17			0.4		0.6			
04:20	0.1		0.4		0.6		0.6	0.6
11:10		2.9	1.9			0.3		0.2
11:12		2.9	1.9			0.3	0.4	0.2
13:04			0.9	0.7	1.4	1.1		
13:10			0.2	0.8	0.2	0.8		

 Table 2. Quasi specific HLA-DRB1 alleles found in Greeks in common with Sub-Saharan populations. AF: allele frequency.

Greeks and Sub-Saharans

Mediterranean Area was a densely populated region between Sahara Desert and European Ices by thousands of years after 10,000 years BC (Arnaiz-Villena *et al.* 1999b; 2002). This "Mediterranean" people (broad cultural sense) comprised a World stretch from Atlantic British and Canary Islands, Western Europe and Africa to North India, including Caucasus, big Persia and Egypt. A very important cultural input was most probably given by displaced Saharans (**Fig. 3**) to starting all Mediterranean Area civilizations. Thus, the "Classical Mediterranean Culture" was originated by Saharans, Atlantic Western Europeans, and Africans, Central and East Mediterraneans. It cannot be attributed only to Greece and Rome in the view of past and present scientific advances. In the case of Greece, it was unexpectedly found genetic relatedness with Sub-Saharans (Arnaiz-Villena *et al.* 2001a; Hajjej *et al.* 2006; Dörk *et al.* 1998; Padoa *et al.* 1999) which is not that odd taking into account cultural, genetic, physical anthropology and genetic relationship of Sub-Saharans/North Africans with Iberia and other Europeans. Table 2 shows Greek alleles in common with Sub-Saharans.

Table 3. Greek HLA-DRB1 allele frequencies taken from the data shown in 12 th
International Histocompatibility Workshop (n=295)

(Bodmer *et al.* 1997, pages 676, 677, 678; Clayton & Lonjou, 1997; Hammond *et al.* 1997). Alleles with Sub-Saharan origin are remarked in orange and specifically shown in Table 2.

Allele	F (%)	Allele	F (%)
DRB1*01:01	9,5	DRB1*11:04	15,4
DRB1*01:02	2,5	DRB1*11:06	1
DRB1*01:04	4,9	DRB1*11:08	3,6
DRB1*03:01	11,8	DRB1*11:10	4,8
DRB1*03:04	0,5	DRB1*11:12	4,8
DRB1*03:05	2,5	DRB1*11:G2	4,8
DRB1*03:07	5,4	DRB1*11:18	0,5
DRB1*04:01	3,2	DRB1*11:22	0,3
DRB1*04:02	3,2	DRB1*11:25	23,3
DRB1*04:03	1,1	DRB1*12:01	4,9
DRB1*04G1	0,9	DRB1*13:01	5,3
DRB1*04:05	1,1	DRB1*13:02	9,6
DRB1*04:07	0,5	DRB1*13:03	4,1
DRB1*04:08	0,5	DRB1*13:04	0,9
DRB1*04:09	1,5	DRB1*13:05	0,5
DRB1*04:11	0,4	DRB1*13:10	0,2
DRB1*04:13	2	DRB1*13:27	5,3
DRB1*04:15	0,3	DRB1*14:01	8,1
DRB1*04:16	1,5	DRB1*14:04	1
DRB1*04:17	0,4	DRB1*14:07	3,4
DRB1*04:20	0,5	DRB1*14:15	0,2
DRB1*07:01	19,5	DRB1*15:01	8,4
DRB1*08:01	1,7	DRB1*15:02	4,7
DRB1*08:03	0,4	DRB1*15:06	2,5
DRB1*08:04	0,2	DRB1*16:01	12,5
DRB1*08:05 DRB1*09:01	1,7 0,9	DRB1*16:02 DRB1*16:04	2,2 9
DRB1*09:01 DRB1*10:01	0,9 9,8	DRB1*16:04 DRB1*16:08	9 4,6
DRB1*11:G1	9,8 9,1	DRB1*NULL	4,0 3,6
DRB1*11:02	1		-,~

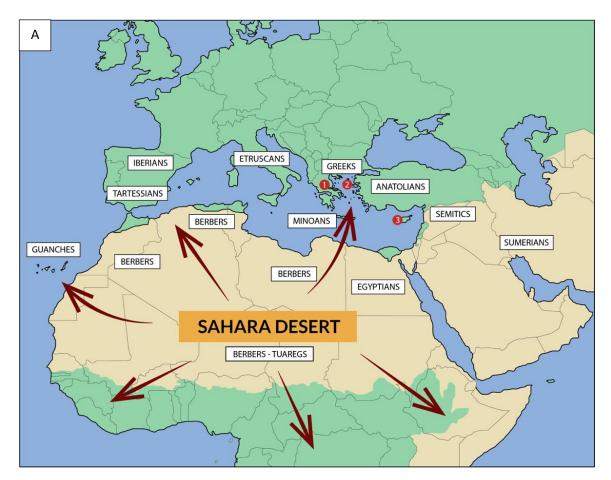
Table **3** shows which Greek HLA-DRB1 alleles were found to be shared and relatively frequent with Greeks; this work was double-blinded performed by several World laboratories I the frame of participants in the 12th International HLA Workshop (See Material and Methods section above; Bodmer *et al.* 1997; Cayton *et al.* 1997; Hammond *et al.* 1997).

Therefore, it is a solid finding. Curiously, Papassavas *et al.* (2000) (Table 4) did not find any of these Greek/African shared alleles with fewer number of Greek individuals of unknown specific origin, 153 less than in 12th HLA Workshop. If they belong to the Workshop work (they are coincidental in time and main authors; see Stavropoulos-Giokas *et al.* 1997, page 325). Thus, a number of Greek samples sent to 12th Workshop (n=295, Table 3 *vs.* n= 246, Table 4) might have been left out by many reasons or be altogether different in Papassavas *et al.* (2000) with Greeks of undetermined origin. In any case, we still put forward that Greeks/Africans genetics is shared (Arnaiz-Villena *et al.* 2001a; Hajjej *et al.* 2006; Dörk *et al.* 1998; Padoa *et al.* 1999) and stick to 12th Workshop results regarding to HLA. This Greek/African genetic sharing is not unusual in the more extensive studies done in Iberia, Canary and other Atlantic Islands and North Africans (Arnaiz-Villena *et al.* 2017; 2019b; Hajjej *et al.* 2018).

Table 4. HLA-DRB1 frequencies found in Greek populations as shown in Papassavaset al. (2000) (n=246).

It is striking the lack of all Sub-Saharan alleles that have been found in Greeks at the 12th International HLA Workshop (see Table 3).

Allele	F (%)	Allele	F (%)
DRB1*01:01	11	DRB1*11:02	2
DRB1*01:02	3,7	DRB1*11:04	34,1
DRB1*03:01	12,6	DRB1*12:01	1,6
DRB1*04:01	2	DRB1*12:03	0,4
DRB1*04:02	3,7	DRB1*13:01	8,5
DRB1*04:03	5,7	DRB1*13:02	6,1
DRB1*04:04	0,4	DRB1*13:03	2,8
DRB1*04:05	5,3	DRB1*13:05	0,4
DRB1*04:07	0,8	DRB1*14:01	8,1
DRB1*04:13	0,4	DRB1*14:04	0,4
DRB1*07	13,4	DRB1*14:10	0,4
DRB1*08:02	0,8	DRB1*15:01	11,4
DRB1*08:03	0,4	DRB1*15:02	4,9
DRB1*08:04	0,4	DRB1*15:03	0,4
DRB1*08:05	0,4	DRB1*16:01	22,4
DRB1*09:01	1,2	DRB1*16:02	3,7
DRB1*10:01	2,4	DRB1*16:05	0,4
DRB1*11:01	15,9		



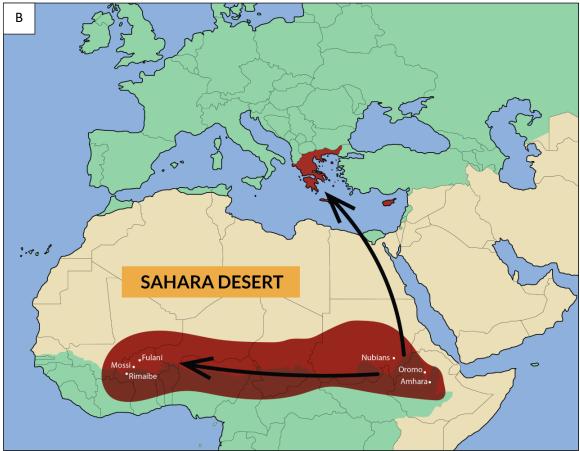


Fig. 3 (**A**). Mediterranean area showing classic populations (squares). Arrows represent population movements before 3,000 years B. C. (Sellier & Sellier 1993). Etruscans have their highest development in the first millennium B.C.; however, their culture was a continuity of a more ancient "Villanovan" (Villanova, Bologna) and pre-Villanovan cultures (2nd millennium B.C.) (Elvira 1988). Semitic people were nomadic people, comprising Jews, Arabs, and Phoenicians. Further details can be seen in references (Martinez-Laso *et al.* 1996; Gomez-Casado *et al.* 2000; Arnaiz-Villena *et al.* 1997; 1999a; 2001a; 2001b; 2001c; 2002). In the map: 1) Attika Region, continental Greece territory; 2) Aegean Greek Islands; 3) Geek Cyprus part.

Fig. 3 (B). Map showing postulated migrations of Sub-Saharan populations. Arrows show postulated migrations from Ethiopia to both West Africa and Greece, the latter probably occurring in pharaonic times, to give rise to other Sub-Saharan populations (Fulani, Mossi, Rimaibe; Burkina Faso) and Greeks. Humid Sahara Desert harboured people density before around 6,000 – 5,000 years BC (Chandan & Peltier 2020).

Conclusions

- Saharan and North African peoples emigrated to North when Sahara started to become dry about 6,000 years BC or before.
- They probably influenced many of the primitive Mediterranean Cultures from Atlantic British and Canary Islands to Persia and North India, including Greeks and Iberians.
- The appearance of ancient linear writings i.e.: Berber/Tuareg, Iberian, Etruscan, Minoan, Runes, and other linear scripts may have a common Saharan origin.
- 4) Agricultural/domestic breeding demic diffusion model from Middle East to Iberia (West Europe) *does not exist*: physical anthropology (skeletons and teeth studies, genetics, writing and languages. Most likely these technologies were locally acquired among Sahara, Iberia and North Africa, both Mediterranean and Atlantic: in fact domesticated animal rock paintings exist in Sahara 1,000 years before than these technologies are reported in Middle East.
- Genetics in Iberia is difficult to separate from North Africa and Prehistoric gene flow is postulated.
- 6) Genetics in Greeks have also shown similarities with Sub-Saharans and it is also possible that admixture occurred because of the Sahara desertification, migrations and/or fights in Egypt within different ethnic groups (i. e.: Danao's Daughters).

7) Iberian/Basque equivalences and discoveries of Iberian scripts in Canary Islands and Sahara (Ti-m Missaou, Hoggar area. Algeria) may be a starting of Lineal/Mediterranean writings evolving from Lineal Megalithic scripts. Those findings are crucial and may be important for understanding main Atlantic/Mediterranean cultures in the context of the "Saharo-Canarian Circle".

Aknowledgements

We thank University Complutense of Madrid for its continuous support. PI18/00721 grant is hold from Ministerio de Ciencia, Innovación y Universidades and FEDER funds.

Conflict of interests: The authors declare no conflict of interest

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To cite this article:

International Journal of Modern Anthropology. 2 (15): 484 – 507 DOI: <u>http://dx.doi.org/10.4314/ijma.v2i15.5</u>



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Arnaiz-Villena A., Juarez I., Palacio-Grüber J., Lopez-Nares A., Suarez-Trujillo F. 2021. The Northern Migrations from a drying Sahara (6,000 years BP): cultural and genetic influence in Greeks, Iberians and other Mediterraneans