

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 with MCMC chain length of 100,000,000 and 10% burn-in to determine time of introduction and its population dynamics

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



Fig. 1 Phylogenetic tree of HCV-3a sequences

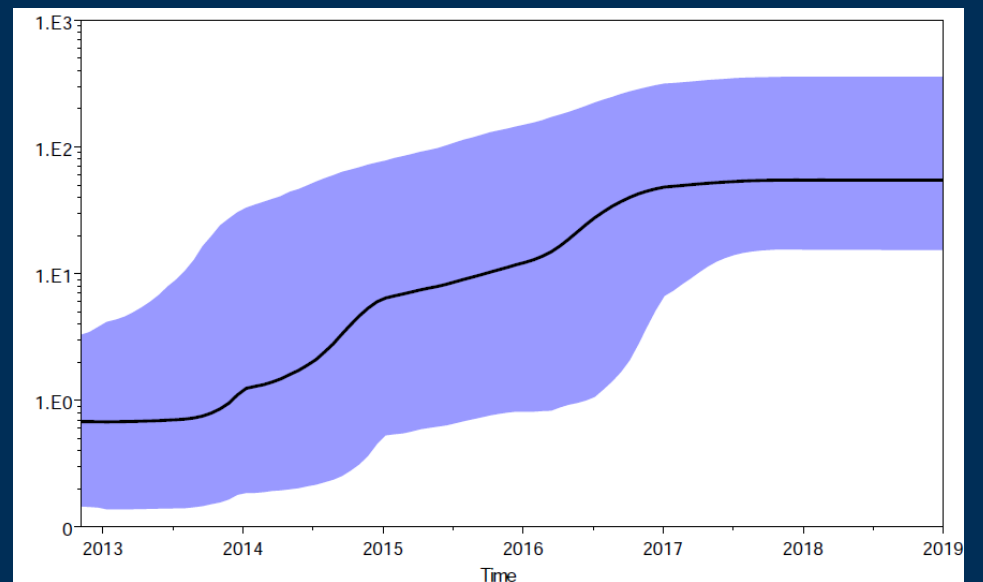


Fig. 2 Bayesian skyline plot

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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