Abstract WEPEC667

Inferring the transmission dynamics of acute hepatitis C virus infection in HIV-positive MSM in Hong Kong

D.P.C. Chan¹, A.W.C. Lin², K.H. Wong², N.S. Wong¹, S.S. Lee¹

¹Chinese University of Hong Kong, Stanely Ho Centre for Emerging Infectious Diseases, Shatin, Hong Kong ²Special Preventive Programme, Department of Health, Hong Kong, Hong Kong

Background: Sexual transmission of hepatitis C virus (HCV) infection has been increasingly recognized among men who have sex with men (MSM) in Western countries. Recently, there has been a marked rise of acute HCV infection in HIV-positive MSM in Hong Kong. The aim of our study was to characterize the transmission dynamic and genetic diversity of acute HCV infection in HIV-positive MSM in Hong Kong.

Methods: A retrospective analysis was carried out on HIV-positive MSM diagnosed with acute HCV infection between 2009 and 2014. Additional HCV RNA detection and genotyping were performed for all HCV seroconverters. Phylogenetic analysis of the HCV-NS5B region was conducted by neighbor-joining method to examine the local molecular epidemiology of HCV co-infection.

Results: Of 24 HIV/HCV co-infected MSM, the median age at HCV infection was 32 years (IQR 27-41), and the median time from HIV to HCV diagnosis was 3.1 years (IQR 1.2-6.5). The majority of patients (87.5%) were Chinese, and 23 (95.8%) were on antiretroviral treatment. None of them reported history of injection drug use. Among 22 (91.7%) HIV-positive MSM with detectable HCV RNA, infection with HCV genotype 3a (63.6%) was the most common, followed by genotypes 1a (18.2%), 6a (9.1%), 1b (4.5%) and 2a (4.5%). Acute HCV infection identified before 2012 were mostly of genotypes 1a and 6a, whereas genotype 3a predominated in the majority of acute HCV cases diagnosed between 2013 and 2014. Phylogenetic analyses revealed a monophyletic cluster of HCV-3a lineage from 2013 onwards, and a homologous pair of MSM-specific HCV-6a strain that were separate from those circulating in local injection drug users.

Conclusions: Our study indicates the existence of MSM-specific networks that has contributed to the sexual transmission of HCV in HIV-positive MSM in Hong Kong. Recent finding of the emergence of an independent and non-injecting HCV-3a cluster further implicates the rapid spread and increasing burden of sexually acquired HCV infection within our local HIV-positive MSM community.