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

Chaturaka Rodrigo
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

1a

3a

NA

AUS

(a)

(b)

(c)

(d)
Results

• Genotypes 1a is older (early 20\textsuperscript{th} century) than 3a (mid-20\textsuperscript{th} 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

Figure 2: Global production and unit price of injecting equipment (1898–1998)
WW=World War.

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
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