Risk Factors and Patterns of HCV Transmission in Men who Have Sex with Men in England

Public Health England

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BACKGROUND and AIMS

An epidemic of HCV has been observed in high income countries over the last 20 years in HIV-infected men who have sex with men (MSM), transmitted through sex or injecting drug use (IDU). By contrast, reports of HCV in HIV-uninfected MSM have been uncommon, although increases have been seen in recent studies of PrEP-users in France and the Netherlands.

We sought to identify the demographic and clinical characteristics of MSM with recently-acquired HCV in England and to describe the patterns of HCV transmission in this cohort.

METHODS

MSM with recently-acquired (<12 months) HCV were prospectively recruited from five clinics in England between January 2017 and August 2017 ('clinic cohort'). Clinical data and risk behaviours were identified by notes review and questionnaires. Sexually transmitted infection screening was performed. Blood was obtained for HCV next generation, whole genome sequencing. Phylogenetic analyses were performed, including MSM from the clinic cohort (n=18) and two other UK cohorts of individuals with acute HCV, TARGET3D (n=24) and CHAT (n=10) to identify transmission clusters. The association index (AI) was calculated, a statistic describing whether or not tips clustering in a tree also share the same characteristics.

RESULTS

Sixteen (40.0%) men were HIV-uninfected. Characteristics of HIV- vs HIV+ MSM are shown in Table 1. Most (13, 81.3%) HIV- men had used PrEP in the last year and most (22, 91.7%) HIV+ men were aviraemic on antiretrovirals. HIV- men were younger (p=0.021), more likely to be recruited from London (p=0.030), less likely to be genotype 4-infected (p=0.032), and they reported a greater number of partners in the preceding 12 months (p=0.025). The preferred way of meeting partners was through phone apps, nominated by 34/40 (85.0%) men, with one particular app reported by 26 (65.0%) individuals.

RESULTS

For the question, 'how many partners in the last 12 months did you think had HIV?', a majority thought 'some', 'most' or 'all' partners had HIV (13, 81.3% HIV- vs 20, 83.3% HIV+ men). By contrast, few men thought 'some', 'most', or 'all' partners had HCV (4, 25.0% HIV- vs 3,12.5% HIV+ men).

Table 1. Clinical, demographic and behavioural characteristics of HIV- and HIV+ MSM with recently-acquired HCV

	HIV- N=16		HIV+ N=24		All N=40		P value
	n	% or IQR	n	% or IQR	n	% or IQR	
Median age, years	34	29-43	44	36-50	39	33-49	0.021*
UK-born	9	56.3	18	75.0	27	67.5	0.215
City of recruitment							
London	16	100	17	70.8	33	82.5	0.030*
Jaundice	2	12.5	2	8.3	4	10.0	0.667
Median peak ALT, U/L	648	288-1618	448	276-783	491	279-1007	0.345
HCV results							
HCV antibody negative	1	6.3	3	12.5	4	10.0	0.638
Median HCV RNA, log IU/mL	3.7	3.2-5.7	5.1	4.3-6.3	4.8	3.4-6.2	0.279
HCV genotype[1]							
1a	13	81.3	14	58.3	27	67.5	0.177
4	1	6.3	9	37.5	10	25.0	0.032*
Median duration HCV, months	4.1	3.3-8.3	4.9	2.3-8.0	4.8	2.7-8.2	0.687
Prior HCV episode(s)	4	25.0	5	20.8	9	22.5	1.000
Clinician-assigned IDU acquisition	6	37.5	8	33.3	14	35.0	0.787
Outcome of HCV infection							
Spontaneous HCV clearance	2	12.5	4	16.7	6	15.0	1.000
Treated with DAAs	13	81.3	18	75.0	31	77.5	0.717
SVR12 achieved	13	100	18	100	31	100	1.000
Lost to follow up or declined therapy	1	6.3	2	8.3	3	7.5	1.000
STI at HCV diagnosis	5	31.3	7	29.2	12	30.0	0.888
Drug use							
IDU ever	7	43.8	11	45.8	18	45.0	0.897
Ever injected by another person	5	31.3	8	33.3	13	32.5	0.890
Used needle after someone else	0	0	0	0	0	0	1.000
IDU in last 12 months	6	37.5	8	33.3	14	35.0	0.787
Last drug injected was methamphetamine	7	100.0	10	90.9	17	94.4	1.000
Permucosal drugs in last 12 months	15	93.8	19	79.2	34	85.0	0.373
Sexual history in past 12 months							
Median no. sex partners	36	16-50	16	4-16	16	8-39	0.025*
Sex in a group environment	14	87.5	17	70.8	31	79.5	0.272
Fisting	12	75.0	13	54.2	25	62.5	0.318
Condomless anal sex	16	100	21	87.5	37	92.5	0.262
History of rectal bleeding	7	43.8	8	33.3	15	37.5	0.505

[1] Genotype distribution: 1a (n=27), 3a (n=3), 4d (n=9), 4 no subtype (n=1)
*<0.05 by chi-squared, Fishers exact or Mann Whitney U test
DAAs direct acting antivirals, IDU injection drug use, STI sexually-transmitted infection, SVR12 sustained virologic response at 12 weeks

For 52 genotype 1a sequences in the phylogeny, 47 (90.4%) clustered with at least one other sequence. Six of seven clusters contained both HIV- and HIV+ MSM (Figure 1). Most clusters originated in the 1990s, with time to most recent common ancestor ranging from 1973 to 2001. One mixed HIV-/HIV+ cluster was likely part of a larger cluster described previously for HIV+ MSM (van der Laar *et al*, Gastroenterology, 2009). AI analysis for clusters with > 2 sequences found no structure by participant characteristics for clusters 1-3. For cluster 4, significant structure was observed by HIV status and age (p<0.0001).

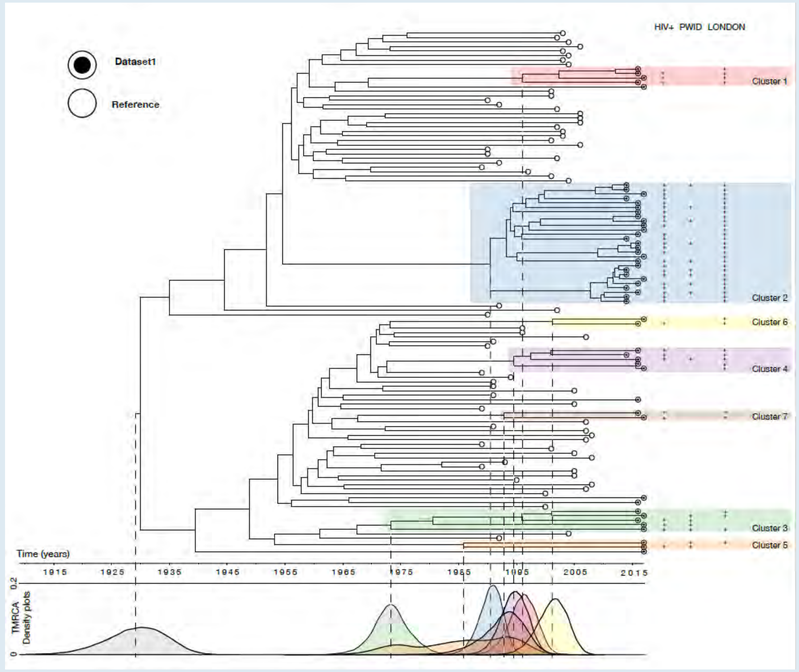

Figure 1. Phylogenetic clustering for HCV genotype 1a with molecular clock analysis

PWID people who inject drugs; TMRCA time to most recent common ancestor

CONCLUSIONS

In this cohort of MSM with recently-acquired HCV, 40% were HIV-uninfected, and the majority of these were PrEP-users. Characteristics of HIV- and HIV+ MSM were broadly similar, with high levels of sexual and drug taking risk behaviours. However, HIV- MSM were younger and had more sexual partners. Around 1/3 in each group was infected with HCV through IDU, and 2/3 through sex. Most HIV- and HIV+ MSM thought partners could be HIV-infected, but few thought partners may be HCV-infected.

HCV phylogenetic analyses identified clusters including both HIV- and HIV+ MSM. In most clusters, sequences were not clustered by HIV-status, suggesting both HIV- and HIV+ men are involved in the same HCV outbreaks. Molecular clock analyses suggested that the majority of clusters originated from the 1990s.

Taken together, these findings highlight that PrEP-using MSM are at risk of HCV, with similar behaviours to HIV+ MSM. Younger age and higher partner number for HIV- MSM raise the possibility of a rapid epidemic, with transmissions likely bridging from the HIV+ population. Few HIV- or HIV+ men demonstrated HCV awareness, and risk reduction strategies should be expanded.

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DISCLOSURES

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