

## TRENDS OF HEPATITIS C VIRUS EPIDEMIC IN AUSTRALIA AND NORTH AMERICA IN 20<sup>TH</sup> CENTURY: BACK PROJECTIONS FROM MOLECULAR EPIDEMIOLOGY

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**Background:** Hepatitis C virus (HCV) was identified in 1989. Its epidemiology prior to 1989 is difficult to reconstruct by epidemiological data. Bayesian evolutionary analysis and phylogenetics of full length genomes was used to model the trends of hepatitis C virus epidemics for subtypes 1a and 3a in North America and Australia in the 20<sup>th</sup> century.

**Methods:** Full length subtype 1a and 3a sequences from early HCV infections identified across nine cohorts in the International Collaboration of Incident HIV and Hepatitis C in Injecting Cohorts (InC3), as well as public databases from a time window of 1989 – 2012 were used in a Bayesian evolutionary analysis with BEAST software. 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:** Subtype 3a had more recent origins (1940-1960) than subtype 1a in both continents (1900 – 1930). Both subtypes showed an exponential increase in the number of infections from 1955 – 1975 in both continents coincident with the epidemic rise in injecting drug use during this period. 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:** The findings support the hypothesis that historical events that fuelled the spread of injecting drug use with population mixing (e.g. World Wars, Korean War) could have been a major driver for cross-continental epidemics.

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