LARGE HEPATITIS C TRANSMISSION CLUSTER IDENTIFIED AMONG HIV POSITIVE MSM IN BANGKOK

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BACKGROUND

- A rapidly emerging HCV outbreak has recently been observed among HIV-positive men who have sex with men (MSM) living in Bangkok, Thailand. Little is known regarding the transmission networks among this population.

METHODS

- MSM with both acute (Fiebig stages 1 to 5) and chronic HIV infection and with incident HCV infections were identified in research cohorts at the Thai Red Cross AIDS Research Centre.
- Incident HCV infections were defined as seroconversion from anti-HCV antibody negative to positive after initiating ART.
- NS5B regions of the HCV genome (404 and 471 bps) were amplified using nested-PCR and sequenced.
- Phylogenetic inference was constructed by Maximum Likelihood methods in MEGA X.0.5 software. Clusters were identified using Cluster Picker with support and genetic distance thresholds of 85% and of 4.5%, respectively.

RESULTS

- A total of 48 (25 acute HIV and 23 chronic HIV) MSM with incident HCV infection and amplifiable NS5B sequences were included in the analysis.
- Median (interquartile range, IQR) HCV RNA at HCV diagnosis was 6.3 (5.3-6.9) IU/mL.

In the phylogenetic analysis, 83% belonged to one of two clusters: one large (n=36, 75%) and one small (n=4, 8%) cluster. Participants with acute HIV infection were more likely to be in a cluster (92%) than those with chronic infection (74%).

- HCV genotype (GT) was 85% GT 1a and 15% GT 3a or 3b. Median age at HCV diagnosis was 34 (IQR, 28-41) years.
- 83.3% (40/48) had history of syphilis infection and 36% (16/44) reported crystal meth use. Only 2 (4%) reported ever injecting drugs, both crystal methamphetamine.
- Six (12.5%) were HBV co-infected, all of whom had chronic HIV.
- All clusters identified were GT 1a. Overall mean genetic distance was 0.10 (SE=0.02).

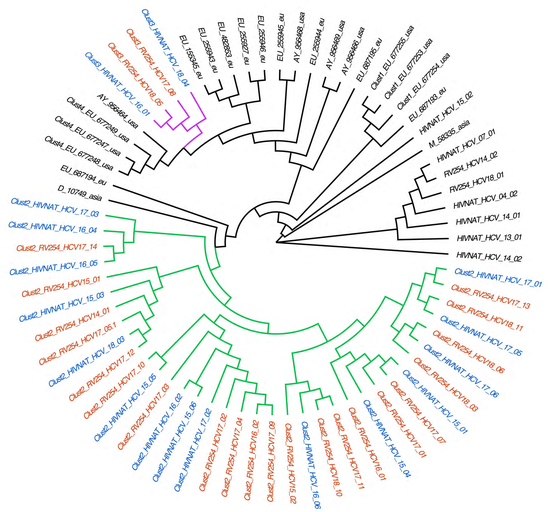

Figure. Cladogram showing phylogenetic clustering of 48 HCV NS5B sequences inferred by Maximum Likelihood methods in MEGA X.0.5 with 1,000 bootstrap sampling. Reference sequences of MSM and PWID population from Asia, Europe and USA were included. Clusters were identified using Cluster Picker software with the support and genetic distance thresholds of 85% and of 4.5%, respectively. Participants with acute and chronic HIV infection are denoted with red and blue tip label colors. NS5B sequences from annotated large transmission cluster (branch label color: green, number = 36 with 21 acute HIV and 15 chronic HIV-positive MSM) and small cluster (branch label color: purple, number = 4 with 2 acute HIV and 2 chronic HIV-positive MSM) are all HCV genotype 1a. From the clusters identified, 83% belonged to one of two clusters: one large (n=36, 75%) and one small (n=4, 8%) cluster.

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CONCLUSIONS

- Phylogenetic analysis showing a high degree of clustering confirms that the HCV epidemic in the HIV-infected MSM community in Bangkok is recent and rapidly expanding. This epidemic is independent of past HCV transmission among people who inject drugs in Thailand, which was largely genotype 3.
- Crystal methamphetamine use is high in participants with HCV infection, and previous reports have identified chemsex and group sex parties as factors associated with HCV transmission.
- HCV antibody testing should be regularly performed for MSM on ART in Bangkok, and direct-acting antivirals being offered to all MSM with HCV infection might contain this HCV epidemic from spreading further.

ADDITIONAL INFORMATION

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Disclaimer

The views expressed are those of the authors and should not be construed to represent the positions of the U.S. Army or the Department of Defense. The investigators have adhered to the policies for protection of human subjects as prescribed in AR 70–25.

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