Phylodynamics of sexually acquired HCV-3a in HIV co-infected patients in Hong Kong

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Background
• Previous studies showed that hepatitis C virus (HCV) transmission in Hong Kong was mainly driven by the continued subtype 3a outbreaks in HIV-positive men who have sex with men (MSM) after HIV infection
• A study was conducted to examine the origin and transmission dynamics of this outbreak

Materials and methods
• HCV NS5B sequences (nucleotides: 8348-8658) were collected from the largest HIV specialist clinic in Hong Kong where over half of all diagnosed patients received clinical care
• After subtyping by Oxford HCV Subtyping Tool, all sequences assigned with subtype 3a were selected for subsequent analyses
• A phylogenetic tree was constructed by maximum likelihood method using generalised time-reversible substitution model incorporating proportion of invariable sites and rate of variation across sites with 1000 bootstraps
• Bayesian coalescent skyline analysis was conducted by BEAST2 using uncorrelated lognormal relaxed molecular clock model

Results
• Between 2013 and June 2019, a total of 93 HCV sequences were collected from HIV patients, 64 of which were of subtype 3a and therefore analysed
• Seventeen of the 3a sequences were identical, forming a closely knit network (annotated)
• From the phylogenetic tree (Fig. 1), no distinct transmission clusters could be identified within the 3a network
• Phylodynamic analysis revealed that the date of most recent common ancestor was 2011.2 (95% highest posterior density interval: 2008.9-2012.8)
• Bayesian skyline plot (Fig. 2) illustrates that the effective population size of HCV-3a has increased between early 2014 and late 2016, but the rise in 2015 was less steep
• A constant effective population size was maintained after 2017

Conclusions
• The HCV-3a epidemic in HIV-positive MSM population was introduced a decade ago
• The spread of HCV-3a could be characterised by two growth periods in 2014 and 2016 respectively
• The reason for the decrease in transmission rate or increase in the number of infections during the two periods required further investigation

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