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Increase in HCV Incidence among Men Who Have Sex with Men in Amsterdam Most Likely Caused by Sexual Transmission

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We retrospectively screened 1836 men who have sex with men (MSM) participating in the Amsterdam Cohort Studies (1984–2003) for hepatitis C virus (HCV) antibodies. HCV incidence was 0.18/100 person-years (PY) in human immunodeficiency virus (HIV)–positive MSM (8/4408 PY [95% confidence interval {CI}, 0.08–0.36]) but was 0/100 PY in MSM without HIV (0/7807 PY [95% CI, 0.00–0.05]). After 2000, HCV incidence among HIV-positive men increased 10-fold to 0.87/100 PY (5/572 PY [95% CI, 0.28–2.03]). Additional hospital cases showed that MSM in Amsterdam who acquired HCV infection after 2000 reported high rates of ulcerative sexually transmitted infections (59%) and rough sexual techniques (56%), denied injection drug use, and were infected mainly with the difficult-to-treat HCV genotypes 1 (56%) and 4 (36%). Phylogenetic analysis showed 3 monophyletic clusters of MSM-specific HCV strains. The emergence of an MSM-specific transmission network suggests that HIV-positive MSM with high-risk sexual behaviors are at risk for sexually acquired HCV. Targeted prevention and routine HCV screening among HIV-positive MSM is needed to deter the spread of HCV.

Hepatitis C virus (HCV) infection occurs mainly by parenteral exposure, particularly injection drug use (IDU) [1]. Its association with sexual transmission remains controversial. Even in the presence of HIV coinfection, HCV is rarely transmitted by heterosexual intercourse [2]. HCV-serodiscordant partners in long-term monogamous heterosexual relationships show only slightly higher rates of HCV infection than the general population [3]. Data obtained from men who have sex with men (MSM) are more conflicting [4, 5]. Previous cross-sectional and cohort studies have reported increased HCV prevalence among MSM and have highlighted unprotected anal intercourse, multiple sex partners, rough sexual techniques, and coinfection with HIV-1 and other sexually transmitted infections (STIs) as potential risk factors [6–10]. However, these associations between sexual risk factors and HCV did not reach statistical significance and were often confounded by concurrent IDU [4].

A growing number of case reports from Europe
Subject, Materials, and Methods

Study population I—the Amsterdam Cohort Studies (ACS) of MSM. The ACS of MSM is an open, ongoing prospective study [20]. Recruitment was started in October 1984 and uses “convenience sampling” (advertisements: brochures at the STI clinic and social venues for MSM) and “chain referral sampling” (recruitment by participants among their acquaintances). The local ethical committee approved the ACS, and all MSM participated only after they provided informed consent. Until 1995, the ACS included MSM of all ages with at least 2 male sex partners during the 6 months preceding enrollment, regardless of HIV status. After 1995, participation was restricted mainly to HIV-negative MSM in Amsterdam, the Netherlands, over the course of nearly 2 decades (1984–2003). Additionally, 5 Amsterdam hospitals provided serum samples and data on parental and sexual risk behaviors of MSM given the diagnosis of an acute HCV infection after 2000. Phylogenetic analysis was used to obtain evidence of sexual transmission of HCV in MSM.

Study population II—hospital case reports. In the Netherlands, the law requires that all acute HCV infections (until 2003, all newly diagnosed HCV infections) be reported to the local health service to enable source tracing and to prevent the further spread of HCV. Through review of these reports and through contact with physicians treating HCV in 5 major hospitals, including the STI clinic in Amsterdam, we identified 34 MSM who acquired HCV after the year 2000 and for whom blood was stored. Of these, 32 men had a confirmed seroconversion of anti-HCV antibodies and detection of HCV RNA after a previously HCV-negative sample. The other 2 men lacked a previous HCV-negative sample but acute HCV infection (jaundice, elevated liver enzymes, and exclusion of hepatitis A and B) had been diagnosed by their physicians. To identify the probable route of transmission, additional data on possible IDU, blood-blood contact, STI coinfection, and sexual risk behaviors were obtained by review of medical charts and notification reports. For all patients, informed consent had been obtained by their treating physician.

HCV RNA isolation and reverse-transcription polymerase chain reaction (RT-PCR) methods. Using the first HCV-seropositive sample obtained for ACS participants and hospital patients, RNA isolation was performed on 100 μL of serum using the TriPure method (Roche Diagnostics). Each RNA isolate was used as input for 2 nested multiplex RT-PCRs. The first PCR, which targets the conserved HCV core region, was devised as a genotyping system to amplify HCV RNA of subtypes 1a, 1b, 2a, 2b, 3a, 4, 5a, and 6a. The second PCR, which targets the NS5B region, was used for phylogenetic analysis. Conditions and primers for both RT-PCRs have been described elsewhere [22].

Sequencing and phylogenetic analysis. The sequencing reaction was performed as described by Van de Laar et al. [22]. First, NS5B PCR products were ethanol precipitated. Sense and antisense strands were separately cycle sequenced using the BigDye Terminator system (version 1.1; Perkin Elmer). Sequence products were purified using DyeEx spin kits (Qiagen) and analyzed on an ABI-310 automated sequencer (Applied Biosystems). Sequence alignment of the 436-bp NS5B fragment was performed using the BioEdit software package [23]. Viral genotype was confirmed after phylogenetic analysis of the NS5B sequences obtained (GenBank accession numbers DQ897975–DQ898026 and EF123061–EF123064) along with 5 GenBank reference sequences [24]. Mega software (version 3.1; available at: http://www.megasoftware.net) was used to construct a phylogenetic tree by the neighbor-joining method, using the Tamura-Nei substitution model with γ-distribution (α = 0.40). Bootstrap values (n = 1000) were calculated to analyze the stability of tree topology. HCV sequences from MSM participants were compared with HCV sequences from HIV-positive Eu-
Table 1. Risk factors associated with positive hepatitis C virus (HCV) serostatus at Amsterdam Cohort Studies entry.

<table>
<thead>
<tr>
<th>Risk factor</th>
<th>HCV status</th>
<th>Univariate analysis, OR (95% CI)</th>
<th>Multivariate analysis, OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Seronegative</td>
<td>Seropositive</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>1812 (100)</td>
<td>24 (100)</td>
<td></td>
</tr>
<tr>
<td>Age, mean ± SD, years</td>
<td>31.7 ± 8.1</td>
<td>36.1 ± 9.1</td>
<td>1.1 (1.0–1.1)</td>
</tr>
<tr>
<td>History of IDU</td>
<td>(117 missing)</td>
<td>(4 missing)</td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>1693 (99)</td>
<td>18 (90)</td>
<td>1</td>
</tr>
<tr>
<td>Yes</td>
<td>2 (0.1)</td>
<td>2 (10)</td>
<td>94.1 (12.5–705)</td>
</tr>
<tr>
<td>History of blood transfusion</td>
<td>(31 missing)</td>
<td></td>
<td>60.5 (7.4–495)</td>
</tr>
<tr>
<td>No</td>
<td>1761 (99)</td>
<td>23 (96)</td>
<td>1</td>
</tr>
<tr>
<td>Yes</td>
<td>20 (1)</td>
<td>1 (4)</td>
<td>3.8 (0.5–29.7)</td>
</tr>
<tr>
<td>HIV status</td>
<td>(10 missing)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Negative</td>
<td>1311 (73)</td>
<td>11 (46)</td>
<td>1</td>
</tr>
<tr>
<td>Positive</td>
<td>491 (27)</td>
<td>13 (54)</td>
<td>3.2 (1.4–7.1)</td>
</tr>
<tr>
<td>History of syphilis</td>
<td>(23 missing)</td>
<td></td>
<td>4.1 (1.6–10.4)</td>
</tr>
<tr>
<td>No</td>
<td>1474 (83)</td>
<td>22 (92)</td>
<td>1</td>
</tr>
<tr>
<td>Yes</td>
<td>305 (17)</td>
<td>2 (8)</td>
<td>0.9 (0.1–1.9)</td>
</tr>
<tr>
<td>Lifetime sex partners, no.</td>
<td>(505 missing)</td>
<td>(6 missing)</td>
<td></td>
</tr>
<tr>
<td>1–19</td>
<td>284 (22)</td>
<td>3 (17)</td>
<td>1</td>
</tr>
<tr>
<td>20–100</td>
<td>357 (27)</td>
<td>6 (33)</td>
<td>0.6 (0.2–2.5)</td>
</tr>
<tr>
<td>&gt;100</td>
<td>666 (51)</td>
<td>9 (50)</td>
<td>0.8 (0.3–2.3)</td>
</tr>
<tr>
<td>Sex partners in the preceding 5 years, no.</td>
<td>(730 missing)</td>
<td>(4 missing)</td>
<td></td>
</tr>
<tr>
<td>1–19</td>
<td>342 (22)</td>
<td>4 (20)</td>
<td>1</td>
</tr>
<tr>
<td>20–100</td>
<td>352 (23)</td>
<td>11 (55)</td>
<td>2.7 (0.8–8.5)</td>
</tr>
<tr>
<td>&gt;100</td>
<td>388 (36)</td>
<td>5 (25)</td>
<td>1.1 (0.3–4.1)</td>
</tr>
</tbody>
</table>

**NOTE.** Data are no. (%) of subjects, unless otherwise indicated. CI, confidence interval; IDU, injection drug use; OR, odds ratio.

* P < .01.

b P < .001.

HCV incidence per annum was calculated as the number of new infections divided by total person-years (PY) under observation for all ACS participants at risk and for HIV-positive and HIV-negative ACS participants separately. The midpoint between the last HCV-negative and first HCV-positive test was defined as the seroconversion date. Differences in HCV incidence before and after 2000 were analyzed using Poisson regression. That year was chosen as the cutoff because increases in sexual risk behaviors [20], STIs [18], and HCV incidence among MSM [15] were apparent thereafter.

**RESULTS**

**Study population—ACS.** The study population included 1836 MSM with ≥2 ACS visits between October 1984 and January 2003. The mean ± SD age at entry was 31.8 ± 8.1 years, 92% were of northwest European nationality, and 28% had at least a college degree. Median follow-up time in the ACS was
6.3 years (interquartile range [IQR], 2.8–11.2 years). These 1836 men made a total of 44,107 visits at a median interval of 91 days (IQR, 49–162 days). Most (89%) identified themselves as (almost) exclusively MSM. Reported rates of risk behavior were high; at ACS entry, 69% had had >20 sex partners during the preceding 5 years, 28% tested positive for HIV-1, and 17% had a history of syphilis. Only 4 ACS participants (0.2%) reported IDU.

**HCV prevalence—ACS.** At study entry, 24 (1.3%) of 1836 MSM tested positive for HCV antibodies. Of these, 2 had injected drugs and 1 had received a blood transfusion before the introduction of standard HCV screening of blood donors (1991). HCV-positive MSM were older than HCV-negative MSM (36.1 vs. 31.7 years; \( \text{p} < .008 \)) and were more likely to have a history of IDU (10% vs. 0.1%; \( \text{p} < .001 \)) or to test positive for HIV (54% vs. 27%; \( \text{p} = .005 \)). In multivariate analysis, only a history of IDU (odds ratio [OR], 60.5 [95% confidence interval [CI], 7.4–495]) and HIV positivity (OR, 4.1 [95% CI, 1.6–10.4]) were significantly associated with a positive HCV status at ACS entry. No other factors reflecting sexual risk behavior—such as the number of partners or a history of syphilis—were associated with HCV prevalence (table 1).

**HCV incidence—ACS.** Between October 1984 and January 2003, 8 MSM seroconverted for HCV and, after December 2000, 5 seroconverted; all 8 HCV seroconverters were HIV positive; their median age was 38.7 years (IQR, 34.5–42.6 years). Overall, HCV incidence was 0.07/100 PY (95% CI, 0.03–0.13/100 PY); it was 0/100 PY among HIV-negative men (95% CI, 0–0.05/100 PY) and 0.18/100 PY among HIV-positive men (95% CI, 0.08–0.36/100 PY). The HCV incidence among HIV-positive MSM increased significantly after the year 2000, compared with previous years—0.87/100 PY in 2000–2003 (95% CI, 0.28–2.03/100 PY), compared with 0.08/100 PY in 1984–1999 (95% CI, 0.02–0.23/100 PY; \( \text{p} < .001 \)) (table 2). The total number of HCV seroconverters in the ACS was too small to allow for a statistical analysis of sexual risk factors.

**Hospital case reports.** For the 34 participants who had a diagnosis of HCV in the 5 participating hospitals in Amsterdam, the median duration between the last HCV-negative test and the first HCV-positive test was 201 days (IQR, 98–472 days). All but 1 subject were HIV positive at the moment of HCV seroconversion; their median age was 40.0 years (IQR, 35.3–46.6 years). Medical chart reviews, performed for 27 of 34 hospital cases, found no IDU during the 6 months preceding

### Table 2. Hepatitis C virus incidence among HIV-positive and HIV-negative men who have sex with men (MSM) participating in the Amsterdam Cohort Studies over time.

<table>
<thead>
<tr>
<th>Years</th>
<th>HIV-negative MSM</th>
<th>HIV-positive MSM</th>
<th>Total MSM</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No. PY Incidence</td>
<td>No. PY Incidence</td>
<td>No. PY Incidence</td>
</tr>
<tr>
<td>1984–1999</td>
<td>0 6811 0.00 0.00–0.05</td>
<td>3 3836 0.08 0.02–0.23</td>
<td>3 10,647 0.03 0.01–0.08</td>
</tr>
<tr>
<td>2000–2003</td>
<td>0 997 0.00 0.00–0.37</td>
<td>5 572 0.87 0.28–2.03</td>
<td>5 1569 0.32 0.10–0.74</td>
</tr>
<tr>
<td>1984–2003</td>
<td>0 7808 0.00 0.00–0.05</td>
<td>8 4408 0.18 0.08–0.36</td>
<td>8 12,216 0.07 0.03–0.13</td>
</tr>
</tbody>
</table>

**NOTE.** CI, confidence interval; PY, person-years.

### Table 3. Hepatitis C virus (HCV) genotype distribution among seropositive men who have sex with men (MSM) in Amsterdam over time.

<table>
<thead>
<tr>
<th>Genotype distribution</th>
<th>HCV infections among MSM over time</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Before 2000: ACS</td>
</tr>
<tr>
<td></td>
<td>Prevalent, no.</td>
</tr>
<tr>
<td>RNA positive*</td>
<td>15/24 (63)</td>
</tr>
<tr>
<td>HCV subset</td>
<td></td>
</tr>
<tr>
<td>1a</td>
<td>2 1</td>
</tr>
<tr>
<td>1b</td>
<td>5 0</td>
</tr>
<tr>
<td>2b</td>
<td>2 0</td>
</tr>
<tr>
<td>3a</td>
<td>4 1</td>
</tr>
<tr>
<td>4d</td>
<td>2 0</td>
</tr>
<tr>
<td>Untypeable</td>
<td>0 1</td>
</tr>
<tr>
<td>Total</td>
<td>15 3</td>
</tr>
</tbody>
</table>

**NOTE.** ACS, Amsterdam Cohort Studies.

* Data are no. positive/total no. of subjects (%).
Figure 1. A, Hepatitis C virus (HCV) NS5B phylogeny of prevalent (P) and incident (S) HCV infections among men who have sex with men (MSM) in Amsterdam. A neighbor-joining tree based on the Tamura-Nei substitution model with γ-distribution (α = .40) is shown. Isolates from MSM who acquired HCV after the year 2000 are outlined (n = 34; hospital cases) or outlined and shaded (n = 5; Amsterdam Cohort Studies [ACS] participants). Isolates not outlined were from ACS participants who contracted HCV before the year 2000 (n = 17). Each isolate code also contains the year of sampling. *Two hospital case patients diagnosed with an acute HCV infection who had no previous HCV-seronegative sample available; †2 hospital case patients who reported no injection drug use (IDU), blood-blood contact, or high-risk sexual contact. B, HCV NS5B phylogeny of HCV genotype 4 infections among different risk groups. A neighbor-joining tree based on the Tamura-Nei substitution model with γ-distribution (α = .40) is shown. Isolates from MSM are outlined, from IDUs are light gray, and from Dutch immigrants are dark gray. Isolate codes contain the city and year of sampling. *Dutch MSM who also admitted to a history of IDU; †Dutch donors without any reported risk behavior; § noninjection drug user from Surinam; ¶ Dutch IDU without any known connection with Egypt. Ali/Cas, Alicante/Castellon (Spain); Ams, Amsterdam (the Netherlands); Inn, Innsbruck (Austria); Mar, Marseille (France); Tur, Turin (Italy).

Seroconversion; 1 MSM reported possible blood-blood contact after assisting at an accident involving a presumed drug user. Sexual risk behaviors among the hospital cases was high; at least 16 (59%) of 27 had had 1 or even 2 ulcerative coinfections within the 6 months preceding HCV seroconversion: lymphogranuloma venereum (LGV; 10/27), syphilis (8/27), and/or herpes simplex virus 2 (3/27). Other STIs mentioned were rectal gonorrhea (10/27), acute hepatitis B virus (2/23), rectal non-LGV Chlamydia trachomatis (3/27), and genital warts (3/27). Of the 27 men, 15 (56%) practiced anal fisting. In total, 23 (85%) of 27 reported either an ulcerative infection and/or anal fisting; 2 of the remainder reported neither IDU, blood-blood contact, nor high-risk sexual contact.

Genotyping and phylogenetic analysis. All HCV seroconversion samples (8 ACS participants) and samples obtained at the time of HCV diagnosis (34 hospital case patients) tested
positive for HCV RNA, as did 15 (63%) of 24 MSM who were positive at ACS entry. Table 3 shows the HCV genotype distribution among Amsterdam MSM infected before and after 2000. HCV infections predating 2000 were mainly of subtypes 1b and 3a (56%), whereas, after 2000, subtypes 1a and 4d predominated (85%).

Figure 1A represents a phylogenetic tree of 56 partial HCV NS5B sequences obtained from the Amsterdam MSM participating in the study. MSM who acquired HCV infection after 2000 had a high degree of clustering, showing 3 monophyletic clusters (cluster I–III) and, additionally, 3 pairs (a–c) of nearly identical HCV strains. When MSM who contracted HCV before 2000 were compared with those who contracted HCV after 2000, 0 of 17 HCV isolates from before 2000 and 33 (85%) of 39 HCV isolates from after 2000 had at least 1 nearly identical HCV isolate. The 2 MSM (S11 and S39) with recent HCV infection who reported no IDU, blood-blood contact, or high-risk sexual contact did not have a clustered or paired HCV isolate, suggesting unrelated routes of transmission. The MSM (S18) who assisted in the incident with the presumed IDU, who also reported unprotected sex, was part of cluster III.

The largest cluster (III) includes 14 MSM infected with HCV genotype 4d. To address whether their HCV strains resemble strains circulating in other risk groups, we constructed a phylogenetic tree (figure 1B) of all 51 HCV genotype 4 sequences in our database [26]: from MSM in the present study (n = 16), IDUs in Amsterdam (n = 17) and other European cities (n = 10), and Dutch blood donors (n = 8). For genotype 4, but also for genotype 1a (data not shown), different risk groups can be distinguished on the basis of phylogeny. Although MSM and IDUs were both infected with strains of HCV subtype 4d, the 14 MSM (cluster III) who contracted HCV infection after 2000 form a separate cluster within this subtype (bootstrap value, 91). Sequences obtained from 2 MSM who acquired HCV infection before 2000 (P2 and P7) were interspersed with sequences of IDUs from Amsterdam; both of them had reported IDU. Interestingly, geographic clustering was observed of IDUs from Amsterdam and those from southern Europe.

**DISCUSSION**

A rapidly increasing number of case reports from Europe [11, 12] the United States [13], and Canada [14] have suggested recent outbreaks of sexually transmitted HCV among HIV-1–infected MSM [15–17]. To our knowledge, this article is the first to suggest an increase in HCV incidence over time among HIV-positive but not HIV-negative MSM on the basis of 20 years of prospective longitudinal cohort data. Additional phylogenetic analysis of HIV/HCV-coinfected cohort and hospital cases strongly supports the presence of an MSM-specific transmission network, probably sexual, in Amsterdam.

As in London, Paris, and Rotterdam [11, 17, 27], phylogenetic analysis of incident HCV infections among MSM in Amsterdam showed at least 3 distinct clusters of independent co-circulating HCV lineages; 83% of Amsterdam MSM infected after 2000 harbored a strain present in at least 1 other MSM in the study. This degree of clustering is typical of a common source of infection and confirms sustained HCV transmission among HIV-positive MSM over the past few years. The low evolutionary distances among recent HCV isolates, the shift in genotypes over time (1b and 3a before 2000 vs. 1a and 4d after 2000), and the lack of clustering among isolates predating 2000 all imply a recent spread of HCV that was absent before 2000. The fact that multiple introductions of different HCV genotypes took place suggests behavioral change in MSM rather than evolution of the virus into a variant that is more easily transmitted.

No sexual transmission of HCV has been reported in recent HCV screenings among MSM in Seattle (n = 833) [28] and Montreal (n = 1085) [4]; 35 (85%) of 41 infections could be traced to IDU. However, persons screened were HIV-negative MSM, a subpopulation almost unaffected by the current HCV outbreaks [29]. Moreover, HCV screening stopped before the onset of the HCV outbreaks reported in Europe. By contrast, Amsterdam MSM infected after 2000 reported no IDU, and, like Parisian MSM [11], they carried MSM-specific HCV strains that differed significantly from those circulating among IDUs. Thus, IDU as an underlying mechanism of HCV transmission among Amsterdam MSM is highly unlikely. In a Swiss cohort study among HIV-infected MSM, increased HCV incidence was associated with sexual risk-taking and inconsistent condom use, especially in younger MSM [5]. Most likely, the current outbreak of HCV is triggered by the increase in sexual risk-taking observed among MSM after the introduction of HAART [20, 21].

How and when might sexual transmission of HCV occur? Among persons infected with HCV alone, >95% intermittently shed HCV RNA in saliva [30], and 42% of HIV/HCV-coinfected subjects shed HCV RNA in semen [31]. The rare event of sexual transmission among MSM, however, suggests that the rectal mucosa is relatively resistant to HCV infection. HIV-1 infection facilitates HCV transmission by increasing both (1) viral infectiousness due to higher viral loads, and (2) viral susceptibility through its detrimental effects to the gastrointestinal-associated immune system [32, 33]. Moreover, ulcerative STIs can enhance the sexual transmission of both HIV-1 and HCV [8, 34] by creating a portal of entry through the mucosal barrier. Quite possibly, HIV infection in itself makes the host vulnerable to HCV infection in combination with the above [35]. The observation that ulcerative STIs facilitate the transmission of HCV infection is consistent with the upsurge in STIs among MSM in countries where HAART is generally available [19, 20] and the high number of ulcerative coinfections reported by MSM with acute HCV infection [16, 17, 27]. However, STIs
and sexual risk-taking have no higher incidence now than in 
the early 1980s, when the sexual transmission of HCV seemed 
absent. What else has changed?

First, current outbreaks of HCV coincide with the recent 
edemic of LGV, a “new” STI that manifests as anorectal ulcers, 
haemorrhagic proctocolitis, and hyperplasia of intestinal and 
perirectal lymphatic tissue. Both HCV and LGV are strongly 
associated with a positive HIV status [36], and, in the Nether-
lands, acute HCV is reported among MSM coinfected with 
LGV [27]. This suggests a potential role for LGV in the outbreak 
of HCV reported in the Netherlands. Second, successive out-
breaks of syphilis, rectal gonorrhoea, Shigella sonnei infection, 
LGV, and acute HCV among MSM in major European cities 
[16, 18, 19, 27, 36, 37] points to the presence of a high-risk 
“core group” of HIV-positive MSM. This “core group” functions 
as a reservoir for STIs and is highly susceptible to new or even inefficiently transmitted infections such as LGV and 
HCV. The popularity of the Internet, trans-European MSM 
weekend tourism, and organized sex parties may have increased 
contacts among HIV-positive MSM who share risky sex and 
are relatively unconcerned about acquiring “treatable” STIs 
[38]. Lesions in the rectal endothelial lineage could occur es-
pecially with rough sexual techniques such as anal fisting, the 
use of toys, and group sex, which favor blood-blood contact 
and, hence, HCV transmission [14, 17, 27, 39]. In 2005, anal 
bleeding during sex was reported by 10% of young (<35 years 
old) HIV-negative participants in the ACS. The use of psycha-
active substances, to enhance sexual pleasure and anal sphincter 
relaxation during receptive anal intercourse or to remove in-
hibition during rough sexual practices, might also cause mu-
cosa trauma or bleeding, especially when substances are applied 
anal [40].

The increased HCV incidence among MSM has clinical im-
lications. HIV/HCV coinfection is associated with lower rates 
of spontaneous HCV clearance, accelerated liver disease, and a 
less favorable HCV treatment outcome [41]. HCV combination 
therapy achieves a sustained virological response in only 17% 
of HIV-positive individuals infected with genotypes 1 or 4 
[42]—the HCV strains that affect the majority (91%) of MSM in 
Amsterdam. In 90%–98% of HIV-negative patients, however, 
HCV chronicity can be prevented when treatment is initiated 
during the acute phase of infection [43]. The results of early 
interferon treatment in HIV-negative MSM infected with HCV 
genotypes 1 and 4 are conflicting but promising [11, 42, 44].

Several limitations should be considered when interpreting 
our results. Despite a significant increase in HCV incidence 
after the year 2000, the low number of HCV incident cases 
among ACS participants makes it necessary to investigate 
whether this trend continued after 2002. All HIV-positive ACS 
participants with extended follow-up after 2002 will be tested 
for HCV prospectively (or retrospectively at their last ACS 
visit). The high number of hospital cases collected after 2002, 
however, indicates sustained HCV transmission among HIV-
positive MSM. Second, hospital cases were collected in a clinical 
setting and not for epidemiological research. Although high 
rates of concurrent STIs and fisting among hospital case pa-
ients are suggestive of percutaneous transmission of HCV during 
sexual contact, a control group is needed to establish whether 
these rates are significantly higher than are those in HIV-posi-
tive MSM without HCV coinfection. Additionally, HIV-posi-
tive MSM visit a physician more frequently and thus are more 
likely to receive HCV and STI testing than those who are HIV 
negative. Testing therefore might have occurred on indication 
and might have biased our conclusions about HCV and high 
levels of STIs. ACS data confirm, however, that HCV mainly 
circulates among HIV-positive MSM, given that no HCV sero-
conversions were identified among HIV-negative MSM. Third, 
retrospective data collection based on self-reported behavior 
may be compromised by report and recall bias. However, all 39 
recently infected MSM in the study denied IDU, which 
accounts for the vast majority of new HCV infections in western 
Europe. Moreover, phylogenetic analysis confirmed a non– 
IDU-related common source of infection. Data on possible 
other confounders (e.g., tattooing/piercing, acupuncture, or 
various nosocomial transmission routes) were not always avai-
labl, but such general routes of incidental transmission cannot 
explain the common source of HCV infection observed among 
MSM. Potential subculture-related confounders such as intra-
anal/anal drug and enema use need further investigation.

Despite these limitations, the present results indicate that 
HCV appears to be emerging as an STI among a restricted 
“core group” of HIV-positive MSM who practice risky sex. 
Given the absence of clear clinical symptoms during acute HCV 
infection, a significant proportion of the HCV epidemic may 
still remain unnoticed. Routine HCV screening among HIV-
positive MSM is needed to identify the magnitude and character 
of the current epidemic and to enhance treatment. Although 
the exact biological mechanism of transmission has yet to be 
determined and should be examined in a prospective cohort 
or retrospective case-control study, targeted prevention can de-
ter further spreading and increase awareness in HIV-positive 
MSM about the additional risks associated with acquiring se-
rious bloodborne coinfections.

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