**Impact of simplified HCV diagnostic strategies on the HCV epidemic among men who have sex with men in the era of HIV oral pre-exposure prophylaxis in Taiwan: a modelling study**

**Technical document**

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This document provides the details of our model, including compartmental structures and transition dynamics, aiming to facilitate a comprehensive understanding of the model.

# **1.Details of model compartments**

The model includes compartments for HCV disease progression and HCV cascade status for MSM. These are denoted , where X denotes the HCV status, denotes the stage of HCV cascade of care and denotes the MSM sub-group (Figure S1).

The possible stages X of HCV infection is for susceptible and never infected with HCV, A for acute HCV infection, F0-F4 for chronic HCV infection classified by stage of liver fibrosis with METAVIR score, DC for decompensated cirrhosis, HCC for hepatocellular carcinoma, LF for liver failure requiring liver transplant and PLF for liver failure followed by liver transplant. Those who have been cured and are susceptible to reinfection are in compartments denoted by with their liver fibrosis stage, for example: an individual cured with liver fibrosis stage at F3 would be .

We denote the cascade status of HCV () for susceptible (including those who spontaneously clear HCV and have been cured) as = 0. For those individuals living with HCV (A, F0-F4, DC, HCC, LF and PLF), the cascade status of HCV () are HCV undiagnosed ( = 1), received HCV antibody testing ( = 2), received HCV RNA testing with HCV ( = 3), initiated HCV treatment ( = 4), andtreatment failure/discontinuing ( = 5).

The overall Taiwanese MSM population ( was compartmentalized into HIV-negative not on PrEP, HIV-negative on PrEP, HIV-positive undiagnosed and HIV-positive diagnosed ( = 1, 2, 3 ,4 respectively). Men transition from one population to another depending on the incidence rate of HIV, the starting and stopping rates for PrEP in those HIV-negative and the testing rate for those living with undiagnosed HIV.

We set annually transition probability among sub-populations in an array (), rows show the probability to transit to population from other sub-population and columns shows the probability to leave from population .

Probability of transition to a given sub-population from each sub-population at each component () would be

Probability of transition to each sub-population from a given sub-population at each component () would be

MSM enter the model when they become sexually active at aged 15 and exit though death at a rate for MSM population (. Additional mortality is included due to advanced liver fibrosis for MSM population(, HCV infection with decompensated cirrhosis , HCV infection with hepatocellular carcinoma , HCV infection with liver failure requiring liver transplant , and HCV infection with liver failure received liver transplant . MSM cured from HCV at these advance liver fibrosis stages still have a background mortality of , , , .

The force of infection for HCV, ,incorporates all the effects of the behaviors contributing to HCV acquisition () and the level of contact between populations (), where N represents the entire modelled population and I represents people living with HCV. In the model it is assumed random interactions occur between sub-populations. Hence,

Once HCV infected, individuals enter undiagnosed acute HCV infection and either spontaneously clear their infection and became susceptible again at a rate or developed chronic HCV infection at a rate. The disease progression between compartments is modelled as follows.

Let be the annual transition probability from compartment X to X’ for sub-population . Then define and .

Then the net movement of people into and out of the is given by

= .

For example, if [1,j] is the first row of the matrix then each element of [1,j] represents the net movement of people into and out of the compartments ,, , , and [4,j] is the fourth row of the matrix then each element of [4,j] represents the net movement of people into and out of the compartments ,, , , .

Those who achieve SVR in the F3, F4, DC stages, and those who achieve SVR at a later stage of liver disease can still progress to DC, HCC, LF and PLF as follows.

Let: is the annual transition probability for those who are cured from HCV and with fibrosis stage at F3 and above to the next fibrosis stage for sub-population . Then define and .

Then the net movement of people into and out of the

= .

For example, [1,j] is the first row of the matrix then each element of [1,j] represents the net movement of people into and out of the compartments .

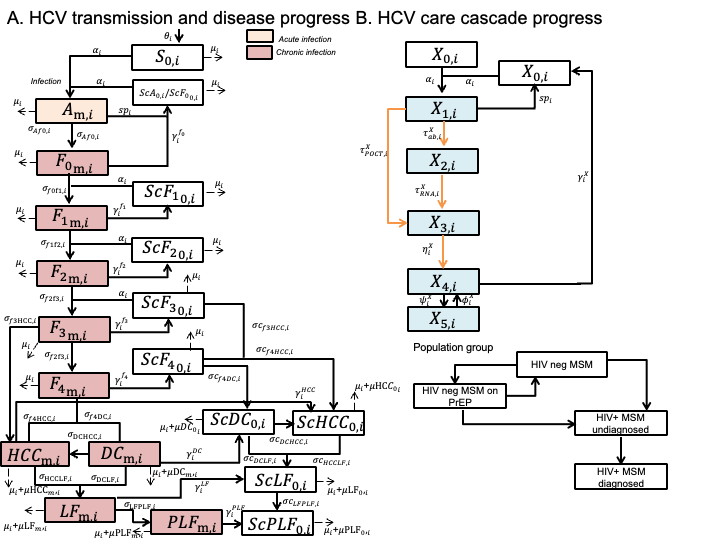
HCV infected individuals in sub-population receive HCV antibody testing at the annually probability followed by receiving HCV RNA testing at annually probability , and then initiating HCV treatment at a annually probability followed by either discontinuing treatment/experienced treatment failure at a rate or achieving SVR at a annually probability . Those who experience treatment failure/discontinuation can re-initiate HCV treatment at a annually probability . This HCV cascade progression annually probability are defined as follows:

* be the annual probability of HCV antibody testing among population and disease progress .
* be the annual probability of HCV RNA testing among population and disease progress .
* be the annual probability of HCV POINT-OF-CARE RNA testing among population and disease progress . This is only for the scenario POINT-OF-CARE RNA. It equals 0 in the status quo and other scenario.
* be the annual probability of treatment initiation among population and disease progress .
* be the annual probability of treatment re-initiation among population and disease progress .
* be the annual probability of treatment failure/discontinuing among population and disease progress .
* be the annual probability of achieving SVR among population and disease progress .
* is the annually probability of spontaneously clearing hepatitis C for sub-population .

These probabilities are used in the model to calculate the net movement of people through the cascade by first defining and , and then

= .

So that [m,j], the m’th row of the matrix represents the net movement of people into and out of the ,, .

Figure S1: Model schematic. (A) HCV transmission and disease progression. Dashed arrows represent mortality, S: susceptible and never infected with HCV, A: acute HCV infection, F0-F4: chronic HCV infection classified by stage of liver fibrosis with METAVIR score, DC: decompensated cirrhosis, HCC: hepatocellular carcinoma, LF: liver failure and requires treatment, PLF: liver failure and received treatment. White blocks represent susceptible, including those spontaneously cleared and cured from HCV. (B) HCV care cascade and HCV testing pathways. Orange arrows indicate the movement influenced by the testing scenarios. (C) Population groups and transitions. The greek symbols represent the parameters related to transition between compartments. 

## **Model equations**

The overall model equations are as follows:

= ,

= .

where

is the inflow of population to the model for sub-population.

is background mortality for sub-population .

is HCV-related mortality for sub-population in DC stage except for .

is HCV-related mortality for sub-population in .

is HCV-related mortality for sub-population in HCC stage except for .

is HCV-related mortality for sub-population in .

is HCV-related mortality for sub-population in LF stage except for .

is HCV-related mortality for sub-population in .

is HCV-related mortality for sub-population in PLF stage except for .

is HCV-related mortality for sub-population in .

is fibrosis progression rate among HCV cured individuals in sub-population .

is the force of infection for HCV for each sub-population denoted by .

For , then for ,

*,*

*,*

*, and*

*.*

If then is given by

If and ,