

Trends of Hepatitis C Virus Epidemic in Australia and North America in 20th Century: Back Projections from Molecular Epidemiology

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Introduction

Bayesian evolutionary analysis (coalescent analysis) based on genetic sequences has been used to describe the origins and spread of rapidly mutating RNA viruses such as Influenza, Ebola and HIV. The rapid mutation rates of RNA viruses bring the evolutionary time-scale to months or years rather than millions of years as in the case of DNA genomes. This makes epidemiological and evolutionary timescales “similar”.

Methods

Full length subtype 1a and 3a sequences generated from early hepatitis C virus (HCV) infections identified in the International Collaborative of Incident HIV and Hepatitis C in Injecting Cohorts (Inc3), as well as from public databases from a time window of 1977 – 2012, were used in a coalescent analysis with BEAST software to estimate the origin and progression of the HCV epidemic during the 20th century. A combination of General Time Reversible model (as the nucleotide substitution model), Bayesian skyline (as the population prior) and lognormal relaxed clock (as the clock model) was used for each subtype and continent-specific dataset.

Results

The subtype 3a epidemic had more recent origins (around 1950) than subtype 1a (around 1920) epidemic in both continents with North America generally preceding Australia. The estimated progression of the size of the epidemics revealed exponential growth between 1955 and 1975 in both continents. All epidemics have stabilized or showed a decline in numbers over the last 20 years probably attributable to a) reduction in intravenous drug use, b) better needle sharing practices with HIV awareness, c) treatment and d) death of older cohorts with infection.

Conclusions

Historical events that fuelled the emergence and spread of injecting drug use, such as the advent of intravenous medical therapies and devices, and growth in the heroin trade, as well as armed conflicts that allowed population mixing are likely to have been the drivers for cross-continental spread of the HCV epidemics.

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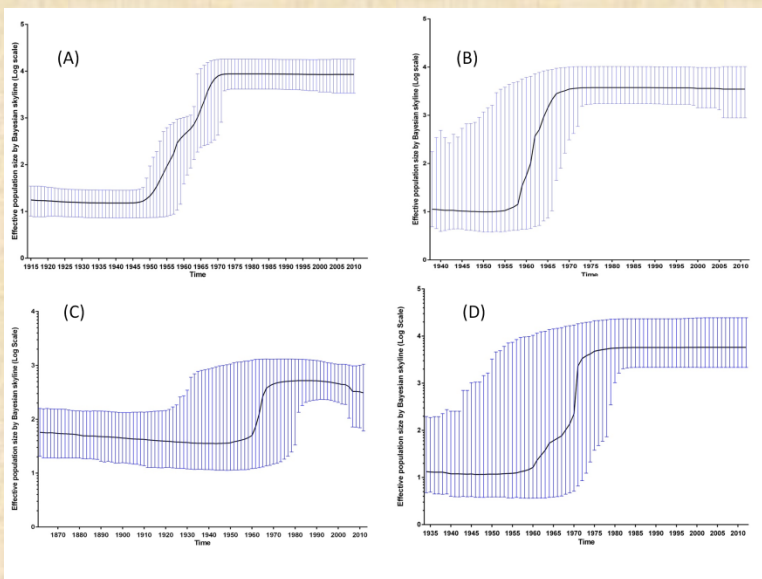


Figure: Projected trends for (A) subtype 1a-North America, (B) subtype 3a – North America, (C) subtype 1a – Australia, (D) subtype 3a - Australia