Phylogeny of HCV acute infection in men having sex with men
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Abstract
HCV is a rapidly-evolving RNA virus, which facilitates sequences (NS5B gene, 322bp) and sampling dates. Phylodynamic inferences use both pathogen phylogenies based on genetic sequences and epidemiological data to estimate the transmission of the pathogen only occurs in a subgroup of individuals.

Epidemiological model
We assumed a Birth-Death model with two host types. Host compartments • I1, “Classical” injection drug users • I2, New MSM hosts
Parameters • β1: transmission rate • β2: transmission rate • γ1: infectious period • γ2: infectious period a1: assortativity a2: assortativity

Prior distributions
We consider 3 time intervals: before new HCV detection tests (t0, 1997), before epidemics onset (t1 estimated). The priors of the parameters follow a uniform distribution.

Results & conclusions
New MSM hosts transmit more than classical IDU hosts.

Model & methods

Data
We witness two ongoing epidemics in two host types:

Classical hosts Injection drug users HIV-

New hosts being detected MSM HIV- and HIV+

Detection during chronic infection

213 sequences (NS5B gene, 322bp) and sampling dates

HCV is a rapidly-evolving RNA virus, which facilitates phylogenetic inference.

Data dimensionality

Parameter values

Prior distributions

Regression ABC

Prior distribution

Posterior distribution

Summary statistics

Branch lengths

LTT (lineage through-time) plot

Topology

New summary statistics

Cherries, triplets

Branch lengths on homogeneous and heterogeneous clusters

LLT 'label' plot

Branch lengths on homogeneous clusters

Cherries, triplets

Branch lengths on heterogeneous clusters

Simulated trees

Simulation and parameter inference

Posterior distributions

Estimations

+ a1 = 0.96

+ a2 = 0.86

+ v = 6.5

+ γ1 = 1.7 yrs

+ γ2 = 0.4 yrs

+ t0 = 1976

+ t1 = 2001

+ R0 = 1.80

+ R0 = 2.35

Cross validation

100 replicates: 1 test data x 60.000 training data

Inference error measurement using relative error (RE)

Given the phylogeny structure, our ABC-regression method has the power to infer most parameters.