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Maternal hepatitis C prevalence and trends by county, US: 2016–2020

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Abstract

Background: Trends in the prevalence of hepatitis C virus (HCV) infection among women delivering live births may differ in rural vs. urban areas of the United States, but estimation of trends based on observed counts may lead to unstable estimates in rural counties due to small numbers.

Objectives: The objective of the study was to use small area estimation methods to provide updated county-level prevalence estimates and, for the first time, trends in maternal HCV infection among live births by county-level rurality.

Methods: Cross-sectional natality data from 2016 to 2020 were used to estimate maternal hepatitis C prevalence using hierarchical Bayesian models with spatiotemporal random effects to produce annual county-level estimates of maternal HCV infection and trends over time. Models included a 6-Ievel rural–urban county classification, year, maternal characteristics and county-specific covariates. Data were analysed in 2022.

Results: There were 90,764/18,905,314 live births (4.8 per 1000) with HCV infection reported on the birth certificate. Hepatitis C prevalence was higher among rural counties as compared to urban counties. Rural counties had the largest annual increases in maternal hepatitis C prevalence (per 1000 births) from 2016 to 2020 (micropolitan: 0.39; noncore: 0.40), with smaller increases

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CONFLICT OF INTEREST

No conflict of interest.

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DISCLAIMER

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the US Federal Office of Rural Health Policy or the National Center for Health Statistics, Centers for Disease Control and Prevention.

SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

among less densely populated urban counties (medium metro: 0.28; small metro: 0.28) and urban counties (large central metro:0.11; large fringe metro: 0.14).

Conclusions: The prevalence of maternal HCV infection was the highest in rural counties, and rural counties saw the greatest average prevalence increase during 2016–2020. County-level data can help in monitoring rural–urban trends in maternal HCV infection to reduce geographic disparities.

Keywords

Bayes theorem; birth certificates; hepatitis C; infections; opioid; pregnancy; rural population

1 | BACKGROUND

Hepatitis C virus (HCV) infection during pregnancy has increased in the US,[1] with higher prevalence estimates found in rural areas.[2,3] We previously reported the prevalence of modelled maternal HCV infection during 2016–2018 was 3.5–3.8 times higher in nonurban counties than in large central metropolitan counties.[3] Counties above the 90th percentile for modelled maternal hepatitis C prevalence in 2018 were concentrated in Appalachia, Northern New England, New Mexico and along the northern border in the Upper Midwest.

In 2020, the Centers for Disease Control and Prevention (CDC) released new HCV testing recommendations that include maternal screening during pregnancy except where HCV infection prevalence is less than 0.1%.[4] The CDC recommendations highlight the need for updated county-level estimates of maternal hepatitis C prevalence to identify areas that meet this threshold. However, maternal hepatitis C prevalence estimates are typically unstable for sparsely populated counties with fewer than 20 cases of maternal HCV infection annually. While aggregation across adjacent counties, by state, or across years can help stabilise estimates, these approaches mask county-level trends, especially in rural counties. The purpose of this study is to use small area estimation methods to provide updated county-level prevalence estimates and, for the first time, calculate trends in maternal HCV infection among live births by county-level rurality.

2 | METHODS

2.1 | Maternal HCV infection

This analysis used restricted-use data from the 2003 revised version of the US Standard Certificate of Live Birth for births occurring between 2016 and 2020 (as of 2016, all states had adopted the revised birth certificate).[5] The revised version of the birth certificate contained checkboxes for infections present and/or treated during pregnancy, including HCV infection, intended to be based on positive test results recorded in the medical record.[6] Information on whether anti-HCV positivity and/or positive HCV RNA test results led to the checkbox being checked was not captured.

2.2 | Maternal county of residence

Analyses were restricted to births among US residents because a US county of residence was required for spatial analysis. Rurality of maternal county of residence was defined using the

2013 National Center for Health Statistics (NCHS) 6-level urban–rural classification scheme (ranging from most urban to most rural: large central metro, large fringe metro, medium metro, small metro, micropolitan and noncore).[7]

2.3 | Maternal characteristics

Maternal characteristics included those previously found to be associated with maternal HCV infection.[2,3,8,9] These were age; race/ethnicity; educational attainment; marital status and, if not married, paternity acknowledgement; participation in the Special Supplemental Nutrition Program for Women, Infants and Children (WIC); expected payment method for delivery; smoking during pregnancy; and pre-pregnancy body mass index (BMI).

2.4 | County characteristics

Federal Information Processing Standards county codes were used to link maternal county of residence with corresponding annual estimates for the following time-varying county-level characteristics predictive of maternal hepatitis C prevalence: percentage of families living below the poverty threshold and drug overdose death rates.[3,10,11]

2.5 | Statistical analysis

2.5.1 | Hierarchical Bayesian spatial models—Hierarchical Bayesian models with spatially and temporally structured random effects were used to estimate county-level prevalence of maternal HCV infection. Log-binomial models were fit using the Integrated Nested Laplace Approximation (INLA) package in R.[12–14] Models included spatially structured random effects,[15] fixed and random effects for year, and a space–time interaction term, which allowed temporal trends to vary by county.

To improve the fit of model-based maternal HCV estimates, models also included county-level drug overdose death rate (as a continuous variable), county poverty rate (as a continuous variable), maternal age category (<20, 20–24, 25–29, 30–34, 35–39, ≥40years), maternal educational attainment (no high school diploma or General Education Diploma [GED], high school diploma or GED, some college, Bachelor's degree or higher), smoking during pregnancy (no, yes), maternal race/ethnicity (Hispanic, non-Hispanic white, non-Hispanic Black, other), marital status (not married and no paternity acknowledgement, not married and paternity acknowledgement, married), expected source of payment for delivery (Medicaid, private, self-pay, other), participation in WIC during pregnancy (no, yes) and pre-pregnancy BMI (underweight, normal, overweight, obese). The best fitting model included covariates where missing and unknown values (generally <2%) were collapsed with the referent group (age, educational attainment, marital status, expected source of payment, WIC participation, pre-pregnancy BMI), included in the 'other' category (race/ethnicity), or included as an indicator variable (smoking during pregnancy). Alternative hierarchical Bayesian regression models (Poisson, zero-inflated Poisson, zero-inflated binomial) were applied; however, none of these alternative models resulted in improvements in fit.

Posterior predicted median county-level prevalence estimates for HCV infection by year and 95% Bayesian credibility intervals (95% BCI) were obtained from the model, and 1000

samples from the posterior distributions were drawn to estimate the median county-level annual change in prevalence and corresponding 95% BCIs (File S1).

To estimate the modelled linear trends in hepatitis C prevalence by NCHS 6-level rurality, annual prevalence of HCV infection was calculated for each urban–rural category and weighted linear regression models (weighted by the number of live births) were used to estimate trends in hepatitis C prevalence by year for each of the urban–rural categories. The mean slope and 95% CI were used to estimate the average annual change in HCV infection (per 1000 live births).

2.5.2 | Missing data—The prevalence of missing data on maternal characteristics was generally <2%. The one exception was marital status, which was missing for 9% of the study population, largely due to a restriction in California beginning in 2017 that limited the release of record-level information on marital status of the mother. Analysing multiply imputed data when covariates have missing values is not straightforward in the R INLA package, so multiple imputation methods were not used to account for missing data on marital status. However, posterior predicted estimates from a model with no covariates were compared with the posterior predicted estimates from the model with the best fit; a near perfect correlation was found overall ($\rho = 1$) and for California individually. This suggested that accounting for missing marital status information through multiple imputation would not have changed this study's findings, as the impact on the posterior predicted prevalence estimates would likely be negligible.

2.5.3 | Sensitivity analyses—To account for potential underreporting of hepatitis C prevalence on the birth certificate, especially as universal maternal screening during pregnancy was not recommended until 2020 and because at least one study suggests that only 40% of pregnancies post-recommendation were screened as recommended,[16] misclassification bias analyses were conducted to explore five different scenarios for the degree of underreporting and whether it was differential over time and by urban–rural category. Previous regional or state-level studies have found 38% (equal to 0.72 sensitivity, assuming 1.00 specificity) to 62% (equal to 0.62 sensitivity, assuming 1.00 specificity) higher prevalence of maternal hepatitis C when birth certificate data were augmented with newborn bloodspot testing[17] or historical laboratory reports of anti-HCV positivity and/or positive HCV RNA test.[18,19] Using the range of hepatitis C sensitivity estimates of birth certificate data from these studies and likely trends in hepatitis C sensitivity over time and across the urban–rural gradient, the following scenarios were examined (1) increasing sensitivity from 2016 to 2020 (0.60–0.80) and same sensitivity across urban–rural category; (2) increasing sensitivity from 2016 to 2020 (0.60–0.80) and decreasing sensitivity from urban to rural category (0.75–0.65); (3) same sensitivity over time and across urban–rural category (0.63); and (4) same sensitivity over time (0.63) and decreasing sensitivity from urban to rural category (0.75–0.65). A fifth scenario was also examined, based on rural–urban sensitivity estimates and log-linear extrapolated time trend estimates from a study using 2012–2015 data from Ohio;[18] this study reported a U-shaped relationship for hepatitis C sensitivity from urban to rural category (0.74 for large metro [not disaggregated into fringe vs. central], 0.68 for medium metro, 0.63 for small metro, 0.73 for

micropolitan, and 0.70 for noncore) and increasing sensitivity over time (0.65 in 2012–0.76 in 2015). Adjustment factors (i.e. proportionate increase in hepatitis C prevalence rates after accounting for underreporting) were generated from the inverse of the sensitivity estimates and are shown by urban-county level and year for each scenario in Table S1. To account for the uncertainty around these estimates, for each county-year observation, we generated 1000 random samples from a normal distribution with the mean corresponding to the adjustment factor estimate and a standard deviation of 0.05. These adjustment factors were applied to the 1000 samples drawn from the posterior distributions of hepatitis C prevalence from the models and results were summarised using the median and 2.5th and 97.5th percentiles of the distributions.

Analyses were conducted in 2022 using SAS and R.

2.6 | Ethics approval

This study was determined to be nonhuman subjects research by the University of Southern Maine's Institutional Review Board.

3 | RESULTS

There were 90,764/18,905,314 live births (4.8 per 1000) with maternal HCV infection reported on the birth certificate (HCV infection status was missing for 0.3% [48,960] of live births [we previously reported the impact of these missing data were minimal]).[3] Hepatitis C prevalence increased from 4.2 to 5.1 per 1000 live births from 2016 to 2020 (annual prevalence increase of 0.22 [Table S1]). Maternal characteristics more common among women with HCV infection included non-Hispanic white race/ethnicity; less than college educational attainment; not married, no paternity acknowledgement; Medicaid as expected source of payment for delivery; participation in WIC during pregnancy; having normal pre-pregnancy BMI; smoking during pregnancy; living in a county within the highest drug overdose death rate quartile; and living in a county designated as small metro, micropolitan rural or noncore rural (Table 1).

Using direct estimates from observed data, maternal hepatitis C prevalence was higher among rural counties (non-core, micropolitan) and decreased with increasing urbanicity among urban counties (small metro, medium metro, large fringe metro and large central metro) (Figure 1). Predicted estimates from spatiotemporal models were generally similar to direct estimates; however, predicted estimates were consistently higher than direct estimates for non-core and micropolitan counties each year (especially so for 2019 and 2020), and varied in a non-consistent direction for small metro, medium metro and large fringe metro counties across study years.

The largest increases in average annual predicted hepatitis C prevalence per 1000 live births were in micropolitan and non-core counties (0.39 and 0.40, respectively), with medium metro and small metro counties (both 0.28) and large central metro and large fringe metro counties having smaller annual increases (0.11 and 0.14, respectively) (Table 2).

The counties with predicted maternal hepatitis C increase above 0.44 per 1000 live births per year (corresponding to the 80th percentile of county-level changes) were generally located in Appalachia, Northern New England, New Mexico and along the northern border in the Upper Midwest (Figure 2). Concentrated areas with larger increases were also found along the West Coast, East Coast, in Alaska, the Midwest and Florida. Some counties had decreases in maternal hepatitis C prevalence, such as several counties in Texas and Florida.

The misclassification bias analysis yielded discrepant findings regarding trends in predicted maternal hepatitis C prevalence depending on whether misclassification was assumed to be differential over time and/or by urban–rural category (see Table S3). Scenarios 1 and 2, based on increasing sensitivity of hepatitis C documentation on the birth certificate over time, found higher rates of maternal hepatitis C prevalence in 2016 and *decreasing* rates of prevalence over time—in contrast to the primary analysis—with the largest decreases in rural counties. Scenarios 3 and 4, which assumed the same sensitivity in hepatitis C documentation over time, found higher rates of maternal hepatitis C prevalence in 2016 and more pronounced *increasing* rates of maternal hepatitis C prevalence over time as compared with the primary analysis, with the largest increases in rural counties. Scenario 5, which was based on empirical data from Ohio, found higher rates of maternal hepatitis C prevalence in 2016 and *no change* in rates of maternal hepatitis C prevalence over time overall, with the decreases over time in large fringe metro, small metro and noncore counties.

4 | COMMENT

4.1 | Principal findings

During 2016–2020, the average prevalence of maternal HCV infection was 4.8 per 1000 live births and was highest in rural counties. Rural counties saw the greatest increase in modelled hepatitis C prevalence, approximately 3.5 times that of large central metro counties and 1.4 to 2.8 times that of large fringe metro, medium metro and small metro counties. Most areas of the country experienced an increase in maternal hepatitis C prevalence, but there were some counties that experienced a decrease. Changes in the prevalence of maternal hepatitis C over time could be due to changes in underlying incidence of HCV infection, screening practices and/or treatment or viral clearance rates.[4,20]

4.2 | Strengths of the study

Study strengths include the provision of county-level prevalence and trend estimates of maternal hepatitis C prevalence for all counties in the United States. Aggregation of estimates across space or time can mask distinct sub-state patterns, particularly for rural areas with smaller populations and for regions that span multiple states.

4.3 | Limitations of the data

This study has some limitations. First, prevalence estimates were based on maternal hepatitis C documentation on the birth certificate,[6] which may underestimate HCV infections as screening in pregnancy during the study period was not universal and data transfer from medical records to the birth certificate may be incomplete. Second, the spatial analysis could have resulted in over-smoothing of extreme high or low values, particularly in areas with

small numbers of births, resulting in masking areas with large decreases or increases in maternal hepatitis C prevalence. Third, the misclassification bias analyses were based on available HCV infection sensitivity data from select states and examined several plausible misclassification scenarios, finding that estimated trends were heavily influenced by the magnitude of the assumed differences in misclassification overtime and by urban–rural category. In addition, some of the bias analyses suggested downward trends in maternal hepatitis C prevalence, which is incongruous with the recent syndemics of hepatitis C infection, injection drug use and drug overdose deaths in the US.[21–23]

In the absence of nationally representative data on trends and differences in the degree of misclassification, these sensitivity analyses were considered exploratory, as it is unknown how misclassification has truly changed over time and by urban–rural category. Moreover, studies based on augmenting birth certificate information with laboratory data on history of maternal HCV infection could overestimate the population at risk of adverse outcomes associated with infection during pregnancy because the risk for vertical transmission among children born to anti-HCV positive and HCV RNA negative mothers is negligible (whereas risk among HCV RNA positive mothers is 5.8%).[24] Furthermore, studies of national hospital discharge data have found similar estimates of maternal HCV infection prevalence as the birth certificate,[9,25] suggesting that HCV infection documented on the birth certificate by healthcare providers aligns with clinical estimates of HCV infection during pregnancy from other data sources.

4.4 | Interpretation

Results from this study are consistent with previous studies that have described increases in maternal HCV infection in the United States since 2000,[1,2] and rural–urban disparities.[3] Ko et al. found that maternal HCV infection increased by more than 400% from 2000 to 2015, using national data from an all-payer inpatient healthcare database.[1] While that study examined maternal HCV infection in relation to demographic factors and region (South, West, Northeast and Midwest), it did not examine trends by county or urban–rural residence. Rossi et al. also found increases in maternal HCV infection of 161% from 2009 to 2017 and described differences in maternal HCV infection rates and trends by state and county population size.[2] However, that study relied on direct estimates of HCV infection rates, which are often suppressed and/or unreliable when based on few cases. In our prior study that used hierarchical Bayesian models to estimate spatially smoothed maternal HCV infection rates during 2016–2018, we found that rates were 3.5–3.8 times higher in more rural counties than in large central metropolitan counties.[3] Additionally, counties with the highest prevalence of maternal hepatitis C in 2018 were concentrated in Appalachia, Northern New England, New Mexico and along the northern border in the Upper Midwest. That prior analysis was based on only 3years of data and was therefore unable to examine trends in maternal HCV infection rates over time by county.

Describing trends at the county level, especially in more sparsely populated rural areas, can be particularly challenging because the prevalence of maternal hepatitis C based on observed data can be highly variable year to year. The present study provides smoothed estimates of trends in maternal hepatitis C prevalence by county over time, which have not

yet been estimated due to low hepatitis C case counts in counties with small numbers of births and the somewhat recent (2016) nationwide adoption of the revised birth certificate, which captures HCV infection information. Results suggest that hepatitis C prevalence was higher among rural counties as compared with urban counties, and rural counties had the largest annual increases in maternal hepatitis C prevalence from 2016 to 2020, with smaller increases among more urban counties. The counties with the largest increases in maternal hepatitis C prevalence were in Appalachia, Northern New England, New Mexico and along the northern border in the Upper Midwest, along with pockets across the West Coast, East Coast, in Alaska, the Midwest and Florida. Conversely, some counties, for example in Texas and Florida, exhibited decreases in maternal hepatitis C prevalence. Providing more recent county-level estimates of maternal hepatitis C prevalence and related trends and rural–urban disparities can highlight which areas may be in need of community-level interventions to reduce maternal HCV infections. These interventions could reduce barriers along the cascade of care for maternal HCV infection, from screening to follow-up and treatment postpartum[26] in addition to increased testing of infants perinatally exposed to hepatitis C virus.[27] Examining counties where decreases were seen may yield information on what factors drove improvements over time, and whether those factors can be used elsewhere to reduce maternal hepatitis C prevalence.

5 | CONCLUSION

Using the most recent data available, this study found increasing prevalence of maternal hepatitis C in the United States from 2016 to 2020, with the greatest increases among rural counties. Implementation of universal screening in pregnancy may lead to greater detection of cases and could affect future trend estimates. Monitoring rural–urban prevalence and trends in maternal hepatitis C can help identify areas for focused efforts on hepatitis C testing and treatment to reduce geographic disparities.[28]

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the National Center for Health Statistics. Restrictions apply to the availability of these data, which were used under license for this study. Data are available from https://www.cdc.gov/nchs/nvss/nvss-restricted-data.htm with the permission of the National Center for Health Statistics.

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Synopsis

Study question

- What are the current trends in maternal hepatitis C virus (HCV) infection by county-level rurality in the United States (US)?

What's already known

- In the US, women living in rural counties have a higher prevalence of HCV infection during pregnancy as compared to women living in urban counties. However, estimating trends by county-level rurality is challenging because of sparse data issues.

What this study adds

- After accounting for sparse data issues, the prevalence of maternal HCV infection is the highest among those living in micropolitan rural and non-core rural counties and lowest among those living in large central metropolitan counties. In addition, rural counties are experiencing the greatest annual increase in prevalence of maternal HCV infection.

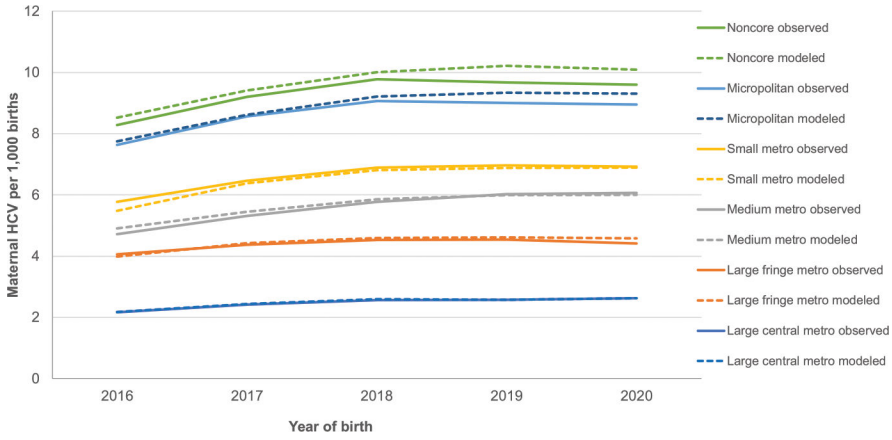

FIGURE 1.

Observed (solid line) and modelled (dashed line) prevalence of maternal HCV infection by 2013 National Center for Health Statistics' 6-Level Urban–Rural classification scheme for counties: US birth certificate data, 2016–2020 (n = 3142). See footnote for Table 2 for model information

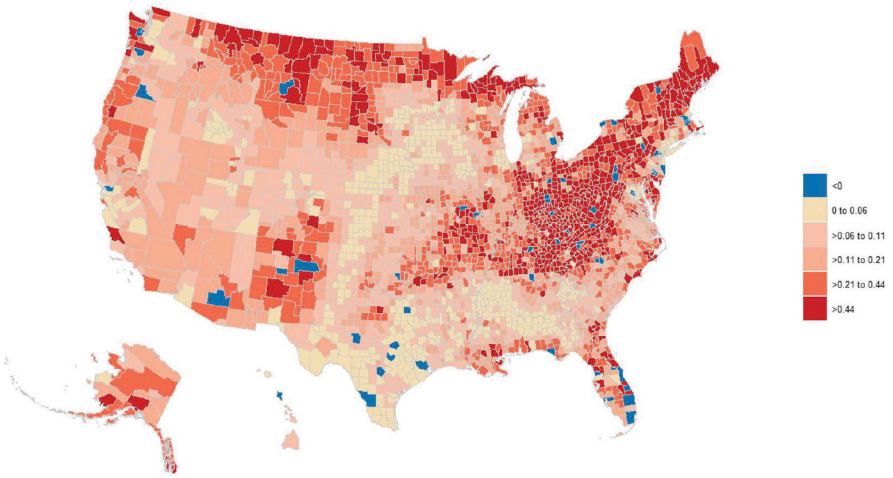

FIGURE 2.

Modelled within-county linear trends overtime in predicted maternal HCV infection per 1000 live births, 2016–2020.

Choropleth map shows the average annual prevalence change (linear trend) within county. Counties coloured in blue show decreasing trends (<0 per 1000 live births) and counties in yellow show no trend or slight increasing trend (0–0.06 per 1000 live births [2nd–20th percentile]). Counties in shades of red show increasing trends: lightest red (>0.06–0.11 per 1000 live births [>20th–40th percentile]), light red (>0.11–0.21 per 1000 live births [60th–80th percentile]) and dark red (>0.44 per 1000 live births [>80th percentile]). See footnote for Table 2 for model information

TABLE 1

Maternal hepatitis C virus (HCV) infection by selected maternal characteristics: US birth certificate data, 2016–2020

	Total[a]		Maternal hepatitis C virus (HCV) infection			
			No		Yes	
	n	Col %	*n*	Col %	*n*	Col %
All	18,905,314	100.0	18,814,550	100.0	90,764	100.0
Maternal age at birth (years)						
Under 20	920,592	4.9	919,285	4.9	1307	1.4
20–24	3,654,875	19.3	3,639,695	19.4	15,180	16.7
25–29	5,460,459	28.9	5,426,671	28.8	33,788	37.2
30–34	5,439,734	28.8	5,413,019	28.8	26,715	29.4
35–39	2,798,710	14.8	2,787,082	14.8	11,628	12.8
40 or greater	630,944	3.3	628,798	3.3	2146	2.4
Maternal race/ethnicity						
Hispanic	4,446,189	23.5	4,439,204	23.6	6985	7.7
Non-Hispanic white	9,741,474	51.5	9,668,820	51.4	72,654	80.1
Non-Hispanic black	2,740,822	14.5	2,736,644	14.6	4178	4.6
Other[b]	1,976,829	10.5	1,969,882	10.5	6947	7.7
Marital status						
Not married, no paternity acknowledgement	1,993,144	10.5	1,961,347	10.4	31,797	35.0
Not married, paternity acknowledgement	4,879,767	25.8	4,843,567	25.7	36,200	39.9
Married	10,242,377	54.2	10,221,923	54.3	20,454	22.5
Missing	1,790,026	9.5	1,787,713	9.5	2313	2.6
Maternal educational attainment						
No high school diploma or GED	2,387,172	12.6	2,365,201	12.6	21,971	24.2
High school diploma or GED	4,816,882	25.5	4,779,639	25.4	37,243	41.0
Some college	5,301,635	28.0	5,275,923	28.0	25,712	28.3
Bachelor’s degree or higher	6,148,397	32.5	6,144,222	32.7	4175	4.6
Missing	251,228	1.3	249,565	1.3	1663	1.8
Expected source of payment for delivery						

	Total[a]		Maternal hepatitis C virus (HCV) infection			
			No		Yes	
	n	Col %	*n*	Col %	*n*	Col %
Medicaid	7,967,454	42.1	7,896,273	42.0	71,181	78.4
Private	9,357,051	49.5	9,344,336	49.7	12,715	14.0
Self-pay	767,044	4.1	764,434	4.1	2610	2.9
Other	696,300	3.7	693,017	3.7	3283	3.6
Missing	117,465	0.6	116,490	0.6	975	1.1
WIC use during pregnancy						
Yes	6,734,099	35.6	6,683,824	35.5	50,275	55.4
No	11,958,635	63.3	11,920,160	63.4	38,475	42.4
Missing	212,580	1.1	210,566	1.1	2014	2.2
Pre-pregnancy body mass index						
Underweight	588,903	3.1	584,622	3.1	4281	4.7
Normal	7,792,317	41.2	7,749,144	41.2	43,173	47.6
Overweight	4,908,640	26.0	4,885,952	26.0	22,688	25.0
Obese	5,175,742	27.4	5,158,662	27.4	17,080	18.8
Missing	439,712	2.3	436,170	2.3	3542	3.9
Pregnancy smoking status[c]						
Yes	1,208,180	6.4	1,154,334	6.1	53,846	59.3
No	17,611,033	93.2	17,575,658	93.4	35,375	39.0
Unknown/not stated	86,101	0.5	84,558	0.5	1543	1.7
County-level characteristics						
County of residence (percentage below poverty threshold)[d]						
Less than 10%	5,078,080	26.9	5,058,948	26.9	19,132	21.1
10–19%	12,167,019	64.4	12,105,676	64.3	61,343	67.6
20–29%	1,545,377	8.2	1,536,275	8.2	9102	10.0
30% or greater	114,731	0.6	113,544	0.6	1187	1.3
County overdose death rate per 100,000 population[e]						
Quartile 1	2,396,251	12.7	2,392,958	12.7	3293	3.6
Quartile 2	3,335,149	17.6	3,328,778	17.7	6371	7.0

	Total[a]		Maternal hepatitis C virus (HCV) infection			
			No		Yes	
	n	Col %	*n*	Col %	*n*	Col %
Quartile 3	4,186,500	22.1	4,173,871	22.2	12,629	13.9
Quartile 4	8,987,414	47.5	8,918,943	47.4	68,471	75.4
6-Level urban–rural county classification scheme[f]						
Large central metro	6,157,620	32.6	6,142,476	32.7	15,144	16.7
Large fringe metro	4,523,607	23.9	4,503,797	23.9	19,810	21.8
Medium metro	3,978,882	21.1	3,956,740	21.0	22,142	24.4
Small metro	1,692,076	9.0	1,681,118	8.9	10,958	12.1
Micropolitan	1,536,072	8.1	1,522,816	8.1	13,256	14.6
Noncore	1,017,057	5.4	1,007,603	5.4	9454	10.4

Abbreviation: GED, General Education Diploma; WIC, Special Supplemental Nutrition Program for Women, Infants, and Children.

[a]Among birth records with maternal hepatitis C virus infection as ‘Y’ or ‘N’.

[b]Includes Asian or Pacific Islander, American Indian or Alaska Native, Other and Hispanic origin unknown or not stated; and unknown.

[c]Smoking during any trimester of pregnancy.

[d]Generated by merging restricted-use data files with Census Bureau data on families below the poverty threshold by county Federal Information Processing Standard Publication (FIPS) for mother’s county of residence at the time of birth.

[e]Generated by merging restricted-use data files with vital records published data on overdose death rates by county Federal Information Processing Standard Publication (FIPS) for mother’s county of residence at the time of birth.

[f]2013 National Center for Health Statistics 6-level urban–rural classification scheme.

TABLE 2

Modelled linear trends in maternal hepatitis C virus (HCV) infection by 2013 National Center for Health Statistics' 6-Level Urban–Rural classification scheme for counties: US birth certificate data, 2016–2020 (n = 3142)

	Model-based estimates (95% confidence interval) per 1000 live births	
6-Level urban–rural county classification scheme	**Intercept**[a]	**Average annual prevalence change in HCV infection**
Large central metro (n = 68)	2.27 (2.21, 2.33)	0.11 (0.08, 0.13)
Large fringe metro (n = 368)	4.15 (4.07, 4.24)	0.14 (0.11, 0.17)
Medium metro (n = 372)	5.09 (4.99, 5.18)	0.28 (0.24, 0.31)
Small metro (n = 358)	6.04 (5.88, 6.20)	0.28 (0.23, 0.34)
Micropolitan (n = 641)	8.08 (7.87, 8.26)	0.39 (0.32, 0.45)
Noncore (n = 1335)	8.85 (8.63, 9.07)	0.40 (0.33, 0.47)
Total (n = 3142)	4.46 (4.41, 4.52)	0.21 (0.19, 0.23)

Note: Analysis included 18,905,322 births. Hierarchical Bayesian log-binomial models were fit using the Integrated Nested Laplace Approximation package in R, version 4.1.2. Models included county-level maternal characteristics, drug overdose death rate and poverty rate; spatially structured random effects; fixed and random effects for year; along with a space × time interaction term, which allowed temporal trends to vary by county.

[a]Intercepts represent the modelled prevalence of maternal HCV infection among live births in year 2016.