

COMBINING BIOLOGICAL MARKERS OF RECENT HEPATITIS C VIRUS INFECTION TO ESTIMATE INCIDENCE AMONG PEOPLE WHO INJECT DRUGS

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Background:

Eliminating hepatitis C (HCV) as a public health threat requires preventing new infections among people who inject drugs (PWID) whom are at highest risk of transmission. As prevalence and incidence decline, cost-effective methods to estimate incidence are increasingly needed. We present a method to estimate HCV incidence using combined biological markers from a cross-sectional survey.

Methods:

Dried blood spot samples from the Unlinked Anonymous Monitoring Survey, which recruits PWID through specialist services in England, Wales and Northern Ireland were tested (for 2016, 2018, 2022 and 2024 survey years). Analyses were restricted to HIV-antibody-negative participants to minimise bias from impaired immune response.

Two biomarkers of recent HCV infection were evaluated. The “RNA” marker classified acute infection as RNA antigen-positive and antibody-negative. The “Avidity” marker measured antibody-antigen binding strength (increasing with duration of infection); recent infection was defined as a low avidity score of $\leq 40\%$.

HCV incidence was estimated separately for each biomarker and as a combined estimate using random-effects meta-analysis. Temporal trends were examined using meta-regression.

Results:

Estimated HCV incidence declined from 2016 to 2024 for both markers; RNA: from 10.4 (95%CI: 6.3-15.8) to 6.8 (95%CI: 3.8-10.9) per 100 person-years and Avidity: from 9.9 (95%CI: 7.0-13.5) to 3.0 (95%CI: 1.6-5.2) per 100 person-years. Pooled estimates suggested borderline evidence of similar reductions, from 10.1 (95%CI: 7.7-13.2) to 4.6 (95%CI: 2.1-10.1), although uncertainty in 2022 weakened the statistical evidence for the overall trend.

Conclusion:

Both biomarkers indicated declining HCV incidence from 2016 to 2024. Using biomarkers of recent infection offer a practical alternative to longitudinal or large cohort studies. Given the short window period of acute infection requiring a large sample size for the RNA-based estimation, combining biomarkers provides a more accurate approach as we approach elimination and HCV transmission declines. Further work is needed to confirm these trends and triangulate findings with modelled estimates.

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Figure 1: HCV incidence estimates among PWID using biological markers of recent infections

