Hepatitis C virus infection: Spread and impact in the Netherlands
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Hepatitis C in the general population of various ethnic origins living in the Netherlands: Should non-Western migrants be screened?

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Background & Aims: Little is known about the HCV prevalence in non-Western migrant populations. To determine whether targeted HCV screening and prevention programs for migrants are needed, we examined HCV prevalence and determinants among non-Western, Western migrants, and the native Dutch population in the Netherlands.

Methods: Data were obtained from four surveys: (1) 3895 heterosexual visitors recruited during biannual surveys at the STI-clinic Amsterdam, 2007–2009; (2) random sample of 4563 pregnant women in Amsterdam, 2003; (3) population-based random sample of 1309 inhabitants of Amsterdam, 2004; (4) population-based random sample of 4428 people living in the Netherlands, 2006–2007. Characteristics associated with HCV-positivity were examined and phylogenetic analysis was used to obtain insight in the geographical origin of HCV strains.

Results: HCV seroprevalence in the four surveys was low (0.3–0.6%). In total 4860/14,195 (34%) were non-Western and 9329/14,195 (66%) Western participants (including Dutch). First-generation non-Western migrants were more likely to be HCV-positive (0.7–2.3%) than Western participants (0.1–0.4%). Except for survey 3, second-generation non-Western migrants had a lower HCV prevalence than first-generation migrants, comparable to Western migrants and the Dutch population. Phylogenetic analysis showed that the majority of the HCV-positive, first-generation non-Western non-European migrants were infected with endemic strains which are rarely observed in Europe.

Conclusions: First-generation non-Western migrants are at increased risk for HCV. Phylogenetic analysis suggests that transmission likely took place in the country of origin, causing introduction but no further transmission of endemic HCV strains in the Netherlands. HCV screening and prevention programs should target first-generation, but not second-generation, non-Western migrants.

Keywords: Hepatitis C; Migrants; Epidemiology; Phylogeny; Prevalence; Population-based.

Introduction

Hepatitis C virus (HCV) is primarily a blood-borne virus and causes persistent viremia in 50–85% of those infected [1]. Chronic infection can lead, over decades, to liver cirrhosis, and eventually death. In high-income countries, health-care associated HCV transmission was effectively halted by the introduction of donor blood screening in 1991. As a result, the vast majority of new HCV infections occur among specific risk groups, in particular injecting drug users (IDUs) who share injection equipment. In contrast, in low- and middle-income countries, the majority of HCV transmissions remain health-care associated because of the use of inadequately sterilized syringes and medical equipment [1].

HCV prevalence and the related burden of disease in high-income countries might have increased over the past decades as a result of the growing number of people immigrating from low- and middle-income countries [2–5]. In most European countries, a substantial proportion of the migrant population resides in large cities. In the Netherlands, Amsterdam has the largest proportion of migrants; 35% of the population in Amsterdam is of non-Western ethnicity and 14.9% are migrants from Western countries [6]. The three largest non-Western migrant groups living in Amsterdam originate from Surinam (9.0% of the total Amsterdam population), Morocco (9.0%) and Turkey (5.3%) [6]. The estimated HCV prevalence in Morocco, Surinam, and Turkey (1.1–2.9%, 1–5.5%, and 1.5–2.9%, respectively) is much higher [7,8] than that estimated for the Netherlands (0.1–0.4%) [9,10].

In the Netherlands, information campaigns advise migrants originating from endemic countries to test for HCV [9]. This advice is based on estimated HCV prevalences in the country of
HCV epidemiology among subpopulations in the general Dutch population

Materials and methods

Four different population-based surveys in Amsterdam (survey 1–3) and the Netherlands (survey 4) were used to study the seroprevalence of HCV among the various ethnic groups living in the Netherlands and the native Dutch population. Survey 1, 3, and 4 are all approved by a medical ethics committee. For the anonymous testing of sera of pregnant women (survey 2), the medical ethics committee established that the project did not require IRB (Institutional Review Board) approval.

Survey 1: sexually transmitted infections (STI) outpatient clinic

In a total of five waves – in May and November 2007, in April and October 2008, and in May 2009 – 7716 attendees of a large STI outpatient clinic in Amsterdam, ≥16 years of age, were asked to participate in a biannual anonymous survey that has been conducted since 1991 [12]. An informed consent was signed by 5228 (67%) of the participants. Since recent data have shown that HCV is emerging as an STI among HIV-infected men who have sex with men (MSM), and highly prevalent in this group [13], all MSM (N = 1282) were excluded in this analysis. In addition, 49/3946 of heterosexual participants were excluded due to missing laboratory results, leaving 3895 heterosexual participants for analysis, of whom 42% were of non-Dutch ethnicity.

Survey 2: random sample of pregnant women

In the Netherlands, all pregnant women are routinely tested for hepatitis B virus (HBV), syphilis, and HIV around their 12th week of pregnancy at local antenatal clinics and local hospitals [14]. In the region of Amsterdam, 10,000–14,000 pregnant women are annually tested and basic demographic characteristics are collected.

Of the 13,644 samples tested in 2003, 12,676 samples were tested and stored at the Public Health Service Laboratory. Of those, we randomly selected and anonymously tested 5146 (40.6%) for HCV antibodies. Demographic data were lacking for 583 samples (including two HCV positives). These samples were therefore excluded, leaving 4563 samples of pregnant women for the analysis: 49% of the participants were of non-Dutch ethnicity.

Survey 3: random selection of the Amsterdam population

From April till June 2004, a random sample of 4042 persons of ≥18 years and living in Amsterdam was asked to participate in the Amsterdam Health Monitor [15]. Non-Dutch participants were oversampled. Of the 4042 invited persons, 1736 (42.9%) were interviewed of whom 1364 (78.6%) donated blood. For the present study, all MSM were excluded (N = 55), leaving 1309 participants for inclusion, of whom 68% were of non-Dutch ethnicity.

Survey 4: national survey (Pienter study)

The Pienter study aims to establish a serum bank of a representative sample of the Dutch population to facilitate sero-epidemiological studies [16]. This population-based cross-sectional zero-survey was conducted in 1996–1997 and again in 2006–2007; we only used data from the second survey. Subjects were selected through a stratified random selection for age and region. Non-Dutch participants were oversampled. A total of 17,223 subjects were invited to participate of which 6243 (36.2%) were tested for anti-HCV: participants ≤14 years (N = 1797), MSM (N = 16) and two non-responders were excluded, leaving 4428 participants as our study population of whom 19% were of non-Dutch ethnicity.

HCV antibodies were detected using a third-generation commercial microparticle EIA system (AxSYM HCV version 3.0, Abbott) with immunoblot confirmation (Chiron RIBA HCV 3.0 SIA; Ortho-Clinical Diagnostics or HCV Score, Innogenetics). Anti-HCV-positive samples were tested for the presence of HCV–RNA by either the VERSANT(r) HCV–RNA Qualitative Assay, Siemens (survey 1 and 2) or an in-house PCR as described by van de Laar et al. [17] (survey 3 and 4).

In survey 2, 1811/5146 (35.2%) pregnant women tested anti-HCV-positive when using the cutoff rate provided by the manufacturer (AxSym ratio ≥1). 1682/1811 (92.9%) had a AxSym ratio between 1 and 2. Based on these results a new cutoff was determined; samples that lacked HCV immunoblot confirmation were classified anti-HCV-positive only when the AxSym ratio exceeded 10.

For survey 1, 2, and 3, samples were all tested for hepatitis B core antigen (anti-HBc) by means of a microparticle enzyme immunoassay (AxSym CORE, Abbott). All anti-HBc-positive samples were subsequently screened for HBsAg (AxSYM HBsAg V2, Abbott) and confirmed with an enzyme-linked fluorescent assay neutralization test (VIDAS HBsAg, BioMerieux). In addition, in survey 1, 2, and 3, HCV testing was performed using a third-generation commercial microparticle EIA system (AxSYM Hepatitis A/B Combo, Abbott) with immunoblot confirmation (RIBON-LIA HCV UR Score; Innogenetics N.V.).

HCV RNA amplification, sequencing, and phylogenetic analysis

For all HCV–RNA-positives, part of the HCV NS5B region (436 bp) was amplified and sequenced using genotype-specific primer sets [18]. The viral genotype was determined after phylogenetic analysis of the NS5B sequences obtained, along with established GenBank reference sequences [19]. A HCV phylogenetic tree was constructed by the maximum likelihood method in PHYML version 3.0 [20] using the KKY substitution model with γ-distribution of among-site rate heterogeneity. Bootstrapting (n = 1000) was used to analyze the stability of the tree topology. The HCV sequences of migrants in the Netherlands were compared to those obtained from 81 HCV–RNA-positive Dutch donors in the period 1997–2002 [17, 19]. HCV genotype 2-infected and 133 HCV genotype 4-infected patients (of varied ethnic origin) diagnosed in the Netherlands between 2000 and 2008 [21,22] as well as to sequences from the migrants’ (or their parents) country of origin were submitted to GenBank.

Statistical analysis

We calculated HCV prevalence and its corresponding 95% confidence interval (CI) by ethnicity. A p-value <0.05 was considered statistically significant. Confidence intervals around prevalence were calculated via the Wilson method, using the binomial statistical package in R [23,24]. Odds ratios (OR) and CI in a 2 x 2 table with one zero cell count were calculated via penalized logistic regression using the logistf package in R [23,24]. Otherwise, logistic regression in SPSS 17.0 was used.

Since the study-population and inclusion criteria of the surveys differ, each survey was presented separately. In addition, we also present the results of the four surveys combined for the largest migrants groups.

Definitions

Ethnicity was determined by the country of birth of the participant’s mother. If the mother was native Dutch, ethnicity was determined by the country of birth of the participant’s father. First- or second-generation was determined by the native country of the migrant; migrants who were born in the Netherlands were considered first-generation; migrants’ descendants born in the Netherlands were considered second-generation.
Results

Characteristics of participants

All surveys included more women than heterosexual men (Table 1). As expected, the median age was lower among STI-clinic attendees and pregnant women (25 years; IQR 22–31 years; and 48 years, IQR 31–63 years, respectively). The proportion of non-Western participants varied from 14.1% (national survey) to 48 years, IQR 31–63 years, respectively). The proportion of non-Western participants varied from 14.1% (national survey) to

<table>
<thead>
<tr>
<th>Characteristics of participants</th>
<th>Western ethnicity</th>
<th>Dutch</th>
<th>Other Western</th>
<th>1st-generation</th>
<th>2nd-generation</th>
<th>Non-Western ethnicity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Survey 1 Heterosexual visitors, STI-clinic</td>
<td>n = 3,895</td>
<td>2,206/3,895</td>
<td>2,206/3,895</td>
<td>2,206/3,895</td>
<td>2,206/3,895</td>
<td>6/1,393</td>
</tr>
<tr>
<td>Median age (IQR)</td>
<td>25 years (22-31)</td>
<td>49 years (39-60)</td>
<td>31 years (28-34)</td>
<td>49 years (39-60)</td>
<td>48 years (31-63)</td>
<td>12/3,895</td>
</tr>
<tr>
<td>Female</td>
<td>100%</td>
<td>100%</td>
<td>100%</td>
<td>100%</td>
<td>100%</td>
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</tr>
<tr>
<td>HCV prevalence</td>
<td>95% CI</td>
<td>6%</td>
<td>6%</td>
<td>6%</td>
<td>6%</td>
<td>6%</td>
</tr>
<tr>
<td>Survey 2 Pregnant women</td>
<td>n = 4,563</td>
<td>4,563/4,563</td>
<td>4,563/4,563</td>
<td>4,563/4,563</td>
<td>4,563/4,563</td>
<td>4/4,563</td>
</tr>
<tr>
<td>Median age (IQR)</td>
<td>25 years (22-31)</td>
<td>49 years (39-60)</td>
<td>31 years (28-34)</td>
<td>49 years (39-60)</td>
<td>48 years (31-63)</td>
<td>15/4,563</td>
</tr>
<tr>
<td>Female</td>
<td>100%</td>
<td>100%</td>
<td>100%</td>
<td>100%</td>
<td>100%</td>
<td>100%</td>
</tr>
<tr>
<td>HCV prevalence</td>
<td>95% CI</td>
<td>6%</td>
<td>6%</td>
<td>6%</td>
<td>6%</td>
<td>6%</td>
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<tr>
<td>Survey 3 Amsterdam population</td>
<td>n = 1,309</td>
<td>734/1,309</td>
<td>734/1,309</td>
<td>734/1,309</td>
<td>734/1,309</td>
<td>13/1,309</td>
</tr>
<tr>
<td>Median age (IQR)</td>
<td>49 years (39-60)</td>
<td>48 years (31-63)</td>
<td>49 years (39-60)</td>
<td>48 years (31-63)</td>
<td>49 years (39-60)</td>
<td>81/1,309</td>
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<td>100%</td>
<td>100%</td>
<td>100%</td>
<td>100%</td>
<td>100%</td>
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<tr>
<td>HCV prevalence</td>
<td>95% CI</td>
<td>6%</td>
<td>6%</td>
<td>6%</td>
<td>6%</td>
<td>6%</td>
</tr>
<tr>
<td>Survey 4 Dutch population</td>
<td>n = 4,428</td>
<td>2,518/4,428</td>
<td>2,518/4,428</td>
<td>2,518/4,428</td>
<td>2,518/4,428</td>
<td>30/4,428</td>
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<tr>
<td>Median age (IQR)</td>
<td>49 years (39-60)</td>
<td>48 years (31-63)</td>
<td>49 years (39-60)</td>
<td>48 years (31-63)</td>
<td>49 years (39-60)</td>
<td>144/4,428</td>
</tr>
<tr>
<td>Female</td>
<td>100%</td>
<td>100%</td>
<td>100%</td>
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<tr>
<td>HCV prevalence</td>
<td>95% CI</td>
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HCV prevalence estimates among STI-clinic attendees, pregnant women, and the national population was 0.3%. The HCV prevalence in the Amsterdam population was estimated at 0.6%. The HCV prevalence among non-Western migrants, and 0%, 0.4%, 1.9%, and 0% for other Western migrants (excluding Dutch participants).

The combined data of the four surveys result in an HCV prevalence estimate among first-generation migrants from Morocco 0.3% (2/810, 95% CI; 0.07–0.90), Surinam 0.6% (4/626, 95% CI; 0.20–0.94), Turkey 0.8% (6/764, 95% CI; 0.33–1.57), and 0% for other Western migrants (including Dutch participants).
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0.25–1.63), and Turkey 0.2% (1/606, 95% CI; 0.01–0.93) compared to native Dutch 0.2% (13/8609, 95% CI; 0.09–0.26). None of the second-generation migrants from Morocco, Surinam, and Turkey tested positive for HCV-antibodies.

Determinants of HCV infection

First-generation non-Western migrants were more likely to be infected with HCV when compared to people of Western ethnicity: pregnant women (OR 5.67, 95% CI; 1.73–18.6), national survey (OR 20.5, 95% CI: 6.76–62.2), and although not statistically significant, STI-clinic attendees (OR 2.94; 95% CI: 0.83–10.43) and the Amsterdam population (OR 1.56, 95% CI; 0.30–8.08) (Table 2).

In univariate analysis, also being HIV-positive (OR 117.6, 95% CI; 11.3–1219.7), reporting IDU (OR 645.2, 95% CI; 171.1–2432.8), having chronic HBV infection (HBsAg positive) (OR 58.7, 95% CI; 6.53–529.2), and of older age (OR 1.08 for every year older 95%

Table 2. Univariate analysis of risk factors and other characteristics for HCV for survey 1–4.

<table>
<thead>
<tr>
<th></th>
<th>Survey 1 Heterosexual visitors, STI-clinic n = 1,895</th>
<th>Survey 2 Pregnant women n = 4,563</th>
<th>Survey 3 Amsterdam population n = 1,309</th>
<th>Survey 4 Dutch population n = 4,428</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Seronegative n = 3,883 n (%)</td>
<td>Seropositive n = 12 n (%)</td>
<td>Seronegative n = 4,548 n (%)</td>
<td>Seropositive n = 15 n (%)</td>
</tr>
<tr>
<td>Median age (IQR)</td>
<td>25 (22-31) 41 (26-49) 1.08 (1.04-1.13)</td>
<td>31 (28-34) 35 (29-40) 1.14 (1.02-1.27)</td>
<td>49 (39-60) 53 (45-60) 1.03 (0.98-1.08)</td>
<td>48 (31-63) 54 (40-61) 1.02 (0.99-1.05)</td>
</tr>
<tr>
<td>Ethnicity</td>
<td>Western</td>
<td></td>
<td>Western</td>
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<tr>
<td></td>
<td>2,496 (64.3) 6 (50.0) 1</td>
<td>2,543 (55.9) 3 (13.3) 1*</td>
<td>474 (36.6) 2 (25.5) 1</td>
<td>3,801 (86.1) 4 (28.6) 1*</td>
</tr>
<tr>
<td></td>
<td>1st generation non-Western</td>
<td></td>
<td>759 (58.5) 5 (82.5) 1.56 (0.30-0.80)</td>
<td>432 (9.8) 10 (71.4) 20.5 (6.76-62.2)</td>
</tr>
<tr>
<td></td>
<td>2nd generation non-Western</td>
<td></td>
<td>83 (4.9) 1 (12.5) 3.76 (0.34-42.1)</td>
<td>181 (4.1) 0 2.33 (0.12-43.7)</td>
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<tr>
<td></td>
<td>2 (0.2)</td>
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<td>1.721 (99.8) 8 (100) 1</td>
<td>Not available</td>
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<td>28</td>
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<td>1.269 (98.8) 8 (100) 1</td>
<td>Not available</td>
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<td>16 (0.2)</td>
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<td>16</td>
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<td></td>
<td>718 (55.2) 2 (25.0) 1</td>
<td>Not available</td>
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<td>0 (0)</td>
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<td></td>
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<td></td>
<td>583 (44.8) 4 (50.0) 2.07 (0.46-10.5)</td>
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</tbody>
</table>

95% CI, 95% confidence interval; HCV, hepatitis C virus; IQR, interquartile range; MSM, men who have sex with men; STI, sexually transmitted infections.

Overall p smaller or equal to 0.001.

Overall p smaller or equal to 0.05.
CI; 1.04–1.13) were associated with HCV infection among STI-clinic attendees (Table 2). Among pregnant women, being HIV positive (OR 87.3, 95% CI; 16.9–451.1), having a chronic HBV infection (OR 11.5, 95% CI; 1.47–90.7), and of older age (OR 1.14, 95% CI; 1.04–1.13) were associated with HCV infection (data on IDU not available). In the Amsterdam and the national population, IDU was associated with HCV infection (OR 1437, 95% CI; 28.5–72,489 and OR 285.9, 95% CI; 59.3–1379.5, respectively).

Data on HIV and HBV were not available in the national survey. In the Amsterdam survey, those with active HBV or HIV infection were also at increased risk but the effect was not statistically significant (Table 2).

### Genotyping and phylogenetic analysis

HCV–RNA was detected in 9/15 (60%) of Western participants and 28/34 (82%) non-Western participants. HCV genotyping succeeded for all HCV–RNA-positive participants (Table 3). Phylogenetic analysis revealed that Western participants were exclusively infected with so-called epidemic HCV strains of genotype 1a (2x), 1b (2x), 3a (4x), and 4d (1x). These strains have a worldwide distribution, due to their rapid spread in the 20th century via effective transmission routes such as IDU and contaminated blood products.

Non-Western migrants were infected with a wider range of subtypes: 13/28 non-Western migrants were also infected with the epidemic HCV strains: 1a (1x), 1b (4x), 3a (6x), and 4d (2x); but 15/28 were infected with so-called endemic HCV strains. Endemic HCV strains are geographically restricted, and typically have high genetic variation due to long-term local persistence; they are rarely observed in the Netherlands. All participants infected with an endemic HCV strain were first-generation migrants from non-Western non-European countries; a Philippine participant with an aberrant strain of subtype 2a, two North African participants with subtype 2i, a Dominican participant with subtype 2r, four migrants from Surinam all infected with a distinct and unrecognized subtype of HCV genotype 2, a Pakistani subject infected with genotype 3a, three Egyptian participants infected with HCV genotype 4a, an Ethiopian and a Turkish participant with aberrant strains of genotype 4d, and an Angolan participant with a yet unrecognized subtype of HCV genotype 4. Phylogenetic analysis of these strains showed a high degree of phylogenetic clustering with HCV strains obtained from the migrant’s country of origin (Fig. 1).

In contrast, 11/13 non-Western migrants who were infected with an epidemic HCV strain were either first-generation migrants from Eastern or Southern Europe, or second-generation migrants born in the Netherlands (Indonesian and Tunisian). The HCV strains obtained from Eastern European migrants were all from the group of epidemic subtypes, particularly those linked to injecting drug use (1a, 3a, and 4d). The two first-generation non-Western non-European participants infected with an epidemic strain came from Pakistan (genotype 3a) and Indonesia (genotype 1b). Hence, these two participants might have been infected in the Netherlands, but due to the rapid worldwide expansion of these epidemic strains during the 20th century, we are unable to clearly distinguish between sequences of epidemic HCV subtypes obtained from different geographic locations (i.e., the Netherlands or the migrant’s country of origin) using phylogenetic analysis of our NS5B fragment [26,27].

### Discussion

In this large-scale study, conducted in a country of low HCV prevalence, we generally found a higher level of HCV prevalence...
among first-generation non-Western migrants compared to second-generation (except for one survey) or Western participants, but a lower prevalence than in the country of origin. These results indicate that second-generation non-Western migrants have a HCV prevalence comparable to that of the native Dutch (or generally Western) population. In the Netherlands no other properly large-scale study was done before. Other community-based studies in the Netherlands with HCV prevalence ranging from 0.2% to 1.1% (no distinction between first and second-generation) [28–30] were relatively small and not representative for the general Dutch population [28,30], and/or large migrant populations were underrepresented [28,29]. In our study, survey 2, 3, and 4 were all representative studies for the general Amsterdam or Dutch population. In survey 3 and 4 non-Western migrants were oversampled. Survey 1 was not representative for the general population but provides a good insight in the HCV spread among sexually active younger (second-generation) migrants.

The combined results of four large-scale surveys, showed a lower HCV prevalence in first-generation migrants from the three largest migrant groups in the Netherlands (i.e., Surinamese, Turkish, and Moroccan) than the estimates in the country of origin supporting our hypothesis. This is in also line with the

Fig. 1. Hepatitis C virus NS5B phylogenetic tree of study participants (bold) along with related and unrelated reference strains. Endemic HCV strains are depicted in red, epidemic strains in black. The risk factors allocated for each HCV strain are listed opposite each sequence: first-generation migrant (X). Injecting drug use (●), transfusion/Nosocomial (○).
findings of Uddin et al. in their study of HCV prevalence among almost 5000 south Asian migrants living in England [5]. The difference between HCV prevalence in migrant communities living in Western countries and the prevalence in the home country might be explained by a shorter exposure period to HCV in the home country, the selection of individuals that emigrated (healthy migrant effect), or migration from a region of low prevalence in the country of origin [5]. It could also be caused by an overestimation of the HCV prevalence in the country of origin of migrants due to a lack of data [5] or to the salmon bias (i.e., severely ill migrants return to die in their home country).

We also hypothesized that HCV prevalence among the three largest non-Western groups living in the Netherlands is higher than among the general population of the Netherlands. However, the observed prevalence, even among first-generation migrants in our study, is in the range of the estimated HCV prevalence in the Netherlands (0.1–0.4%) [9], with the exception of first-generation migrants from Surinam. However, the HCV prevalence among first-generation Surinamese participants differs between the surveys. The lower HCV prevalence found in survey 1 and 2 (STI-clinic visitors and pregnant women) compared with survey 3 and 4 (general populations) is likely to be explained by the higher median age in the latter surveys. The relationship between HCV and increasing age suggests that most infections occurred further in the past, possibly in the era before the introduction of donor blood screening and reduced hospital hygiene.

Phylogenetic analysis showed that HCV sequences obtained from first-generation non-European, non-Western migrants had a high degree of phylogenetic clustering with HCV strains circulating in their country of origin. This suggests that the participants acquired their infection in their country of origin, possibly by parental transmission via unsterile medical equipment or by contaminated blood transfusions [1]. The fact that second-generation migrants as well as the native Dutch population are unaffected by these typical HCV migrant strains suggests that no (or only sporadic) HCV transmission occurs once first-generation migrants live in low-endemic countries. Hence, being a HCV-negative at the time of migration and not participating in specific high-risk behavior for HCV such as injecting drugs, the risk of acquiring HCV for first-generation migrants living in the Netherlands, most likely is similar to that of the general Dutch population. However, (frequent) traveling between the country of residence and the country of origin might increase the risk of acquiring HCV, especially when undergoing medical procedures in the country of origin.

We are aware that for some ethnic groups the numbers were small, resulting in wide confidence intervals around the prevalence. However, since there are not many large-scale population based studies of multi-ethnic populations, our study provides important information for accurate estimation of the prevalence and disease burden of HCV in the Netherlands. Our findings on migrants are not restricted to the Netherlands and may also be informative for HCV estimates for other European countries and the country of origin of the migrant groups studied. Other population-based studies in Europe were either focussing on specific ethnic groups or did not distinguish between first- and second-generation [5,31].

In conclusion, first-generation non-Western migrants, but not second-generation migrants, are at higher risk for HCV infection compared to the native Western population. Phylogenetic analysis confirms that the majority of HCV infections among first-generation migrants were probably acquired in the country of origin. Targeted screening programs for migrants, should be focussed at first-generation non-Western migrants. However, for migrants from Morocco and Turkey, specific screening programmes based on country of origin are not recommended because of the low HCV prevalences found in first-generation migrants from these countries. Although migrants will need a culturally adequate approach for prevention and screening options [32], the criteria to define the population at HCV risk (based on risk factors, such as IDU, blood transfusion in endemic country, etc.) for screening should not differ from that for the Dutch native population.

Conflict of interest

The authors who have taken part in this study declared that they do not have anything to disclose regarding funding or conflict of interest with respect to this manuscript.

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References

HCV epidemiology among subpopulations in the general Dutch population

Research Article


