

Trends of Hepatitis C Virus Epidemic in Australia and North America in 20th Century

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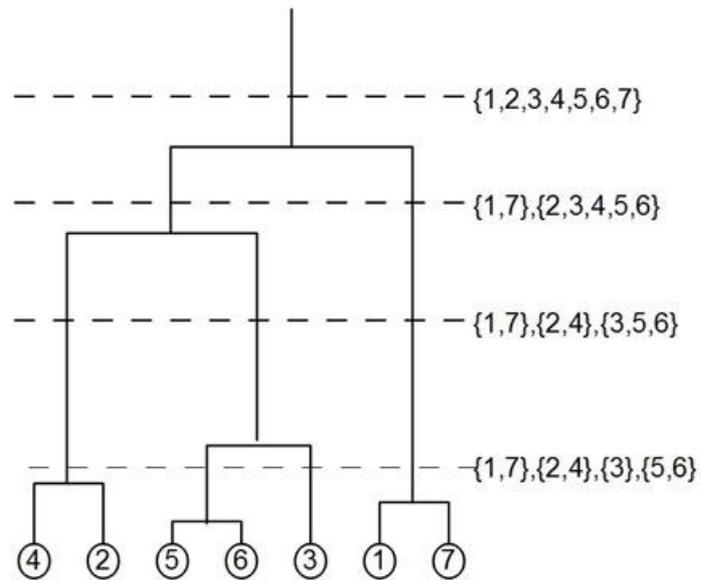
Hepatitis C virus

- Identified and cloned in 1989
- Time of origin is unknown
- Virus genomes have been uncovered from samples stored as far back as 1953
- Important to study the progression of the epidemic
 - Typical example of a blood borne virus spread
 - Important for epidemiological monitoring

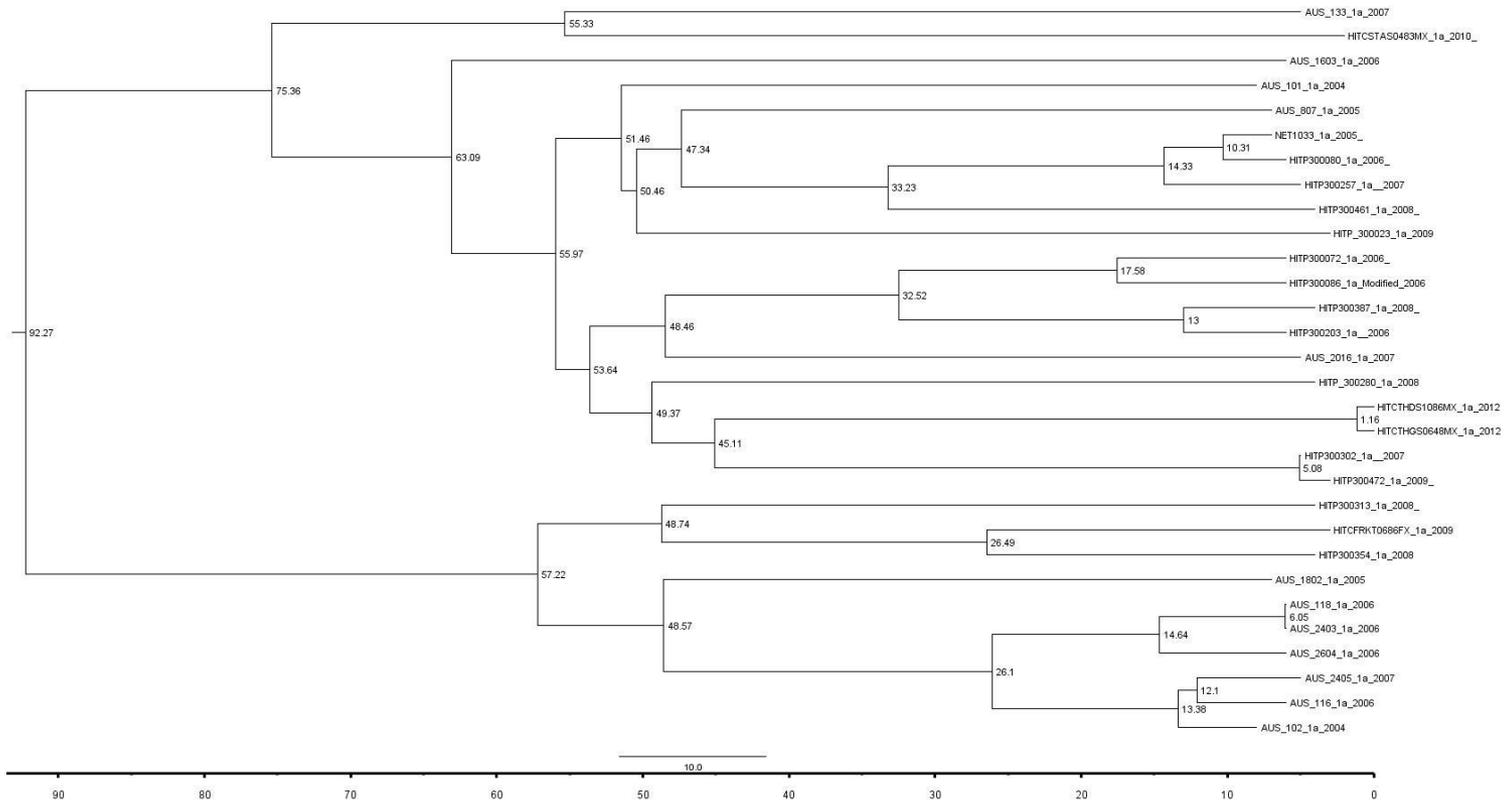
Objectives

- To reconstruct the trends of the HCV epidemic in two continents using currently existing sequences

A phylogenetic tree



A phylogenetic tree with a timeline



Sample selection – Full length Genomes

- For genotype 3a
 - InC3
 - Los Alamos HCV database
 - Genbank
- For genotype 1a
 - InC3
 - Los Alamos HCV database

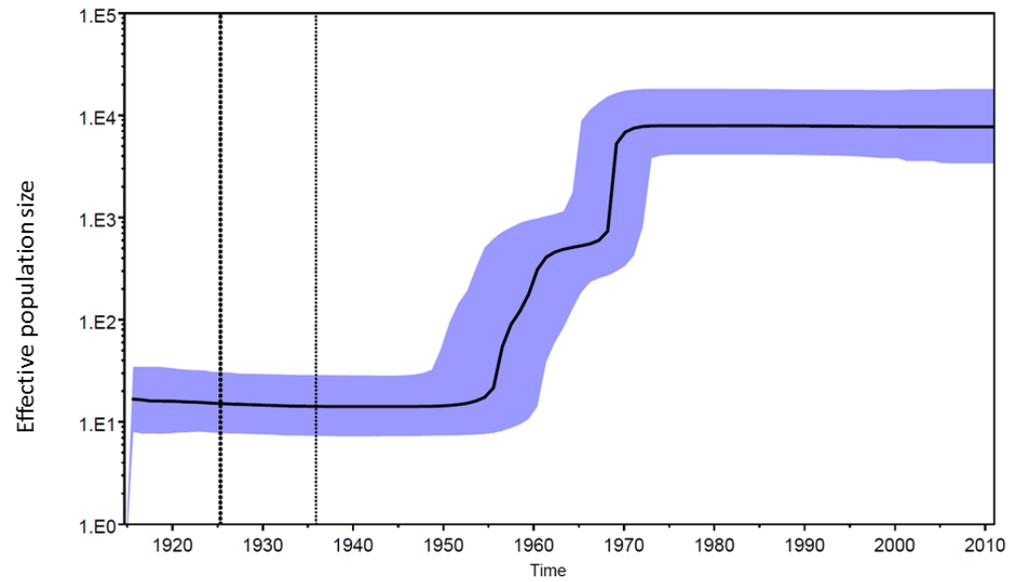
Methods

- Geneious
 - For alignment preparation and conversion of files
- MEGA
 - Substitution rate priors
- Path-O-Gen
 - Temporal signal of data
 - Priors for substitution rates
 - Priors for MRCA

Methods

- Beauti
 - XML file preparation
- BEAST
 - Run the analysis
- Tracer
 - Read the analysis and model comparison
 - Bayesian skyline plot
- Figtree / Geneious
 - Graphics, trees etc.

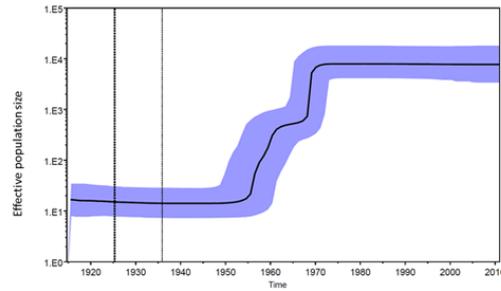
Subtype 1a NA



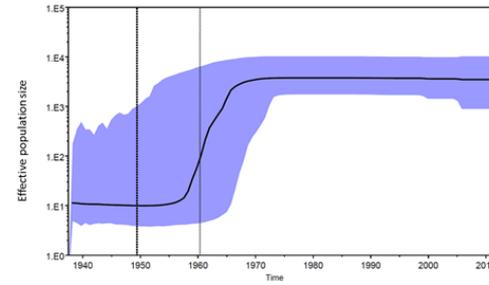
All Projections

NA

1a



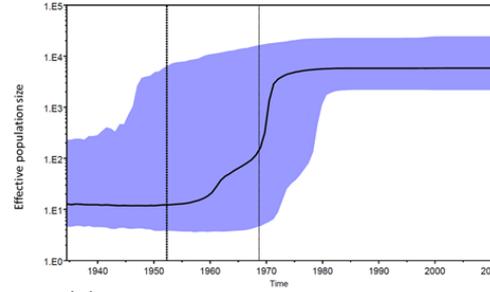
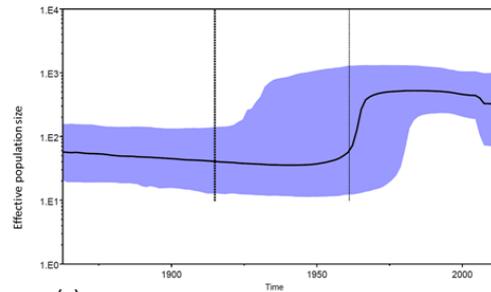
3a



(a)

(b)

AUS

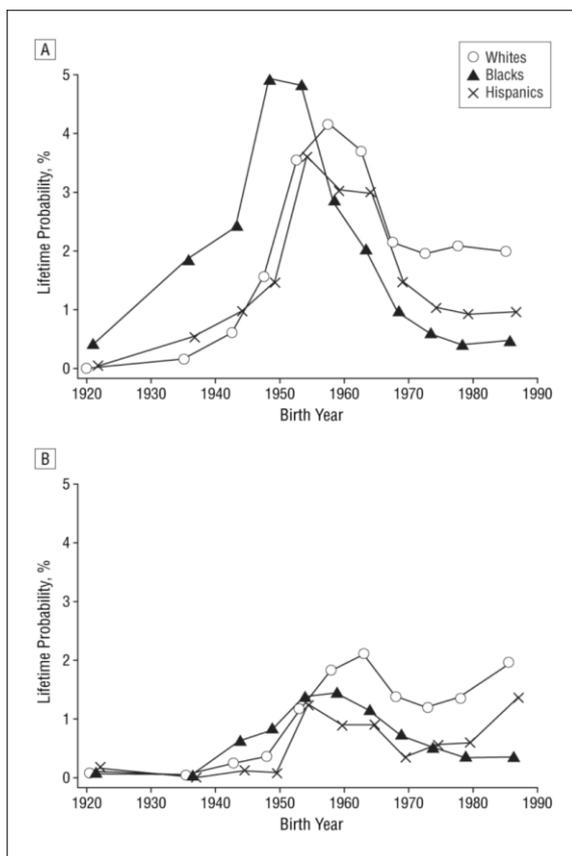


(c)

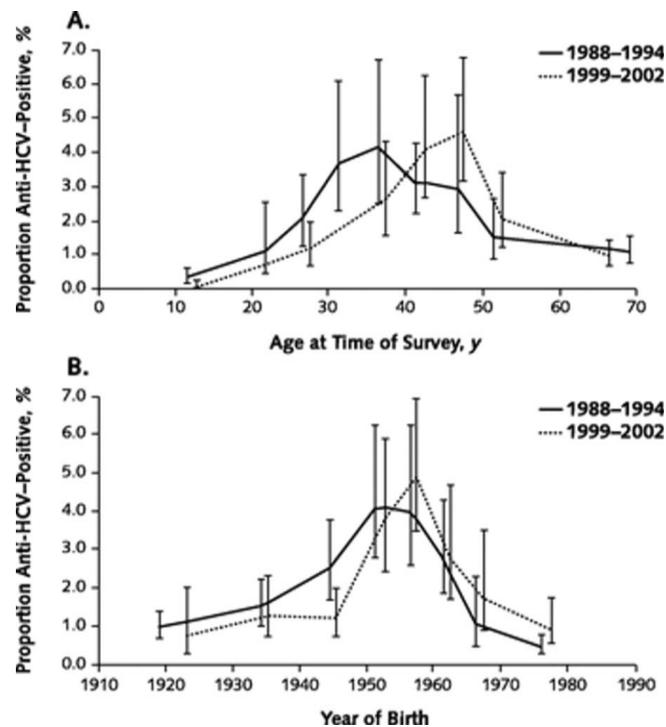
(d)

Results

- Genotypes 1a is older (early 20th century) than 3a (mid-20th century)
- 1a probably originated at the same time in both continents. ? Source (Asia or Africa)
- There is a rapid rise in cases between 1955-1975
- All show a decline after 2000 except 3a in AUS which is stable



a) Modelled life time probability of IVDU in US



b) HCV ab prevalence by birth year in US

Arch Intern Med. 2007;167(2):166-173. doi:10.1001/archinte.167.2.166

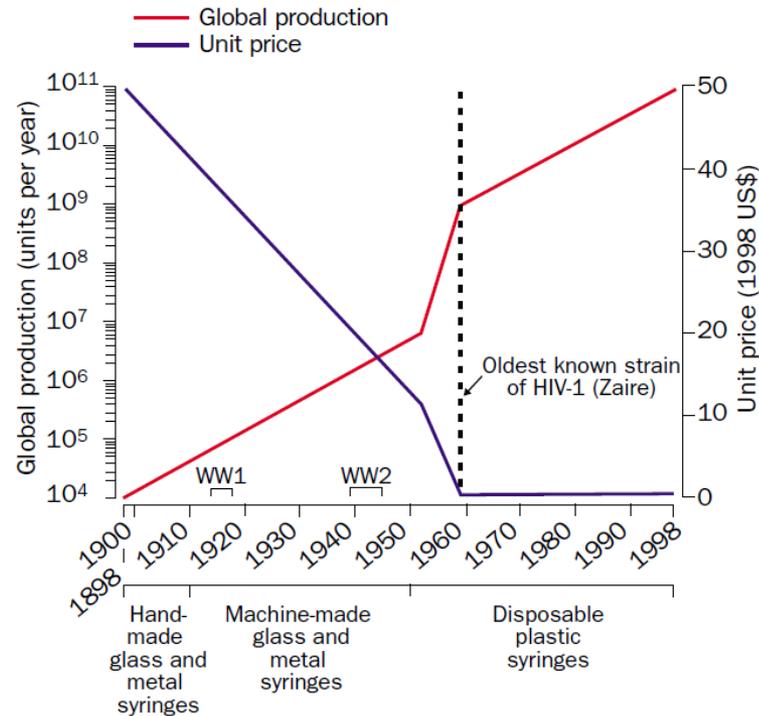


Figure 2: **Global production and unit price of injecting equipment (1898–1998)**

WW=World War.

Drucker E, Alcabes PG, Marx PA. The injection century: massive unsterile injections and the emergence of human pathogens. *Lancet* 2001; 358:1989-92

Decline in number of infections

- Awareness of HIV and HCV
- Harm minimisation strategies
- Death of older people with infections
- ? Treatment effect

Conclusions and future applications

- Bayesian evolutionary analysis is an attractive alternative to predict trends of HCV infection
- For comparison of trends in pre and post DAA era

References

Rodrigo C, Eltahla AA, Bull RA, et al. Historical trends in the hepatitis C virus epidemics in North America and Australia. *J Infect Dis*, **2016**
doi: 10.1093/infdis/jiw389

Rodrigo C, Eltahla A, Bull RA, et al. on behalf of InC3 investigators. Phylogenetic analysis of full-length, early infection, hepatitis C virus genomes among people with intravenous drug use: the InC3 Study. *J Viral Hepat*. 2016. In Press

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