

Phylogenetic clustering of acute hepatitis C virus infection in Australia is associated with HIV co-infection and genotype 1a infection

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Aims of this study

Among people with acute HCV infection in Australia

1. Determine the HCV genotype distribution
2. Identify and characterise the composition of phylogenetically reconstructed pairs and clusters
3. Investigate factors associated with pair/cluster membership

➔ Characteristics of highly connected populations

Methods and statistical analysis

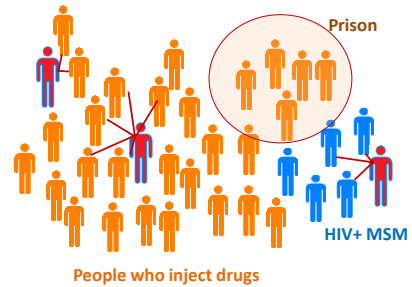
Method

- Core-E2 region amplified and sanger sequenced (1300bp)
- Phylogeny inferred using maximum likelihood (RAxML)
 - 1000 bootstrap replicates

Statistical analysis

- Clusters and pairs identified (ClusterPicker)
 - 90% bootstrap support
 - 5% genetic distance cut offs
- Factors associated with being in a cluster identified
 - Multivariate logistic regression in Stata 11

HCV transmission



➔ Inform treatment as prevention strategies

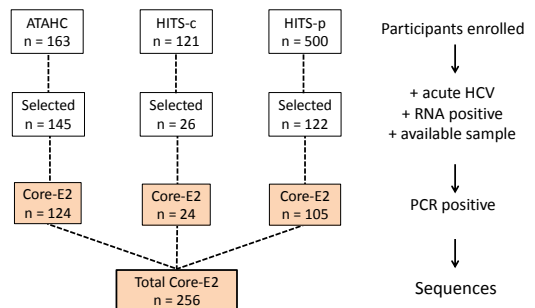
Study population

ATAHC	Australian Trial in Acute Hepatitis C infection
HITS-p	Hepatitis C Incidence and Transmission Study in prison
HITS-c	Hepatitis C Incidence and Transmission Study in community

Acute HCV defined by initial positive anti-HCV antibody test and either;

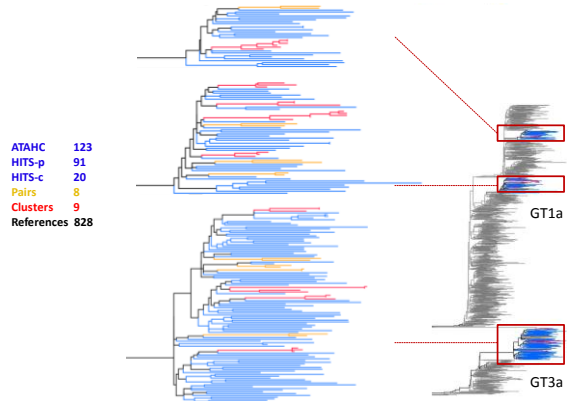
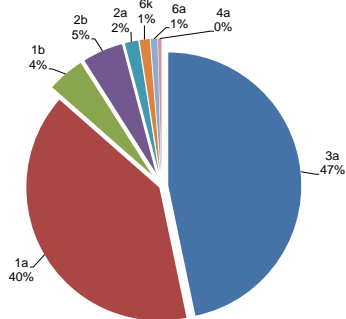
- Negative anti-HCV antibody test within two years prior, OR
- Acute clinical hepatitis (jaundice or ALT >400 IU/mL) within 12 months prior

Sample selection and sequencing





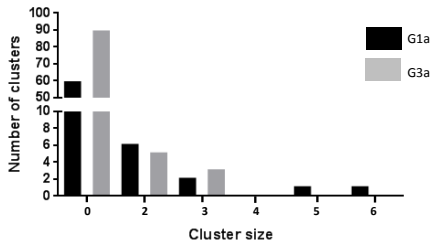
Genotype distribution



Cluster size and distribution

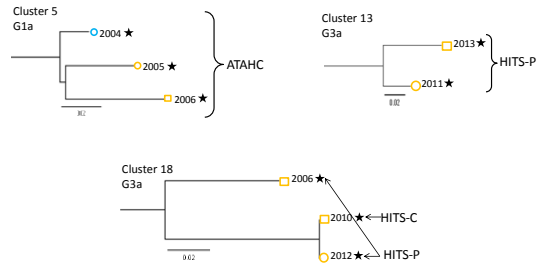
32% G1a in pair/cluster (29/88, mean genetic distance=0.034)

18% G3a in pair/cluster (19/108, mean genetic distance=0.028)



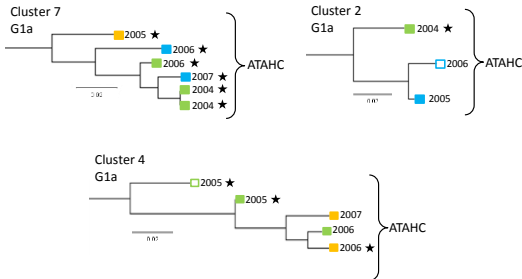
Examples of interesting clusters

- Male HIV+ (black square)
- Female HIV+ (black circle)
- < 30 years old (yellow square)
- 30-40 years old (green square)
- Male HIV- (white square)
- Female HIV- (white circle)
- IDU ever (star)
- > 40 years old (blue square)



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Factors associated with being in a cluster/pair

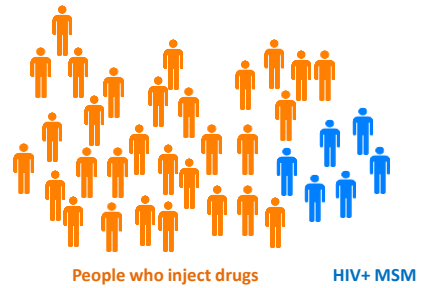
Characteristic	Total n (%)
Age	
< 30	
> 30	
Sex	
Male	
Female	
HIV infection	
Negative	
Positive	
HCV Gt	
3a	
1a	
Cohort	
ATAHC	
HITS-p	
HITS-c	

Conclusions

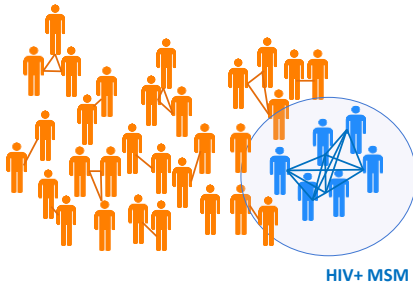
Among people with acute HCV infection in Australia

- HCV genotype 3a and 1a are predominant
- 20% of participants demonstrated phylogenetic clustering
- Some large clusters displayed distinct characteristics
- Being in a cluster/pair was independently associated with
 - Being infected with genotype 1a (vs. 3a)
 - HIV co-infection

Implications?

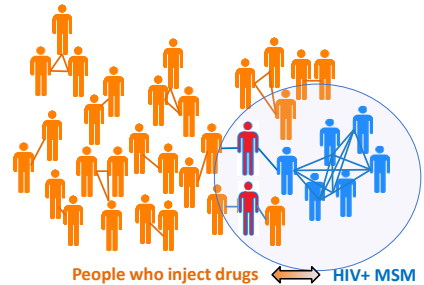


1. HIV+ MSM community highly connected

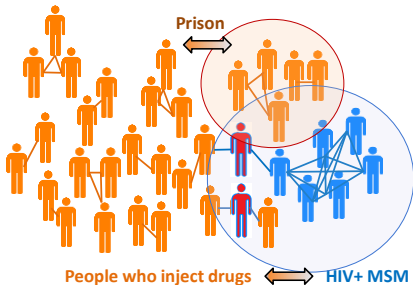


➔ Transmission patterns may assist public health strategies

2. Overlapping modes of HCV transmission

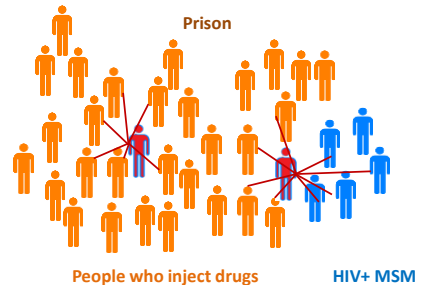


2. Overlapping modes of HCV transmission




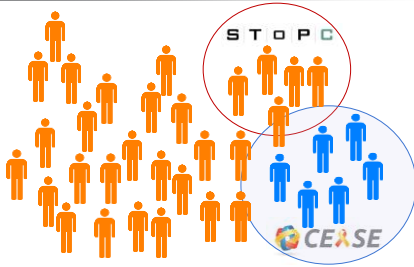
➔ Need to monitor bridging between communities


3. Characteristics of highly connected groups

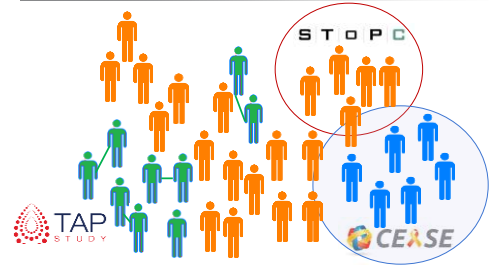


➔ Target and monitor treatment as prevention programs


Australian "Treatment as Prevention" trials 



Australian "Treatment as Prevention" trials 



➔ Universal IFN- free DAA treatment to reduce viral burden and eliminate new transmissions

Acknowledgements 

- ATAHC, HITS-P & HITS-C study participants and coordinators
- Kirby Institute, UNSW
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 - Prof Greg Dore
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- Inflammation and Infection Research Centre, UNSW
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 - Ms. Suzy Teutsch
 - Prof Andrew Lloyd
- The Burnett Institute, Melbourne
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Thank you 