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Short Communication

HLA genetic study in Iran Saqqez-Baneh Kurds: no genetic trace of Aryan invasions in Anatolian Turks and Kurds is found

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ABSTRACT

Kurds are living at Middle East region comprising several countries (38 million people) and also have emigrated to Asia, Europe and America. Kurds from Iran have been HLA typed in the present work from Saqqez and Baneh towns, Kordestan province, Iran. Origin of Kurds is considered autochthonous from Anatolia and surrounding mountains: they have been referred as “the mountain people” by classic Persian, Greek and Roman authors. Present day Turks are also autochthonous from Anatolia, but they were not recognized by classical authors as living in the mountains and they speak a language of Asian origin that was imposed to Anatolia by a “elite” invasion without a noticeable high Asian gene input. Most frequent class I and class II HLA alleles found in Iranian Kurds population are: HLA-A*24:02, A*02:01 and HLA-B*35:01, and HLA-DRB1*11:01, DRB1*03:02 and HLA-DQB1*03:01; also, most frequent HLA extended haplotypes from this Iran Kurdish sample are not shared with Iranians but with Mediterranean, Turkish and Caucasus people. This is confirmed by Neighbour-Joining and correspondence analysis studied together with the corresponding populations. Finally, our studies show that both Kurds and Turks are genetically original from Anatolian Peninsula and surrounding countries and that an apparent Asian genetic or Aryan invasion does not exist in the area.

Both Kurds and Turks show that they genetically belong to the Old Mediterranean people stock. Kurds are also close to Caucasian peoples [1–6]. Kurdish ancestral culture may be traced to Halaf Culture (6000 BCE, Tell Halaf, Southern Diyarbakir, Turkish Kurdistan) [7,8]; Hurrians (3000 BCE), who spoke a non-Indo-European Caucasian language, may be the basis of present-day Kurdish substratum [8]. Probably, other later invasions modified initial Kurdish language. Kurds have always been referred as mountain people since they have lived at mountains according to Persians, Greeks and Romans [8]. Anatolian Turks have also a genetic Mediterranean background; Central Asia Turkish people brought a language and cultural change, but Central Asia invasion genetic input is not noticed: an “elite” invasion occurred [2].

Some authors have identified Hittite Anatolian main culture as the basis of ancient Anatolia and Europe Indo-European invasion: this invasion has been shown not to exist [9] and Hittite language is probably another Dene-Caucasian one [10].

Distribution of present-day Kurds are as follows [2,3,6,11]: Turkey (15–20 million), Iran (10–12 million), Iraq (8–8.5 million), Syria (3–3.6 million), Armenia (37.5 thousands), Georgia (13.9 thousands), Azerbaijan (6.1 thousands), Europe (1.82–2.12 million), Asia (160–260 thousands), Canada/USA (37 thousands) (Figure 1, [Supplementary Material](#)).

However, 38 million Kurds do not have their own recognized country because different interests that other European, Asian and American countries had and also nowadays have [12]. In the present work, we aim to study the Iranian Kurds HLA genetics in order to genetically compare them with other Kurds and also unrelated populations.

Sixty unrelated and healthy Kurd individuals volunteered to donate blood for this study after signed consent. They lived in Saqqez and Baneh towns, in the Kurdistan territory of Iran (Figure 1, [Supplementary Material](#)). Their four grandparents were originally from the same area and all of them spoke Kurd language. These Kurd volunteers were typed for their HLA-A, -B, -DRB1 and -DQB1 loci by high resolu-

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tion PCR-SSOP-Luminex method (Amplicor, Hoffmann La Roche, Basel, Switzerland) [13]. HLA-DRB1 and HLA-DQB1 typing was done by DNA sequencing in a Perkin Elmer 310 automated DNA sequencer when ambiguities were found at the time of typing (Foster City, CA, USA) [14]. Statistical analyses were performed with Arlequin v3.0 software [15] to obtain HLA-A, -B, -DRB1 and -DQB1 allele and extended haplotypes frequencies (Tables 1 and 2, [Supplementary Material](#)). IMGT 3.1.20 (December 14th 2018) version was used to analyze data.

HLA class I allele frequencies show that HLA-A*24:02 (0.1750), A*02:01 (0.1250) and A*03:01 (0.1166); and HLA-B*35:01 (0.2167), B*51:01 (0.0917), B*18:01 (0.0583) and B*50:01 (0.0583) were the most frequent alleles in Irani Kurd sample studied in present work (Table 1, [Supplementary Material](#)). On the other hand, HLA-DRB1*11:01 (0.2000), DRB1*03:01 (0.1583) and DRB1*04:01 (0.1250); and HLA-DQB1*03:01 (0.2417), DQB1*02:01 (0.2083) and DQB1*05:01 (0.1000) were the most frequent HLA class II alleles in Kurds (Table 1, [Supplementary Material](#)). Most frequent HLA extended haplotypes found in Iranian Kurd sample studied in present work are: HLA-A*02:01-B*35:01-DRB1*01:01-DQB1*05:01 (3.33%), A*24:02-B*18:09-DRB1*11:01-DQB1*03:01 (3.33%), A*03:01-B*18:01-DRB1*11:01-DQB1*03:01 (2.50%), A*03:01-B*35:01-DRB1*11:01-DQB1*03:01 (2.50%), A*24:02-B*35:01-DRB1*03:01-DQB1*02:01 (2.50%), HLA-A*24:02-B*52:01-DRB1*15:01-DQB1*06:01 (2.50%), HLA-A*01:01-B*35:01-DRB1*11:01-DQB1*03:01 (1.67%), HLA-A*24:02-B*58:01-DRB1*03:01-DQB1*02:01 (2.50%), A*01:01-B*08:01-DRB1*03:01-DQB1*02:01 (1.67%), and HLA-A*24:02-B*51:01-DRB1*04:01-DQB1*04:01 (1.67%) (Table 2, [Supplementary Material](#)).

First most frequent haplotype found, HLA-A*02:01-B*35:01-DRB1*01:01-DQB1*05:01 (3.33%), is identified as a Mediterranean ancestry haplotype being shared with Italians, Spaniards and Caucasian populations of Brazil and USA [16]. This haplotype is found with the highest frequencies in our Iranian Kurd population. The second (HLA-A*24:02-B*18:09-DRB1*11:01-DQB1*03:01) and tenth (A*24:02-B*51:01-DRB1*08:01-DQB1*04:01) most frequent haplotypes found in present work seem to be specific of Kurds and not shared with any other population in the world. It is remarkable that they all share the A*24:02 allele in their structure. Third most frequent haplotype found in Iranian Kurds (A*03:01-B*18:01-DRB1*11:01-DQB1*03:01; 2.5%) is also shared with Mediterranean/European populations like Spaniards and Germans [16]. The fourth (A*03:01-B*35:01-DRB1*11:01-DQB1*03:01; 2.50%), fifth (A*24:02-B*35:01-DRB1*03:01-DQB1*02:01; 2.5%) and sixth (A*24:02-B*52:01-DRB1*15:01-DQB1*06:01; 2.50%) most frequent extended haplotypes found in Iranian Kurds are also present in Mediterranean and Oriental populations with lower frequencies [16]. The seventh most frequent haplotype found, HLA-A*01:01-B*35:01-DRB1*11:01-DQB1*03:01 (1.67%), is also found in Caucasian populations [16].

Neighbour-Joining dendrogram constructed from HLA-DRB1 frequencies and the calculation of Nei genetic distances (DA) (results not shown) [11] showed that Kurds from Iran are genetically close to the following populations : Gorgan (DA = 13.41), Russians (14.86), Italians (15.73), Croatians (16.09) and Georgians (16.26) [11]. Other populations such as Iranians (31.37), Palestinians (33.47), Ashkenazi Jews (34.57) or Lebanese (39.78) are genetically more distant from Kurds [11]. Correspondence analyses (results not shown) confirm genetic relatedness of Kurds with Mediterraneans and Caucasus populations [11].

Therefore, HLA alleles and extended haplotypes frequencies found in Iranian Kurds studied in present work are a reflection of uniqueness of this population. Kurds do not share any of the most frequent extended haplotypes with Iranian populations showing close relatedness with other Mediterranean, Caucasus, Turkish and South Russian

populations. Thus, our present paper Kurd HLA data confirms that present day Iranians (including Kurds) and also Anatolian Turks genetic stock comes from and autochthonous people and not from a now dismissed Aryan invasion from East [2,3,10,17].

All genotype data included in this paper are held in <https://www.allelefreqencies.net> and identifier number is 3774. Population is named “Iran Saqqez-Baneh Kurds” [16].

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary material

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.humimm.2022.07.005>.

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