Supplemental Material: The cost-effectiveness of hepatitis C virus screening in hemodialysis patients





# <span id="page-1-0"></span>Supplemental Table 1: CHEERS 2022 Reporting Checklist







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#### <span id="page-5-0"></span>Supplemental Exhibit 1: HEP-CE Model Structure

#### Model Description:

The Hepatitis C Cost Effectiveness (HEP-CE) model is an individual-based stochastic microsimulation model programmed in C++. A cohort of individuals enters the model with a user-programmed age and liver disease (fibrosis) distribution, and injection-drug use, HCV seropositivity, and chronic infection prevalences. These individuals cycle through various health, disease, and care states, accrue costs and utilities (quality-adjusted life years; QALYs), and are exposed to background and HCV-related mortality each one-month cycle. The major disease and care states are represented in the model diagram below with additional detail on modules explained below and on hemodialysis-related HCV outbreaks detailed in Supplemental Table 3. HCV Screening, Linkage, and Treatment:

All individuals who are not already diagnosed with and in care for HCV are exposed to HCV screening at a frequency determined by the strategy programmed (never, one-time, or periodic at a specified interval). Each time an individual is screened for HCV, they accrue testing costs. Testing occurs as reflex testing with HCV antibody followed immediately (the same cycle) by HCV RNA, only if HCV antibody testing is positive. False negative and false positive antibody and RNA tests can occur, at rates according to literature-informed test sensitivity and specificity, respectively. When a hypothetical individual enters the model, he/she has a true HCV infection status assigned, and a flag indicating whether that diagnosis (if positive) is known. Each time he/she is screened for HCV, the model calculates, based on test sensitivity and specificity, whether the test will reveal to the patient and clinician the true infection status, or a false negative/positive. If a false negative, the patient continues to have progression of liver disease until either re-screening with a true positive occurs or they die from liver-related or background mortality. If a false positive occurs, the patient goes on to have further HCV evaluation, including a genotype test. The genotype test should then reveal lack of HCV viremia, and the patient incurs the cost of the additional tests and evaluation and then returns to the susceptible pool and does not continue further in HCV care until the time of a new positive screen, if that occurs again.

If an individual has a positive HCV antibody and RNA on screening, they are then exposed to a probability of linking to care each cycle, and once linked to care they go through additional HCV evaluation including genotype testing, clinical visits, and liver disease (fibrosis) staging evaluation. This evaluation can occur the same cycle an individual is linked to care or can be programmed to take multiple cycles to complete. In this study, we programmed it to take at least 1 cycle (month) to complete. Once fibrosis evaluation is completed, individuals then enter the treatment module. In this module, they are exposed to a likelihood of starting treatment and assigned a treatment course and cost. Individuals can also be lost to follow-up any cycle that they are linked to care and/or in treatment. Once unlinked, they are also exposed to a lower, literature informed re-linkage rate each cycle, or they can be re-linked if they are screened again.

Treated individuals experience a literature-informed probability of completing treatment or withdrawing due to toxicity or a non-toxicity related reason. Those who complete treatment are exposed to a literature-informed probability of achieving cure, and those who do not complete treatment can still clear spontaneously if within the first 6 months of infection.

#### HCV Infection:

Outside of a programmed hemodialysis center outbreak, HCV infection is possible only through injection drug use. Individuals with current injection drug use experience a monthly probability of HCV infection, and once infected can either spontaneously clear during the first 6 months after infection or can be treated as above.

#### Liver Disease:

Only individuals with HCV infection enter the fibrosis progression module. In the fibrosis progression module, if they have current HCV infection, they experience a monthly probability of their fibrosis advancing to the next stage (F0 to F1, F1 to F2, F2 to F3, F3 to F4, and F4 to decompensated). Once HCV is cured, they remain in the fibrosis stage they reached prior to the last treatment month. If they are re-infected, fibrosis progression resumes. Their fibrosis stage determines their monthly costs due to liver disease, their mortality (higher only for F4 and decompensated stages), and their monthly utilities. Mortality, Costs, Utilities:

Each cycle, each individual is exposed to a risk of background and liver-disease related mortality. For each individual still alive during a given cycle, the model sums the individual's current background healthcare costs with any costs incurred during the cycle from screening, care/treatment, and injection drug use or liver disease-related care. It also multiplies their ageand sex-defined background utility (QALY) by any disease- or treatment-related utilities they incur that cycle – i.e., from HCV infection, a particular fibrosis stage/liver disease, injection drug use, treatment or toxicity.

#### Injection Drug Use:

Individuals begin in one of three injection drug use states: never, current, or former. Once in current injection drug use, they move to former use at a literature-informed, age- and sexstratified probability each month. Individuals can move into or back into current use from never or former states at a literature-informed probability each month as well. In this study's base case, we assumed no new injection drug use begins while on hemodialysis, so movement only occurs from current to former use states.

# **HEP-CE Model Diagram**



<span id="page-8-0"></span>Supplemental Table 2: Hemodialysis Center Hepatitis C Virus Outbreak Literature Review and Calculations

| Description of<br>Source                                  | N   | <b>HCV</b><br>cases | Time<br>Period<br>(months) | Person-<br>months<br>followed | Outbreak<br>Rate.<br>monthly | Outbreak<br>Probability,<br>monthly | Source |
|---|-----|---------------------|----------------------------|-------------------------------|------------------------------|-------------------------------------|--------|
| NY State HD center<br>outbreak 2001-2008                  | 90  | 9                   | 88                         | 3590                          | 0.002507                     | 0.002504                            |        |
| 2016 Cochrane   | 254 | $\overline{4}$      | 9                          | 2268                          | 0.001764                     | 0.001762                            | 2, 3   |
| Review of 1 trial<br>that randomized HD                   | 192 | 9                   | 9                          | 1688                          | 0.005333                     | 0.005319                            | 2, 3   |
| centers to dedicated/                                     | 160 | $\overline{2}$      | 9                          | 1431                          | 0.001397                     | 0.001397                            | 2, 3   |
| non-dedicated<br>machines for those<br>with HCV infection | 121 | 7                   | 9                          | 1058                          | 0.006619                     | 0.006598                            | 2, 3   |
| Mean  |     |                     |                            |                               | 0.0035                       | 0.0035                              |        |

Outbreaks described in literature that detail person-time:

We averaged the HCV incidence rates related to hemodialysis center outbreaks over the described New York state outbreak and the randomized trial arms (initial and subsequent 9 months of follow-up for each trial arm). We assumed all participants in the randomized trial were followed for the duration of the trial as only participants tested at the end of the trial were reported in the results. For the NY state outbreak, we assumed non-case tested individuals at the time of investigation had on average been utilizing the given center for half of the study period, similar to the cases average reported person-time in the center and given average lifespan. The overall mean outbreak HCV incidence was 0.0035 cases/person-month or 4.23 cases per 100 person-years. For sensitivity analyses, we varied this number between the lowest reported HCV incidence rate (0.001397 cases/person-month or 1.68 cases/100 person-years) and 4 times the highest reported incidence rate (0.02648 cases/person-month or 31.8 cases/100 person-years).

Determination of outbreak duration:

We estimated an antibody window period (time between infection and when HCV antibody is detectable on current assays) of 6 months/180 days based on the longest estimates from the literature. <sup>4</sup> We then used half the baseline screening period to account for the index case acquiring infection, on average, halfway through the screening interval (i.e. 6 months in if yearly strategy) and it therefore taking half the screening interval, on average, to pick up the index case. We then assumed that the index case could have transmitted HCV within that time period, and it would take up to 6 months for secondary cases to be detectable by antibody testing (given the window period and an outbreak screening interval of every 3 months). A case is then potentially contagious if the same infection prevention lapses continue until that case is linked to care and treated, which we estimate will take 4 months on average (1 month to make a referral, 2 months to link, complete fibrosis staging, and prior authorization for medications, and 1 month on treatment until viral load is undetectable). Altogether that equates to 16 months plus half the baseline screening interval, for periodic screening intervals as depicted in the formula and table

below. For the non-periodic screening intervals (no testing and testing only at dialysis center entry), we used literature-informed screening durations (multiple lasting approximately 5-7 years with variable screening practices occurring but usually less than guideline-recommended intervals)5, 6 balanced with overall life-expectancy for the population from our simulations (about 5 years). For the screening at dialysis entry scenario, we assumed a shorter outbreak duration than no screening because of at least baseline known HCV status for an individual identified through likely diagnostic screening after elevated ALT or symptoms or background screening in another setting.

Outbreak Duration Formula:

Outbreak Duration = Antibody window period +  $0.5*$ Baseline Screening Interval +  $2*$ Outbreak Screening interval (3 months) + Time from diagnosis until 4 weeks into HCV Treatment, at which point HCV RNA should be undetectable

 $= 6$  months + 0.5\*Screening Interval (months) + 6 months + 4 months



Outbreak duration based on Screening Interval:

Outbreak duration in RNA testing only sensitivity analysis (no 'window period'):



Outbreak Diagram:



### **Modelling of Outbreaks within Hemodialysis (HD) Centers**

|       | Sex    | Proportion HCV |  |  |
|-------|--------|----------------|--|--|
| Age   |        | Seropositive   |  |  |
| 18-24 | male   | 0.01839978     |  |  |
| 18-24 | female | 0.02075406     |  |  |
| 25-29 | male   | 0.03396505     |  |  |
| 25-29 | female | 0.02814523     |  |  |
| 30-34 | male   | 0.04228198     |  |  |
| 30-34 | female | 0.03455368     |  |  |
| 35-39 | male   | 0.05730906     |  |  |
| 35-39 | female | 0.04678727     |  |  |
| 40-44 | male   | 0.08667965     |  |  |
| 40-44 | female | 0.06421291     |  |  |
| 45-49 | male   | 0.13999133     |  |  |
| 45-49 | female | 0.09515614     |  |  |
| 50-54 | male   | 0.18427662     |  |  |
| 50-54 | female | 0.10253617     |  |  |
| 55-59 | male   | 0.17029166     |  |  |
| 55-59 | female | 0.09131393     |  |  |
| 60-64 | male   | 0.11242212     |  |  |
| 60-64 | female | 0.06767342     |  |  |
| 65-69 | male   | 0.06131423     |  |  |
| 65-69 | female | 0.04515619     |  |  |
| 70-74 | male   | 0.03482455     |  |  |
| 70-74 | female | 0.03366514     |  |  |
| 75-79 | male   | 0.02371474     |  |  |
| 75-79 | female | 0.02804273     |  |  |
| 80-84 | male   | 0.01763923     |  |  |
| 80-84 | female | 0.02466199     |  |  |
| 85-99 | male   | 0.01467136     |  |  |
| 85-99 | female | 0.01451613     |  |  |

<span id="page-11-0"></span>Supplemental Table 3: HCV seropositivity and fibrosis stage data, initial cohort



Proportions HCV seropositive and with each METAVIR fibrosis stage (F0-F4) calculated from secondary data analysis from Sawinski et. al., 2019.<sup>7</sup> Fibrosis stages based upon Fibrosis-4 (FIB-4) scores, with cutoffs <1.45 for F0-F1, 1.45-3.25 for F2-F3, and >3.25 as F4.

#### <span id="page-12-0"></span>Supplemental Figure 1: Calibration Results



A. Modeled Versus Predicted Survival

Figure Legend:

Lines represent proportion of population still alive in a given time step (month) in the base case simulation (Non screening or treatment and every 6-month screening strategies shown; results are very similar and lines overlap). Dots represent United States Renal Data System (USRDS) 2017 survival data for incident hemodialysis patients entering the USRDS cohort 1, 2, 3, 5, and 10 years before  $2017$ .<sup>11</sup>

#### B. Hepatitis C Virus Incidence:



Figure Legend:

Absolute number of new hepatitis C virus (HCV) infections each cycle during outbreak and nonbreak scenarios in base case simulation, no screening, no treatment strategy with a total cohort size of 1,000,000 hypothetical individuals.

#### C. Cirrhosis Cases over Simulation



Figure Legend:

Absolute number of cirrhotic individuals each cycle during outbreak and non-break scenarios in base case simulation, no screening, no treatment strategy with a total cohort size of 1,000,000 hypothetical individuals.



#### D. Sample size needed to minimize stochastic variation

Figure Legend:

Panels each demonstrate the difference in mean quality-adjusted life years (QALYs) between the strategies noted when 1000 runs of increasing cohort sizes were used in the base case model simulation, up to a maximum of 400 million. The mean difference is graphed as the solid black line, and purple shaded area represents 95% confidence bands on the mean difference. The dashed black line indicates a mean difference of zero for reference (no difference in QALYs between strategies).

Abbreviations: QALY, quality-adjusted life year



<span id="page-16-0"></span>Supplemental Table 4: Full list of model parameters



<sup>a</sup> All probabilities, incidences, and costs are monthly unless otherwise indicated

**b**Based on age- and sex-stratified annual mortality rates from USRDS 2019 Reference Sheet

H.8\_1 with overall mortality across all ages of 183.4 deaths per 1000 person-years

<sup>c</sup> Lower antibody sensitivity range represents estimate halfway in between historical low HCV antibody sensitivity estimates $^{31,32}$  and more recent, small studies with sensitivity 94-100% in dialysis patients $33-35$ 

<sup>d</sup> False positive test costs include an HCV genotype and two established physician visits

Abbreviations: IDU, injection drug use; HCV, hepatitis C virus; SMR, standardized mortality ratio; HD, hemodialysis; PY, person-years; SVR, sustained virologic response (cure); RNA, ribonucleic acid



<span id="page-18-0"></span>Supplemental Table 5: Breakdown of HCV Testing and Treatment Costs, Base Case Model

<sup>a</sup> All per person costs represent the total number of tests or treatments completed or toxicity events recorded, multiplied by the individual cost per test, treatment, or toxicity (treatment costs include drug costs as well as visit costs for 2 months), divided by the total cohort size  $(N=200,000,000)$ .

Abbreviations: HCV, hepatitis C virus; RNA, ribonucleic acid



<span id="page-19-0"></span>Supplemental Table 6: Comparison of testing using RNA versus antibody testing



Abbreviations: RNA, ribonucleic acid; QALYs, quality-adjusted life years; ICER, incremental cost-effectiveness ratio; Ab, antibody



# <span id="page-20-0"></span>Supplemental Table 7: Additional Sensitivity Analysis Results





#### **H. Low HD Center Outbreak-Related HCV Incidence (1.68 cases/100 PY)**



#### **L. Background HCV Screening Simulated (20.8% over 5 years)**  $H<sub>0</sub>$  $\overline{\mathbf{S}}$



#### **M. HCV Antibody and RNA Test Cost Lower Estimate (25th% Gamma Distribution)**



#### **N. HCV Antibody and RNA Test Cost Higher Estimate (75th% Gamma Distribution)**



Abbreviations: HCV, hepatitis C virus; SVR, sustained virologic response (cure); QALYs, quality-adjusted life years; ICER, incremental cost-effectiveness ratio; SMR, standardized mortality ratio; HD, hemodialysis



Supplemental Table 8: Probabilistic Sensitivity Analysis Results

<span id="page-25-0"></span>Abbreviations: HCV, hepatitis C virus; QALYs, quality-adjusted life years; ICER, incremental cost-effectiveness ratio

<span id="page-26-0"></span>Supplemental Figure 2: Probabilistic Sensitivity Analyses Cost Effectiveness Acceptability Curve



Cost Effectiveness Acceptability Curve

Figure Legend:

This graph represents the cost effectiveness acceptability curve (CEAC) for the probabilistic sensitivity analysis varying several parameters (HCV antibody and RNA test cost, treatment cost, outbreak-related HCV incidence, mortality from cirrhosis, and antibody and RNA test sensitivity and specificity). The x-axis is the willingness-to-pay threshold in \$US and the y-axis is the probability that a given strategy will be the 'winner' at the corresponding willingness-to-pay threshold: the strategy that yields the highest number of quality adjusted life years (QALYs) for a cost under the willingness-to-pay threshold. The probability was determined by doing 1000 runs, each with a different set of parameters drawn from the probability distributions noted in Supplemental Table 5, and then calculating the strategy with the highest net monetary benefit  $(NMB; NMB = OALYs$  gained  $*$  willingness-to-pay threshold – incremental costs comparing each strategy to the next least expensive, non-dominated strategy) at each willingness-to-pay threshold.

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