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Travel Medicine and Infectious Disease (2016) xx, 1–10

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Epidemiology of hepatitis C virus and genotype distribution in immigrants crossing to Europe from North and sub-Saharan Africa

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Received 28 January 2016; received in revised form 7 April 2016; accepted 4 May 2016

Summary *Background:* The association between the prevalence of hepatitis C virus (HCV) and immigration is rarely studied, particularly for the immigrants crossing to the resettlement countries. Most of the published data are confined to those immigrants who were resident in European countries and rarely immigrated before they reach the final destination. Libya is a large country in North Africa with the longest coast of the Mediterranean Sea facing the European Union. It has been considered as the main transient station for African immigrants to Europe. The objectives of this study were to determine: (1) the prevalence of HCV in African immigrants gathered in Libya from different African countries on their way to Europe and (2) HCV genotype distribution in these immigrants and its correlation with different demographic factors.

Methods: A total of 14 205 serum samples were collected in a 3-year period (2013–2015) from different immigrants from North and sub-Saharan Africa who resided in the African immigrant campus, Tripoli, Libya. The participants were interviewed, and relevant information was collected, including socio-demographic, ethnic, and geographic variables. Each serum sample was tested for anti-HCV antibody using ELISA. The genotypes were determined and assigned using a specific genotyping assay and correlated with demographic and potential risk factors of the recruited individuals.

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http://dx.doi.org/10.1016/j.tmaid.2016.05.020
1477-8939/

Results: Of the immigrants studied, 1078 (7.6%) were positive for HCV. The prevalence of HCV infection ranged from 1.4% to 18.7%; it was higher among individuals arriving from Nile river (3.6–18.7%) of North Africa, followed by those who arrived from the West African region (2.1–14.1%), Horn of Africa (HOA, 6.8–9.9%), and Maghreb countries (1.4–2.7%). The relative risk factor attributable to gender variation was not significant (95% CI: 0.8513–1.2381). Five genotypes were detected in 911 African immigrants. Genotypic analysis showed that the predominant HCV genotypes in this group were genotypes 4, 1, and 2 that accounted for 329 (36.1%), 326 (35.8%), and 131 (14.4%) strains, respectively, followed by genotype 3 that accounted for 87 (9.5%) strains. Genotype 5 was isolated mainly from 18 HOA (2%) and 20 West African (2.2%) individuals.

Conclusions: The prevalence of HCV is considered high with a unique disparate distribution among African immigrants crossing to Europe. This indicated that the prevalence of HCV is high among these immigrants and thus may be reflected on the HCV prevalence in the guest countries. The broad genetic heterogeneity of HCV genotypes detected here may impact the efficacy of prevention and control efforts for HCV in both Europe and North and sub-Saharan Africa; hence, an integrated global policy of actions is needed.

1. Introduction

Hepatitis C virus (HCV) is a leading cause of liver-related morbidity and mortality worldwide. The epidemiology of the infection is highly variable between and within countries; North and sub-Saharan African countries are of great interest because they have been considered as high prevalence regions with the highest HCV prevalence rate of up to 23% within these countries [1,2]. Strategies to deal with HCV identification and treatment must be tailored to the geographic location and the political and economic environment of the region. Although great strides have been made in reducing HCV transmission risk acquired iatrogenically through contaminated needles, medical procedures, or receipt of unscreened contaminated blood products, new challenges related to the changing patterns of disease incidence are emerging. These may include in particular immigrants and intravenous drug users (IVDUs) [3,4]. Hence, fresh evaluation and new approaches to disease prevention are needed.

Immigration is an inexorable process; in 2013, 3.2% of the global population (231 million individuals) migrated to a new host nation. This newly emerged population may suffer from infectious diseases that are usually more exotic or prevalent in their own countries [5]. In reality, migrants are often initially healthier overall than the host country population, although they are at a higher risk of carrying latent forms of some infectious diseases [6]. Some groups may also be disproportionately at risk of specific infectious diseases due to increased exposure to risk in their country of origin, during the migration journey, and because of adverse socioeconomic conditions in the destination country [7]. The association between the introduction of infectious diseases and migration has long been recognized. The global distribution of HCV genetic variation has likely been influenced by historical and contemporary trends in human migration. For example, strains from West Africa appear to have been transferred to the Americas through the trans- Atlantic slave trade [8,9]. Migration from an endemic area to new regions is also thought to be responsible for changing the HCV genotype landscape [10]. An example is the emergence of genotype 6 in industrialized countries such as Canada and Australia, which is genetically similar to the most isolated genotype of Southeast Asian linage. More recently, a newly identified genotype 7 has been isolated from a Congolese immigrant in Canada [11,12]. Yet, the link between migration and recent increase in the prevalence of HCV in Europe remains unclear and is further complicated by the increase in HCV in the nonmigrants as well.

With the growing ease of travel, globalization of the world economy, and lack of political settlement, mass migration has been on the upswing in recent years, particularly from North and sub-Saharan Africa [13,14]. Libya is a large country in North Africa with the longest coast of the Mediterranean Sea facing the European Union (EU). It has been considered as the main landing (transient) station for African immigrants to Europe; annually, over 80 000 African immigrants gather at the Libyan coasts to attempt crossing to Europe [15,16]. The epidemiological data on immigrants to Europe are sparse and fragmentary. There is paucity of information regarding the epidemiological characteristics of HCV in African immigrants from these countries; most of the published data are confined to those immigrants who were resident in European countries and rarely migrated before they reach the final destination [17,18]. The investigation of HCV prevalence and subtype characteristics in African immigrants to Europe will help to understand the spreading pattern of HCV infection within Europe and other developed nations. Here, we report the prevalence of HCV and genotype distribution in African immigrants from North and sub-Saharan Africa as they resided in the traverse country before reaching the final destination in Europe.

2. Materials and methods

2.1. Study population and recruitment

The study was carried out over 3 consecutive years in 4 selected nationally recognized African immigrant campus

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supervised and guarded by the Libyan National authority. Immigrants who were in apparent good health and did not report signs or symptoms in the recent or remote past were asked if they wished to undergo the testing after its importance had been explained by the healthcare assistant or practice nurse once a patient had permanently registered. Participation in the study was completely voluntary, and signed informed consent, which was written in the immigrants' language, was obtained from each participant. Blood samples for hepatitis C test were then taken from each participant. All the studied specimens were anonymous with a coding number for analysis and used exclusively for academic research, and the patients were not remunerated. Serum samples were collected from 14205 African immigrants aged between 15 and 58 years. The samples were collected from newly arrived immigrants from January 2013 to December 2015 to avoid the increased potential for de novo HCV infection from the guest country. The immigrants were from different parts of Africa, including sub-Saharan countries of Central Africa, East Africa, and West Africa as well as North African countries as shown in Table 1.

2.2. Laboratory tests

A blood sample of 5–10 ml was collected and transported immediately to the local Reference laboratory in Tripoli Central Hospital. Serum was prepared and stored at −20 °C until tested as previously described [19]. All samples were tested for anti-HCV antibodies by using a third-generation enzyme immunoassay (Axsym; HCV EIA 3.0; Abbott Laboratories, Abbott Park, Illinois) as previously published [19]. Samples that were positive for anti-HCV antibodies were retested by the same method and considered as positive only if the retest was positive.

2.3. Determination of hepatitis C virus genotypes

HCV genotyping was performed by gene amplification using the COBAS-Amblicor HCV test (this test involves reverse transcription of HCV RNA into cDNA by PCR, hybridization of the amplified cDNA with an oligonucleotide probe that binds enzyme, and catalysis of the conversion of a substrate to a colored product recognized by COBAS AMBLICOR Analyzer (Roche Diagnostic, Basal, Switzerland)). This analysis is used worldwide and covers all the seven internationally recognized HCV genotypes as previously described [20,21].

2.4. Data analysis

Data were coded and entered into a database, which was then cleaned and verified. Data were analyzed using the Chi square test with Yates' correction or Student's *t*-test for univariate analysis. The results for all variables are expressed in the form of rates (%). A multivariate analysis was conducted using logistic regression to verify the variables that had a statistically significant influence on HCV infection as previously described by Daw et al. [20]. The data were analyzed using SPSS version 11.5 to identify the distribution of different genotypes and their association with gender, age, and year of diagnosis.

Table 1 Study population of African immigrants crossing to Europe according to the region and country of origin: 2013–2015.

Region/Country	No. of immigrants/year			Sample size (%)	Ratio[a]
	2013	2014	2015		
Central Africa					
Chad	379	978	1200	2557	1:6
Central Africa total	379	978	1200	2557 (18)	1:6
West Africa					
Burkina Faso/Ivory Coast	160	177	230	567	1:25
Niger/Mali	750	1038	1687	3475	1:4
Nigeria/Ghana	300	305	346	951	1:13
West Africa total	1210	1520	2263	4993 (35.2)	1:3
Horn of Africa (East Africa)					
Eritrea	320	250	227	797	1:18
Somalia	660	715	637	2012	1:7
Ethiopia	270	230	215	715	1:20
East Africa total	1250	1195	1097	3.524 (24.8)	1:4
North Africa					
Nile River Region					
Egypt	326	153	138	617	1:23
Sudan	459	580	859	1898	1:7
Maghreb Region					
Maghreb countries[b]	238	197	181	616	1:23
North Africa total	1023	930	1178	3131 (22)	1:6
Total	3862 (27.2)	4623 (32.5)	5720 (40.3)	14 205	

[a] Correspondence to the Total no of Immigrants.
[b] Tunis, Algeria, Morocco.

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Table 2 Prevalence of HCV Infection in African immigrants and its association with demographic factors and region of origin. Q12

Demographic characteristics	Prevalence of anti-HCV				
	Total	No (%)	OR	95%CI	
				Upper	Lower
Age group					
≤20	1269	13 (1.03)	0.0104	0.0060	0.0180
21–30	5391	253 (4.69)	0.0492	0.0432	0.0562
31–40	4502	329 (7.31)	0.0788	0.0700	0.0889
≥41	3043	444 (14.60)	0.1708	0.1525	0.1910
Gender					
Male	13 159	1369 (10.4)	0.1161	0.1092	0.1234
Female	1046	106 (10.1)	0.1128	0.0906	0.1403
Region of Origin					
Central Africa	2557	146 (5.7)	0.0605	0.0529	0.0691
West Africa	4993	405 (8.1)	0.0883	0.0792	0.0984
Horn of Africa	3524	296 (8.4)	0.0917	0.0807	0.1042
North Africa	3131	314 (10.0)	0.1108	0.0905	0.1357

3. Results

A total of 14205 different serum samples were collected from newly arrived African immigrants on their way to Europe via Tripoli over 3 consecutive years (2013–2015). Of these, 1313 (22%) samples were collected from North African (NA) immigrants, 2515 (17.7%) from the Nile river region (Egypt and Sudan), 616 (4.3%) from the Maghreb region (Tunis, Algeria, and Morocco), 2557 (18%) from Central African (CA) (Chad), 4993 (35.2%) from West African (WA) (Niger, Mali, Burkina Faso, Ivory Coast, Nigeria, and Ghana), and 3524 (24.8%) from Horn of Africa (HOA) (Somalia, Eretria, and Ethiopia) immigrants as shown in Table 1.

All the subjects were aged between 14 and 58 years, with an average age of 24.17 ± 5.14 years. Male gender predominated among the immigrants, with 13159 (92.6%) males and 1046 (7.4%) females (M:F; 12:1). Data were arbitrarily aggregated into 10 years interval according to the age at the enrollment. The patients were non-homogeneously distributed into the different age groups, with a decreasing trend observed for age; approximately 72% of the patients were below 40 years of age. The overall majority of the studied subjects were within 24–28 years of age.

The overall prevalence of HCV in the African immigrants was 7.6% though it varied according to the origin of the immigrants, ranging from 5.7% to 10.0% as shown in Table 2. NA Subjects at the Nile river region showed the highest prevalence of up to 18.7% in Egyptians and 3.6% in Sudanese, while the Maghreb immigrants showed the lowest

Table 3 Distribution of HCV genotypes in African immigrants from North and Sub-Saharan Africa.

Region/Country/of origin	Strains typed (%)	Genotype number (%)				
		1	2	3	4	5
Central Africa						
Chad	97	32	27	0	38	0
Total	97 (10.4)	32 (33)	27 (27.8)	0	38 (39.2)	0
West Africa						
Burkina Faso/Ivory Coast	73	41	16	0	12	4
Niger/Mali	105	49	29	3	19	5
Nigeria/Ghana	119	62	21	0	27	9
Total	297 (32.6)	152 (51.2)	66 (22.2)	3 (1)	58 (19.5)	18 (6.1)
Horn of Africa (East Africa)						
Eretria	69	20	2	14	26	7
Somalia	78	18	0	20	38	2
Ethiopia	121	27	3	33	47	11
Total	268 (29.4)	65 (24.3)	5 (1.9)	67 (25)	111 (41.42)	20 (7.5)
North Africa						
Nile River	198 (21.7)	66 (33.3)	28 (14.1)	6 (3)	108 (54.5)	0
Egypt	63	9	3	6	45	0
Sudan	135	57	25	0	63	0
Maghreb countries	51 (5.6)	21 (41.2)	5 (9.8)	11 (21.6)	14 (27.5)	0
Total	911	326 (35.8)	131 (14.4)	87 (9.5)	329 (36.1)	38 (4.1)

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prevalence ranging from 1.4% to 2.7%. In CA subjects, the prevalence ranged from 2.3% to 5.7% in Chadians. The prevalence of HCV in CA immigrants was 5.7%, ranging from 3.6% to 8.2%. Of the samples retrieved from WA immigrants, 8.1% were positive for HCV antibody, ranging 2.1–14.1%. The prevalence was high in the subjects from Nigeria and Ghana (14.2%), followed by Burkina Faso/Ivory Coast (8.3%) and Niger/Mali (7.4%). The prevalence in immigrants from HOA was (8.4%), with a range of 6.8%–9.9%; it was 6.3%, 8.2%, and 9.3% for subjects from Eritrea, Somalia, and Ethiopia, respectively. In NA immigrants, the prevalence was 10.0% and ranged from 1.3% to 18.7%. The Egyptian immigrants and Nigerians showed the highest prevalence rates, while the Maghreb immigrants and Chadians showed the lowest prevalence rates. Male and female immigrants showed similar prevalence rates of HCV (10.4% and 10.1%, respectively). The mean age of anti-HCV-positive males and females was 27.6 ± 19.8 years and 23.7 ± 18.4 years, respectively, and it was higher in those subjects aged over 30 years ($P < 0.001$) in both genders.

The genotyping analysis of HCV among African immigrants is shown in Table 3. Only 911 (84%) of the samples were typable and were assigned to five different genotypes (1, 2, 3, 4, and 5). The remaining samples were not typed due to insufficient sample size. HCV genotypes 4 and 1 were the most predominant ones that accounted for 36.1% and 35.8% of strains, respectively, followed by genotypes 2 and 3 that accounted for 131 (14.4%) and 87 (9.5%) of strains, while genotype 5 accounted only for 38 (4.1%) strains. Genotype 4 was isolated from 111 (%) of HOA immigrants, followed NA and WE immigrants, while genotype 1 was isolated from 152 WA immigrants, followed by HOA and CA immigrants. Genotype 2 was isolated from 66, 52, 5, and 8 WA, CA, HOA, and NA immigrants, respectively. Genotype 3 was isolated from 67 HOA and 17 NA immigrants mainly from the Maghreb region and from only 3 WA immigrants (i.e., Mali and Niger). Genotype 5 was isolated from 20 HOA and 18 WA immigrants.

The prevalence of HCV and the distribution of the genotypes vary significantly according to the geographical regions from where the immigrants arrived as shown in Fig. 1. The frequency and diversity of genotypes appear to differ from one region to another. Although genotypes 1, 2, and 4 were isolated from all the studied population, we found that genotype 4 was widely present in NA and HOA immigrants, followed by CA immigrants. However, the frequency of genotype 4 was significantly lower in WA immigrants in whom genotype 1 dominated in particular. Genotype 5 was isolated only from HOA and WA immigrants in a similar proportion.

4. Discussion

Immigration is a global phenomenon, and immigrants may harbor some infectious diseases. Such new infectious agents may be introduced into the indigenous population and impact public health. Therefore, it is essential to investigate and monitor some infectious agents in the immigrants, especially viral hepatitis [23]. Epidemiological

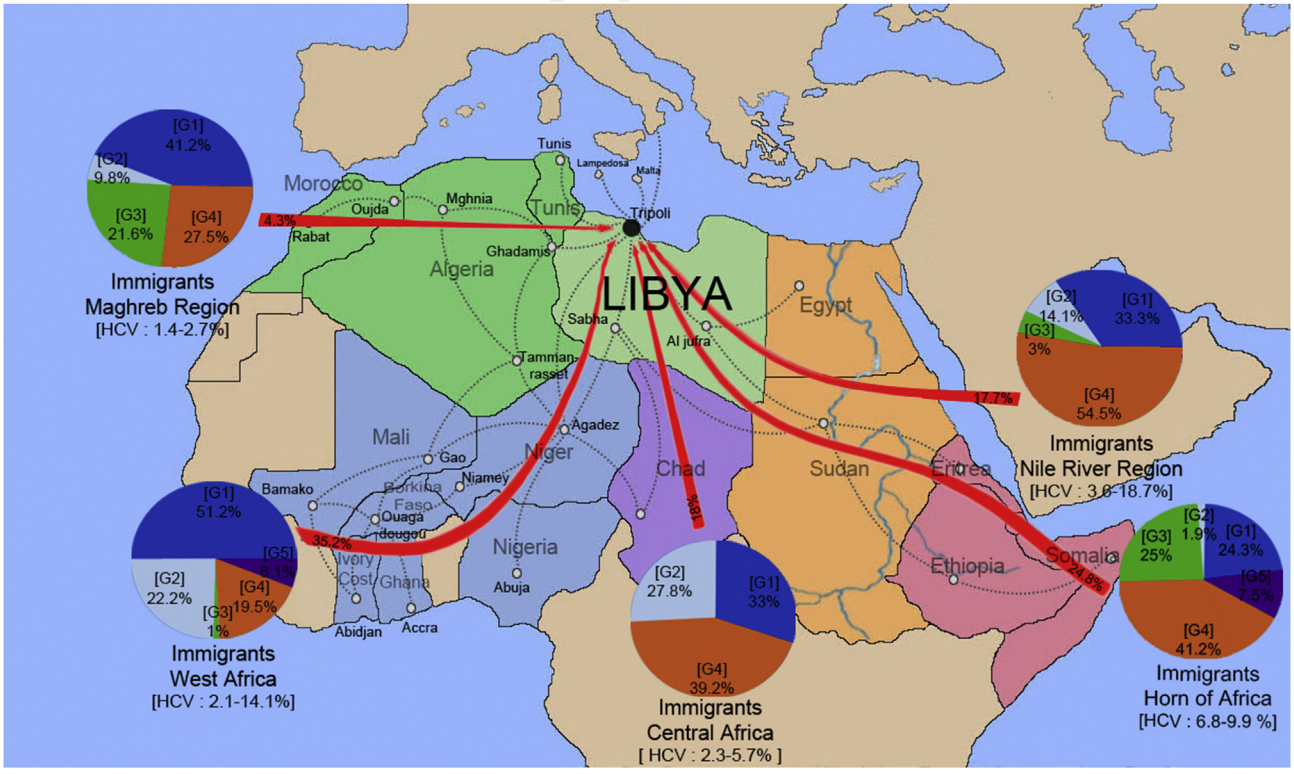

Fig. 1 Detailed mapping of immigrants flow and HCV prevalence and genotype distribution in immigrants from North and sub-Saharan Africa. The thickness of the red arrows is roughly proportional to the percentage of observed immigrants from 2013 to 2015.

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studies of HCV in this group are crucial for the formulation of preventive strategies and planning of healthcare programs worldwide. Africa has experienced severe HCV, HBV, and HIV pandemics, and African individuals are highly prone to risk factors that can easily transmit such infections. North and sub-Saharan African countries have the highest prevalence rate of HCV, with prevalence of up to 26% in some of these countries [24,25]. The frustrating economic and social conditions, lack of security, and personal aspirations have enforced many Africans to leave their native land and seek immigration to Europe [26]. Most of the studies on immigrants focus on disparities between immigrants and native population in the respective host countries, providing insights into differences in exposure to risk factors and access to health services [27]. This approach ignores how different factors affect migrants' health at different stages of their lives—preceding, accompanying, and after the migration process [28]. To date, few studies have investigated the infectious states of immigrants during the traverse and before settlement in the host country [29].

Libya, given its central location in the Mediterranean basin with a longest coast, represents the main gate of entrance for African immigrants into Europe, particularly from North and sub-Saharan Africa. This is clearly evident from the flight of immigrants during the upheaval in North Africa in spring 2011 [17,30]. Data on the prevalence of HCV in the African immigrants during the traverse are rarely available. Researchers should therefore prioritize such studies to articulate the needed policy to prevent and manage HCV infection and the consequent burden on immigrants, transit, and host countries.

In this study, we observed a high prevalence of HCV in immigrant population arriving from North and sub-Saharan Africa. Our results showed that HCV prevalence in African immigrants ranged from 1.6% to 18.7% depending on the country of origin, and revealed that those arriving from West Africa and the Nile region, particularly Egypt, had the highest HCV prevalence among the studied population. The individuals from these countries included in this study were mainly young people with a mean age of 24—35 years, which accounted for a high prevalence of HCV, while the older age groups tend to show even higher prevalence of HCV infection. Both males and females had a high prevalence of HCV, despite the fact that most of the immigrants were adult males. However, further studies are needed to clarify this assumption [31].

Among the NA countries, Tunisian, Algerian, and Moroccan immigrants showed low prevalence of HCV at 1.6%, though it was higher in Sudanese (3.7%) immigrants from the Nile river region. Studies from these countries have shown a considerable variation between the population subsets [1]. Egypt has the highest HCV prevalence globally, hovering around 14.7%, with 15% of the total population having been infected [32,33]. Libya (i.e., the traverse land) borders Egypt, but has a lower endemicity for HCV, which is estimated to be 1.2% [19,34] Tunisia and Morocco have intermediate HCV prevalence, with the rates falling between 1.4% and 7% for the general population [35,36]. There is a paucity of data for Algeria in that the only figure for a national prevalence dates from 2009, and it is estimated that 2.5% of the population is HCV-positive [37]. There is also scarceness of data regarding the prevalence of HCV in general population of Sudan. A limited number of studies on specific groups have shown that the prevalence of HCV varies from 1.8% to 4.7% [38]. However, published data on the prevalence of HCV in the Maghreb region population are incomplete, and further studies are needed particularly among general population and groups with attributable risk factors [1,39].

Sub-Saharan Africa has been considered a region with the highest HCV burden. However, HCV seroprevalence in sub-Saharan Africa is particularly patchy, and there is scarceness of data in some countries. Most of the published data are either based on data analysis or selected group of people. Immigrants from sub-Saharan Africa have shown a considerable variation in HCV prevalence based on the country of origin. The highest rate was reported in WA immigrants coming from Nigeria and Ghana, followed by Burkina Faso and Ivory Coast, though it was low among immigrants from Niger and Mali. In Central Africa, the Chadian immigrants show a moderate prevalence of HCV similar to that in Somalis and Eritreans in the HOA. However, the prevalence reached up to 7.1% in Ethiopian immigrants. Studies from Mali, Ethiopia, and Nigeria have shown a higher prevalence of HCV in these countries; however, no similar studies were published from Chad, Niger, Somalia, and Eretria [40—42]. In a recent review, Riou et al. [43], reported a pooled HCV seroprevalence across low-risk cohorts and general adult African population varying from 6.9% [6.0—7.8] in the central Africa region to 4.3% [4.0—4.7] in West Africa and 0.9% [0.8—1.0] in South-East Africa. Although these studies highlight the concern of high prevalence of HCV in sub-Saharan Africa, they are extremely heterogeneous and did not provide reliable information at the country level. The present study gives more certainty to the robustness of the accurate prevalence of HCV within these countries.

Immigration has influenced the prevalence of HCV within the southern regions of the EU. Greece, Italy, France, and Spain have reported a higher level of HCV (2—7%) than Libya in North Africa [44,45]. Spatial geographic spots in the Netherlands and Germany (with large numbers of immigrants have also shown a higher rate of HCV (7%) than the other regions of the same countries [46]. This indicates emergence of HCV epidemics within these countries. Our results are in concordance with the published data of African refugees in European countries. In a study performed in Verona (Italy) in 2008 among 182 sub-Sahara African refugees, 2.7% of the refugees were anti-HCV positive, while in Greece, 12.5% of the African refugees were anti-HCV positive [47,48]. However, such studies are usually generalized and do not categorize the immigrants based on their home country. Furthermore, being resident in the host country for a longer period of time may influence the HCV seroprevalence of the immigrants. Therefore, further studies are needed on the immigrants as they arrive immediately at the European borders.

Various HCV genotypes were detected among the African immigrants in this study. Certain genotypes are common among all the immigrants (genotypes 1, 2, and 4), though they differ in ratio, while other subtypes such as genotypes 5 and 3 are restricted to certain regions and certain instances, respectively. In NA immigrants, genotype 4 is predominant among the Egyptian and Sudanese immigrants

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and is less common among the Maghreb region immigrants in whom genotypes 1 and 2 are the most common genotypes. This is in agreement with other studies on genotype distribution in NA countries; these studies showed that the predominant HCV genotypes circulating in the general population are 1 and 2, except for Libya and Egypt, which are distinct and exhibit genotype 4 as the most commonly circulating strain [20,49]. The distribution of HCV genotypes among the sub-Saharan African immigrants is distinctive and relatively diversified. Chadians immigrants from Central Africa predominantly harbor genotypes 4, 5, and 3, though those from the WA region carry genotypes 2, 3, and 1. HOA immigrants showed genotypes 4, 2, 5, and 1. This is also in agreement with previous studies from West Africa and Ethiopia [41,50,51]. However, we have no previous study data on HCV genotypes in Sudan, Chad, Eretria, Somalia, and Niger for comparison. Hence, the present study can be considered as the first insight to illuminate the epidemiological nature of HCV among these countries.

Patterns of HCV genotypes observed in the Central and North Africa were quite similar those in the Nile river and HOA regions, although the geographic distribution of genotypes differed among the 4 regions ($p = 0.040$) and showed significantly lower frequency in the North Africa than in the West and HOA regions ($p = 0.027$). Genotype 5 was found only in immigrants arriving from Somalia, Ethiopia, and Burkina Faso, but not in immigrants arriving from North Africa. A prior study in Libya, the traverse land of the African immigrants, demonstrated a mosaic distribution of all these genotypes including genotype 5, with a higher frequency of genotype 4 (26.6%) and 1 (17.6%) [20,21]. This may indicate the influence of African immigrants on the integration of these genotypes within the Libyan community; phylogenetic studies are needed to confirm this speculation.

In this study, we reported a wide variety of HCV genotypes among African immigrants, most of which are rarely seen in native Europeans. This may be reflected on the epidemiological manifestations of HCV in the host countries. The prevalence rates of HCV genotypes has changed and has increased steadily in certain regions of Europe, particularly France, Italy, Greece, and Spain [52]. In France alone, the prevalence of HCV genotype 4 increased from 4% in 1990 to more than 11% in 2000. A recent study showed that genotype 4 was the second most frequently detected genotype and was found in 23% of a large cohort of HIV-positive homosexual men from Europe and Australia [53,54]. Our study showed that HCV genotypes 4 and 1 were the common genotypes among the studied immigrants and accounted for more than 35% of the isolated strains. Similar data were reported among immigrants resident in Italy, France, the Netherlands, and Germany [46,55]. Because of these trends, regional differences in HCV genotype prevalence and epidemiology may warrant consideration of prevention and treatment strategies that are tailored to local and regional needs.

The health dimension of immigration is a critical issue for both transit and final destination countries, and a sensible strategy for evaluating infections in immigrants ultimately requires knowledge of the disease patterns in these immigrants before their integration in the host society [56]. As immigrants reside in their final destination country, they are known to be a marginalized and vulnerable group who experience a range of social and psychological issues, including but not limited to unemployment, low income, and feeling of alienation and detachment from the host country population [57,58]. These factors also expose them to more risky behaviors such as sexual promiscuity and drug addiction. Hence, they may act as a vector of HCV transmission in the host community. The high incidence of HCV infection in these immigrants may indicate that concomitant infectious diseases such as HIV, HBV, and MDR-TB could affect these groups [59]. The emergence of these diseases within the immigrants is likely to threaten EU countries. Therefore, the adoption of national or subnational migrant health policies is not simply one-way traffic, and new persistence and perseverance policies are needed to combat such infections [60].

Our present study was carried on a certain group of population described as immigrants. They are young and healthy section of the African society, and thus, it highlights the heavy burden of HCV in African countries. Although the trend of HCV infection in these immigrants could not be easily extrapolated to the general population [19,32], the present study could be used as a vehicle for further understanding of the epidemiology of HCV in African countries. This study had some limitations. First, we could not estimate the number of viremic HCV cases in immigrants that could benefit from antiviral therapy. Second, diagnosis of HCV infection was based on detection of antibodies rather than on detection of HCV RNA, which might have yielded some false results. Third, the assessment of liver function was not included. Fourth, although biased information is possible, it is unlikely that this could have caused a large impact on the accuracy of the results because the demographic data is collected based on trust of verbal communication with the immigrants as most of them do not carry any personnel documents. Nevertheless, our data provide valuable insights into the burden of HCV infection in these populations.

The strength of our study is that it included a large number of immigrants arriving from different regions of Africa with a high prevalence of HCV. This is more likely to influence EU countries' healthcare systems regarding viral screening and guidelines for antiretroviral therapy [61,62]. Recent studies have revealed that the population dynamics of infectious agents are greatly influenced by a variety of epidemiological factors, including host population size and density, the spatial distribution of the host, and the rate of contact between individuals [63]. Hence, additional studies are needed to be performed on the underlying social factors that may play a key role in determining the rate and pattern of HCV spread among immigrants and influence future intervention policies.

5. Conclusion

In conclusion, our findings show a high prevalence of HCV infection with distinct heterogenic genotypes in various immigrant populations from North and sub-Saharan Africa. Early identification of HCV infection is essential to facilitate treatment of infected individuals, which will confer medical benefits to the individual and curtail the continuing

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spread of HCV infection in the host country, traverse country, and land of origin of the immigrants. Therefore, further studies are needed on the follow up of the epidemiology of HCV in immigrants during their resettlement in the host country. Hence, neoliberal policies of HCV prevention should be introduced and even extended beyond the European borders to reach Africa. In sub-Saharan African countries, the governments generally took a minimalist approach toward their to-be immigrated citizens. Therefore, these policies may include but not limited to economic support, training, infection prevention, and geo-security programs guided by European initiatives at NGOs and government levels [64,65].

Ethical approval

The study was approved by the Libyan National Ethical Committee (Approval No. LY NS; HCV-IM-4012519). It was conducted in accordance with the Helsinki Declaration and under the supervision of the Faculty of Medicine, Tripoli, Libya [22]. All participants signed an informed consent form witnessed by the local health office before collection of data and blood samples. The questionnaire used to collect demographic and epidemiological data was anonymous and linked to the blood sample tube only by a code [20].

Author contributions

Conceived and designed the experiments: MD. Performed the experiments: MD and MA. Analyzed the data: MD and AB. Contributed reagents/materials/analysis tools: MD and MA. Wrote the paper: MD and AB. Designed analysis: MD and AB. Performed cartography: MD and AD. Provided advice and critically reviewed the manuscript: MD, MA, and AD.

Conflict of interest

None.

Acknowledgments

We are deeply grateful to the Libyan Study Group of Hepatitis and HIV: Hana Elasafer, MD, Lulua Bendaref, PhD, Soad Tloba, MSc (Department of Medical Microbiology and Immunology (DMI)) and Mohamed A Daw, MD (group leader-DMI), Faculty of Medicine, Tripoli, Libya. We also thank the staff at the Libyan Reference Laboratory, Tripoli, where the laboratory analyses were conducted.

References

[1] Daw MA, Dau AA. Hepatitis C virus in Arab world: a state of concern. Sci World J 2012;2012:719494. http://dx.doi.org/10.1100/2012/719494. PMID:22629189.
[2] Madhava V, Burgess C, Drucker E. Epidemiology of chronic hepatitis C virus infection in sub-Saharan Africa. Lancet Infect Dis 2002;2(5):293–302. PMID: 12062995.
[3] Zimmerman C, Kiss L, Hossain M. Migration and health: a framework for 21st century policy-making. PLoS Med 2011; 8(5):e1001034. http://dx.doi.org/10.1371/journal.pmed.1001034. PMID:21629681.
[4] Ruta S, Cernescu C. Injecting drug use: a vector for the introduction of new hepatitis C virus genotypes. World J Gastroenterol 2015 Oct 14;21(38):10811–23. http://dx.doi.org/10.3748/wjg.v21.i38.10811. PMID: 26478672.
[5] Gushulak BD, MacPherson DW. Globalization of infectious diseases: the impact of migration. Clin Infect Dis 2004 Jun 15; 38(12):1742–8. PMID: 15227621.
[6] Hargreaves S, Seedat F, Car J, Escombe R, Hasan S, Eliahoo J, et al. Screening for latent TB, HIV, and hepatitis B/C in new migrants in a high prevalence area of London, UK: a cross-sectional study. BMC Infect Dis 2014 Dec 3;14:657. http://dx.doi.org/10.1186/s12879-014-0657-2. PMID: 25466442.
[7] Redditt VJ, Janakiram P, Graziano D, Rashid M. Health status of newly arrived refugees in Toronto, Ont Part 1: infectious diseases. Can Fam Physician 2015 Jul;61(7):e303–9. PMID: 26175382.
[8] Markov PV, van de Laar TJ, Thomas XV, Aronson SJ, Weegink CJ, van den Berk GE, Schinkel J. Colonial history and contemporary transmission shape the genetic diversity of hepatitis C virus genotype 2 in Amsterdam. J Virol 2012 Jul; 86(14):7677–87. http://dx.doi.org/10.1128/JVI.06910-11. PMID:22573865.
[9] An Y, Wu T, Wang M, Lu L, Li C, Zhou Y, Chen G. Conservation in China of a novel group of HCV variants dating to six centuries ago. Virology 2014 Sep;464–465:21–5. http://dx.doi.org/10.1016/j.virol.2014.06.011. PMID:25043585.
[10] Greenaway C, Ma AT, Kloda LA, Klein M, Cnossen S, Schwarzer G, et al. The seroprevalence of hepatitis C antibodies in immigrants and refugees from intermediate and high endemic countries: a systematic review and meta-analysis. PloS One 2015;10(11):e0141715. http://dx.doi.org/10.1371/journal.pone.0141715. PMID:26558905.
[11] Hajarizadeh B, Grebely J, Dore GJ. Epidemiology and natural history of HCV infection. Nat Rev Gastroenterol Hepatol 2013 Sep;10(9):553–62. http://dx.doi.org/10.1038/nrgastro. PMID:23817321.
[12] Murphy DG, Sablon E, Chamberland J, Fournier E, Dandavino R, Tremblay CL. Hepatitis C virus genotype 7, a new genotype originating from central Africa. J Clin Microbiol 2015 Mar;53(3):967–72. http://dx.doi.org/10.1128/JCM.02831-14. PMID: 25520447.
[13] Sharma S, Carballo M, Feld JJ, Janssen HL. Immigration and viral hepatitis. J Hepatol 2015 Aug;63(2):515–22. http://dx.doi.org/10.1016/j.jhep.2015.04.026. PMID:25962882.
[14] Lancet T. Migrant crisis in the mediterranean. Lancet 2015 May 8;385(9979):1698. http://dx.doi.org/10.1016/S0140-6736(15)60875-3. PMID:25943919.
[15] Daw MA, El-Bouzedi A. Dau AA Libyan armed conflict 2011: mortality, injury and population displacement. Afr J Emerg Med 2015:2. http://dx.doi.org/10.1016/j.afjem.2015.02.002.
[16] Pargeter A. The migration of power and North-South inequalities: the case of Italy and Libya. Mediterr Polit 2013 Mar 1;18(1):147–8.
[17] Rechel B, Mladovsky P, Ingleby D, Mackenbach JP, McKee M. Migration and health in an increasingly diverse Europe. Lancet 2013;381(9873):1235–45. http://dx.doi.org/10.1016/S0140-6736(12)62086-8. PMID:23541058.
[18] Owiti JA, Greenhalgh T, Sweeney L, Foster GR, Bhui KS. Illness perceptions and explanatory models of viral hepatitis B & C among immigrants and refugees: a narrative systematic review. BMC Public Health 2015;15(1):151. http://dx.doi.org/10.1186/s12889-015-1476-0. PMID:25886390.
[19] Daw MA, El-Bouzedi A. Prevalence of hepatitis B and hepatitis C infection in Libya: results from a national population based survey. BMC Infect Dis 2014 Jan 9;14:17. http://dx.doi.org/10.1186/1471-2334-14-17. PMID: 24405790.

Please cite this article in press as: Daw MA, et al., Epidemiology of hepatitis C virus and genotype distribution in immigrants crossing to Europe from North and sub-Saharan Africa, Travel Medicine and Infectious Disease (2016), http://dx.doi.org/10.1016/j.tmaid.2016.05.020

[20] Daw MA, El-Bouzedi A, Dau AA. Geographic distribution of HCV genotypes in Libya and analysis of risk factors involved in their transmission. BMC Res Notes 2015 Aug 21;8:367. http://dx.doi.org/10.1186/s13104-015-1310-x. PMID: 26293137.
[21] Elasifer HA, Agnnyia YM, Al-Alagi BA, Daw MA. Epidemiological manifestations of hepatitis C virus genotypes and its association with potential risk factors among Libyan patients. Virol J 2010;7:317. http://dx.doi.org/10.1186/1743-422X-7-317. PMID: 21073743.
[22] World Medical Association Ethics Unit. http://www.wma.net/en/30publications/10policies/b3/index.html; 2009.
[23] Manzardo C, Treviño B, Prat JG, Cabezos J, Monguí E, Clavería I, Navarro R. Communicable diseases in the immigrant population attended to in a tropical medicine unit: epidemiological aspects and public health issues. Travel Med Infect Dis 2008 Jan-Mar;6(1–2):4–11. http://dx.doi.org/10.1016/j.tmaid.2007.11.002. PMID:18342267.
[24] Forbi JC, Ben-Ayed Y, Xia GL, Vaughan G, Drobeniuc J, Switzer WM, et al. Disparate distribution of hepatitis B virus genotypes in four sub-Saharan African countries. J Clin Virol 2013 Sep;58(1):59–66. http://dx.doi.org/10.1016/j.jcv.2013.06.028. PMID:23871163.
[25] Rao VB, Johari N, du Cros P, Messina J, Ford N, Cooke GS. Hepatitis C seroprevalence and HIV co-infection in sub-Saharan Africa: a systematic review and meta-analysis. Lancet Infect Dis 2015 Jul;15(7):819–24. http://dx.doi.org/10.1016/S1473-3099(15)00006-7. PMID:25957078.
[26] Kpessa MW. Ideas, institutions, and welfare program typologies: an analysis of pensions and old age income protection policies in Sub-Saharan Africa. Poverty & Public Policy 2010; 2(1):37–65.
[27] O'Donnell C, Burns N, Dowrick C, Lionis C, MacFarlane A. Health-care access for migrants in Europe. Lancet 2013; 382(9890):393. http://dx.doi.org/10.1016/S0140 6736(13) 61666–9. PMID:23911373.
[28] Keygnaert I, Guieu A, Ooms G, Vettenburg N, Temmerman M, Roelens K. Sexual and reproductive health of migrants: does the EU care? Health Policy 2014;114(2):215–25. http://dx.doi.org/10.1016/j.healthpol.2013.10.007. PMID: 24268324.
[29] Napoli C, Dente MG, Kärki T, Riccardo F, Rossi P, Declich S. Screening for infectious diseases among newly arrived migrants: experiences and practices in non-EU countries of the Mediterranean basin and black Sea. Int J Environ Res Public Health 2015 Dec 8;12(12):15550–8. http://dx.doi.org/10.3390/ijerph121215002. PMID:26670237.
[30] Schmid S. Migration potential from North Africa to Europe. Arbeitskr Weltbevölkerung 2011.
[31] Daw MA, Shabash A, El-Bouzedi A, Aghnya A. Dau in association with the Libyan study group of hepatitis & HIV.Seroprevalence of HBV, HCV & HIV co-infection and risk factors analysis in Tripoli-Libya. PLoS One 2014;9(6):e98793. doi: 10.1371/journal.pone.009879. PMID:24936655. doi: 10.1371/journal.pone.0098793.
[32] Guerra J, Garenne M, Mohamed MK, Fontanet A. HCV burden of infection in Egypt: results from a nationwide survey. J Viral Hepat 2012;19:560–7. http://dx.doi.org/10.1111/j.1365-2893.2011.01576.x. PMID:22762140.
[33] Abdelwahab SF, Hashem M, Galal I, Sobhy M, Abdel-Ghaffar TS, Galal G, Strickland GT. Incidence of hepatitis C virus infection among Egyptian healthcare workers at high risk of infection. J Clin Virol 2013 May;57(1):24–8. http://dx.doi.org/10.1016/j.jcv.2013.01.005. PMID:23375237.
[34] Daw MA, Elkaber MA, Drah AM, Werfalli MM, Mihat AA, et al. Prevalence of hepatitis C virus antibodies among different populations of relative and attributable risk. Saudi Med J 2002;23:1356–60. PMID:12506296.
[35] Gorgi Y, Yalaoui S, Ben Nejma HL, Azzouz MM, Hsairi M, Ben Khelifa H, et al. Detection of hepatitis C virus in the general population of Tunisia. Bull Soc Pathol Exot 1998;91:177. PMID: 9642480.
[36] Benani A, El-Turk J, Benjelloun S, Sekkat S, Nadifi S, et al. HCV genotypes in Morocco. J Med Virol 1997;52:396–8. PMID: 9260687.
[37] Rouabhia S, Sadelaoud M, Chaabna-Mokrane K, Toumi W, Abenavoli L. Hepatitis C virus genotypes in north eastern Algeria: a retrospective study. World J Hepatol 2013 Jul 27; 5(7):393–7. http://dx.doi.org/10.4254/wjh.v5.i7.393. PMID: 23898373.
[38] Mudawi HMY, Smith HM, Fletcher IA, Fedail SS. Prevalence and common genotypes of HCV infection in Sudanese patients with hepatosplenic schistosomiasis. J Med Virol 2007 Sep;79(9): 1322–4. PMID:17607776.
[39] Ezzikouri S, Pineau P, Benjelloun S. Hepatitis C virus infection in the Maghreb region. J Med Virol 2013;85:1542–9. http://dx.doi.org/10.1002/jmv.23643. PMID:23780703.
[40] Bouare N, Gothot A, Delwaide J, Bontems S, Vaira D, Seidel L, Gerard C. Epidemiological profiles of human immunodeficiency virus and hepatitis C virus infections in Malian women: risk factors and relevance of disparities. World J Hepatol 2013 Apr 27;5(4):196–205. http://dx.doi.org/10.4254/wjh.v5.i4.196. PMID:23671724.
[41] Abreha T, Woldeamanuel Y, Pietsch C, Maier M, Asrat D, Abebe A, Liebert UG. Genotypes and viral load of hepatitis C virus among persons attending a voluntary counseling and testing center in Ethiopia. J Med Virol 2011 May;83(5):776–82. http://dx.doi.org/10.1002/jmv.21788. PMID:21351106.
[42] Onyekwere CA, Hameed L. Hepatitis B and C virus prevalence and association with demographics: report of population screening in Nigeria. Trop Doct 2014;45(4):231–5. doi: 10.1177/0049475514560211. PMID: 25515733. doi: 10.1177/0049475514560211.
[43] Riou J, Aït Ahmed M, Blake A, Vozlinsky S, Brichler S, Eholié S, et al. Hepatitis C virus seroprevalence in adults in Africa: a systematic review and meta-analysis. J Viral Hepat 2015 Oct 19. doi:10.1111/jvh.12481. PMID:26558905. doi: 10.1371/journal.pone.0141715.
[44] Esteban JI, Sauleda S, Quer J. The changing epidemiology of hepatitis C virus infection in Europe. J Hepatol 2008 Jan; 48(1):148–62. PMID: 18022726.
[45] Dultz G, Zeuzem S. Hepatitis C virus: a european perspective. Gastroenterol Clin North Am 2015 Dec;44(4):807–24. http://dx.doi.org/10.1016/j.gtc.2015.07.008. PMID: 26600221.
[46] Kauhl B, Heil J, Hoebe CJ, Schweikart J, Krafft T, Dukers-Muijrers NH. The spatial distribution of hepatitis C virus infections and associated Determinants—An application of a geographically weighted poisson regression for evidence-based screening interventions in hotspots. PloS One 2015 Sep 9;10(9):e0135656. http://dx.doi.org/10.1371/journal.pone.0135656. PMID:26352611.
[47] Tafuri S, Prato R, Martinelli D, Melpignano L, De Palma M, Quarto M, et al. Prevalence of Hepatitis B, C, HIV and syphilis markers among refugees in Bari, Italy. BMC Infect Dis 2010 Jul 20;10:213. http://dx.doi.org/10.1186/1471-2334-10-213. PMID: 20646306.
[48] García Comas L, Ordobás Gavín M, Sanz Moreno JC, Ramos Blázquez B, Gutiérrez Rodríguez A, Astray Mochales J, et al. Prevalence of hepatitis C antibodies in the population aged 16–80 years in the Community of Madrid 2008–2009. J Med Virol 2015 Oct;87(10):1697–701. http://dx.doi.org/10.1002/jmv.24219. PMID:25989026.
[49] Abdel-Ghaffar TY, Sira MM, El Naghi S. Hepatitis C genotype 4: the past, present, and future. World J Hepatol 2015 Dec 8; 7(28):2792–810. http://dx.doi.org/10.4254/wjh.v7.i28.2792. PMID:26668691.

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[50] Agwale SM, Tanimoto L, Womack C, Odama L, Leung K, Duey D, et al. Prevalence of HCV coinfection in HIV-infected individuals in Nigeria and characterization of HCV genotypes. J Clin Virol 2004 Dec;31(Suppl 1):S3—6. PMID:15567088.

[51] Zeba MTA, Sanou M, Bisseye C, Kiba A, Nagalo BM, Djigma FW, Simporé J. Characterisation of hepatitis C virus genotype among blood donors at the regional blood transfusion centre of Ouagadougou, Burkina Faso. Blood Transfus 2014 Jan; 12(Suppl 1):s54—7. http://dx.doi.org/10.2450/2012.0089-12. PMID: 23058861.

[52] Marascio N, Liberto MC, Barreca GS, Zicca E, Quirino A, Lamberti AG, et al. Update on epidemiology of HCV in Italy: focus on the calabria region. BMC Infect Dis 2014;14(Suppl 5): S2. http://dx.doi.org/10.1186/1471-2334-14-S5-S2. PMID: 25236184.

[53] van de Laar TJ, Van der Bij AK, Prins M, Bruisten SM, Brinkman K, Ruys TA, et al. Increase in HCV incidence among men who have sex with men in Amsterdam most likely caused by sexual transmission. J Infect Dis 2007;196:230—8. PMID: 17570110.

[54] van de Laar TJ, Matthews GV, Prins M, Danta M. Acute hepatitis C in HIV-infected men who have sex with men: an emerging sexually transmitted infection. AIDS 2010;24(12): 1799—812. http://dx.doi.org/10.1097/QAD.0-b013e32833c11a5. PMID:20601854.

[55] Coppola N, Alessio L, Gualdieri L, Pisaturo M, Sagnelli C, Caprio N, et al. Hepatitis B virus, hepatitis C virus and human immunodeficiency virus infection in undocumented migrants and refugees in southern Italy, January 2012 to June 2013. Euro Surveill 2015 Sep;3:20. http://dx.doi.org/10.2807/1560-7917.ES.2015.20.35.30009. PMID:26530499.

[56] Kauhl B, Heil J, Hoebe CJ, Schweikart J, Krafft T, Dukers-Muijrers NH. The spatial distribution of hepatitis C virus infections and associated determinants—an application of a geographically weighted poisson regression for evidence-based screening interventions in hotspots. PloS One 2015; 10(9):e0135656. http://dx.doi.org/10.1371/journal.-pone.0135656. PMID: 26352611.

[56a] Riccardo F, Dente MG, Kärki T, Fabiani M, Napoli C, Chiarenza A, et al. Towards a European framework to monitor infectious diseases among migrant populations: design and applicability. Int J Environ Res Public Health 2015 Sep 17;12(9):11640—61. http://dx.doi.org/10.3390/i-jerph120911640. PMID: 26393623. Q11

[57] Kouider EB, Koglin U, Petermann F. Emotional and behavioral problems in migrant children and adolescents in Europe: a systematic review. Eur Child Adolesc Psychiatry 2014 Jun; 23(6):373—91. http://dx.doi.org/10.1007/s00787-013-0485-8. PMID: 24132833.

[58] Kouider EB, Koglin U, Petermann F. Emotional and behavioral problems in migrant children and adolescents in American countries: a systematic review. J Immigr Minor Health 2015 Aug;17(4):1240—58. http://dx.doi.org/10.1007/s10903-014-0039-2. PMID: 24851820.

[59] Guarino H, Marsch LA, Deren S, Straussner SL, Teper A. Opioid use trajectories, injection drug use, and hepatitis C virus risk among young adult immigrants from the former soviet union living in New York city. J Addict Dis 2015;34(2—3):162—77. http://dx.doi.org/10.1080/10550887.2015.1059711. PMID: 26132715.

[60] Germinario C, Gallone MS, Tafuri S. Migrant health: the Apulian model. Epidemiol Prev 2015 Jul-Aug;39(4 Suppl 1):76—80. PMID: 26499420.

[61] Daw MA, Dau AA, Agnan MM. Influence of healthcare-associated factors on the efficacy of hepatitis C therapy. Sci World J 2012;2012:580216. http://dx.doi.org/10.1100/2012/580216. PMID:23346018.

[62] Thomas DL. Global control of hepatitis C: where challenge meets opportunity. Nat Med 2013 Jul;19(7):850—8. http://dx.doi.org/10.1038/nm.3184. PMID: 23836235.

[63] Lindahl JF, Grace D. The consequences of human actions on risks for infectious diseases: a review. Infect Ecol Epidemiol 2015 Nov 27;5:30048. http://dx.doi.org/10.3402/iee.v5.30048. PMID: 26615822.

[64] Ronzitti N. The treaty on friendship, partnership and cooperation between Italy and Libya: new prospects for cooperation in the mediterranean? Bull Italian Polit 2009 May;1(1): 125—33.

[65] Ahmed MO, Daw MA. Mapping the travel route of African refugees who traverse Libya to determine public health implications for Libya and the North-African region. Travel Med Infect Dis 2016 Jan 4;1:1—3. http://dx.doi.org/10.1016/j.tmaid.2015.12.007.

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