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Updated national and state-specific prevalence of congenital cytomegalovirus infection, United States, 2018–2022

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Abstract

Context: Congenital cytomegalovirus (cCMV) infection is the most common infectious cause of birth defects and the leading non-genetic cause of sensorineural hearing loss in the United States. Prior national cCMV infection prevalence estimates were based on one multi-site screening study conducted between 2007–2012 and were not adjusted for sociodemographic characteristics, such as maternal race and ethnicity or age.

Objective: This study sought to estimate national and state-specific prevalence of cCMV infection in the U.S., adjusted for maternal race and ethnicity and maternal age group, by pooling estimates from published studies.

Design: We searched PubMed for U.S. cCMV newborn screening studies conducted between 2003–2023. From included studies, we abstracted maternal race and ethnicity- and age group-

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Declarations of Competing Interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Disclaimer

The findings and conclusions in this article are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.

SUPPLEMENTAL MATERIALS

Literature search

72 articles returned on December 5, 2023

Term 1: cCMV

Term 2: Screen[ing studies]

Term 3: Newborn

Term 4: Prevalence

Filters: English language and 2003–2023

((congenital cytomegalovirus[Title/Abstract]) OR (cCMV[Title/Abstract]) OR (congenital CMV[Title/Abstract])) AND (screen*[Title/Abstract]) AND (newborn*[Title/Abstract]) AND (prevalence[Title/Abstract]) AND ((english[Filter]) AND (2003:2023[pdat]))

stratified cCMV prevalence to estimate strata-specific pooled prevalence. We obtained strata-specific weights from live birth data.

Main Outcome Measure: Estimated adjusted national and state-specific prevalence estimates from 2018–2022.

Results: Four studies (conducted 2004–2005, 2008, 2007–2012, and 2016–2021) were included for data abstraction. Overall, infants born to non-Hispanic Black (9.3 [8.2–10.5] per 1,000) or non-Hispanic American Indian and Alaska Native (8.5 [2.1–33.2] per 1,000) mothers had the highest cCMV prevalence. The estimated race and ethnicity-adjusted prevalence was 4.6–4.7 per 1,000 live births nationally and ranged from 3.9–6.5 across states from 2018–2022. Southern states and Alaska consistently had the highest cCMV prevalence. The estimated maternal age group-adjusted prevalence was 4.3–4.4 per 1,000 live births nationally and ranged from 3.8–5.1 across states from 2018–2022.

Conclusions: States with larger proportions of racial and ethnic minorities had higher estimated prevalence of cCMV infection compared to states with larger proportions of White persons. These estimates may be useful for informing cCMV surveillance at the jurisdiction level and developing tailored, culturally relevant education and prevention strategies for persons at higher risk.

Keywords

Congenital cytomegalovirus infection; congenital CMV infection; public health surveillance

INTRODUCTION

Congenital cytomegalovirus (cCMV) infection is the most common infectious cause of birth defects and the leading non-genetic cause of pediatric sensorineural hearing loss (SNHL) and single-sided deafness in the United States.^{1–4} Although the majority of cCMV infections are asymptomatic during the neonatal period, both asymptomatic and symptomatic infants are at risk of long-term sequelae, including SNHL, vision impairment, and neurodevelopmental disabilities. Few U.S. studies have assessed cCMV prevalence based on newborn screening. In the United States, prior cCMV prevalence estimates were based on one multi-site screening study conducted between 2007 and 2012.⁵ Since the publication of those findings, it has been assumed that cCMV infection occurs in approximately 4.5 per 1,000 live births, with considerable variation observed by maternal race/ethnicity and age.^{5–8} However, these estimates were not adjusted for sociodemographic distributions of annual live births in the United States (U.S.) and important differences may be obscured.

Despite the potential severity of disease, cCMV is not nationally notifiable in the U.S. and only 12 states currently conduct surveillance for infection and related conditions.^{9,10} This has contributed to a limited understanding of the state-specific disease burden. As states consider implementing screening or surveillance for cCMV, the availability of more accurate and representative estimates of expected prevalence may inform resource allocation, priority setting, and policy- and decision-making for cCMV. Furthermore, CMV vaccines may come to market within the next five years and addressing this knowledge gap will be especially important to prepare for vaccine effectiveness and impact evaluation. Using

cCMV prevalence reported from U.S. newborn cCMV screening studies, this study sought to estimate the expected national and state-specific live birth prevalence of cCMV infection from 2018–2022, adjusted for maternal race and ethnicity and maternal age group.

METHODS

Literature search

We conducted a rapid literature review for English-language publications describing cCMV prevalence estimates from newborn screening studies conducted in the U.S. within the last 20 years. We consulted a previously published systematic review to aid in the development of the search strategy.¹¹ Among the U.S. newborn screening studies included in the reviewed reference, five were published between 2003–2021; of these, three were from the same study population and only one reported maternal race and ethnicity- or age-stratified prevalence. We did not expect our search to yield many additional publications and limited our search to PubMed. The search strategy is detailed in Supplemental Material. We excluded studies that screened special populations (e.g., premature infants) or whose screening protocols were non-universal (e.g., targeted).

The rapid literature search returned 72 articles: 52 were conducted outside of the U.S., 14 were U.S. studies but did not describe cCMV screening, 1 described screening among premature infants, and 1 described targeted screening among high-risk infants and were not appropriate for inclusion. Four studies, including 1 from the referenced systematic review, were selected for data abstraction (Table 1; Supplemental Materials).

Data abstraction

We abstracted maternal race and ethnicity- and age group-stratified cCMV prevalence estimates, as well as the number of infants tested and positive for cCMV (by strata) from each included study. Additionally, we obtained study data not reported in the publication (e.g., in instances where maternal categories were collapsed) from study authors when possible. Maternal race and ethnicity groups used in the analyses were non-Hispanic White, non-Hispanic Black, Hispanic, non-Hispanic Asian, and non-Hispanic American Indian and Alaska Native (AI/AN); maternal age groups were ≤ 24 years, 25–29 years, 30–34 years, and ≥ 35 years.

Not all studies contributed data for every group of interest: non-Hispanic Asian data were available from three studies,^{5,7,8} non-Hispanic AI/AN data were only available from two studies,^{5,8} and data for the defined age groups were available from three studies.^{6,8} Additionally, two studies collapsed non-Hispanic White, Asian and Pacific Islander (API), and “other” into one category^{6,7} – as described in the original publications, we assumed this category comprised mostly non-Hispanic white mothers and therefore used this prevalence estimate for non-Hispanic White infants but did not include it in the non-Hispanic Asian pooled estimates. Though only one study provided data for infants born to multiracial mothers,⁵ estimates were based on a large sample size ($n=2,436$), and that study included sites in seven states and described data for all the other maternal race and ethnicity groups included in this analysis.

Statistical analysis

We calculated annual, national and state-specific prevalence estimates of cCMV infection following methods similar to what has been reported previously for other birth defects.^{12,13} First, we calculated pooled prevalence estimates and 95% confidence intervals (CIs) per maternal group using random effect models. We conducted the analyses using the “Meta-analysis” function in Comprehensive Meta-Analysis version 4 (CMA v4). Prevalence estimates per maternal group from each study were only included in the pooled calculations if there were at least 100 infants tested. This resulted in some groups (non-Hispanic Hawaiian and Other Pacific Islanders [HOPI] and “Other”) being excluded from all analyses. One study stratified prevalence estimates by time period (before and during the COVID-19 pandemic).⁸ Overall prevalence estimates were lower compared to pre-pandemic estimates; we assumed changes to disease transmission during the pandemic were transient and therefore we included only pre-pandemic prevalence estimates in this analysis. We did not include any estimates for “unknown” maternal race and ethnicity or age group.

We obtained group weights using annual live birth data per state available from the Centers for Disease Control and Prevention (CDC) Wide-ranging ONline Data for Epidemiologic Research (WONDER) natality database.¹⁴ We calculated group weights by dividing the annual number of infants born to each maternal group by the total birth cohort, nationally and per state, from 2018–2022. Persons whose Hispanic ethnicity was unknown or not reported, but reported at least one race category, were classified as non-Hispanic. The number of reported births was suppressed for maternal groups if the data did not meet criteria for confidentiality restraints (<10 records), so total births may be missing for some group-state-year combinations.

Next, we calculated maternal race and ethnicity- and age group-adjusted expected annual live birth prevalence per state as the sum of the products of race and ethnicity- or age group-stratified pooled prevalence and race and ethnicity or age group population weights, divided by the total live birth cohort. In the equation below, E is the expected live birth prevalence, s is the state (or US), y is the year, PP is the pooled prevalence, and g is each group (maternal race and ethnicity or age group, described above).

$$E_{s,y} = \frac{(PP_{g1} \times Population\ weight_{g1}) + (PP_{g2} \times Population\ weight_{g2}) + \dots (PP_{gn} \times Population\ weight_{gn})}{Total\ live\ birth\ population}$$

We then estimated the annual number of infections and disease nationally and per state. To estimate the number of infections, we applied the adjusted prevalence to the total live birth population and rounded to the nearest 100 infections (unless the estimate was <100, in which case we rounded to the nearest 10). We assumed 18% of infections would be symptomatic at birth or result in long-term sequelae (i.e., disease)^{3,15,16} and rounded to the nearest 10 cases.

Finally, we compared the state-specific population demographics and prevalence estimates for California, Florida, and Minnesota to those reported in the respective original publications. We used CMA v4 and SAS v9.4 (Cary, NC) statistical software to conduct all analyses.

RESULTS

Pooled cCMV prevalence estimates by maternal race and ethnicity and maternal age group

The overall pooled prevalence estimate for cCMV infection was 4.8 (4.0–5.7) per 1,000 live births (Table 1). Infants born to non-Hispanic Black mothers (9.3 [8.2–10.5]), non-Hispanic AI/AN mothers (8.5 [2.1–33.2]), and mothers aged ≤ 24 years (8.2 [6.9–9.9]) had the highest prevalence per 1,000 live births; infants born to non-Hispanic Asian mothers (2.5 [0.8–7.5]), Hispanic mothers (3.6 [1.7–7.4]), and mothers aged 25–29 years (3.1 [2.5–3.7]) and ≥ 35 years (2.7 [1.2–5.8]) had the lowest prevalence per 1,000 live births (Table 1). Pooled estimates including all data from Schleiss et al. (i.e., not restricting to pre-pandemic data) were similar and reported in Supplemental Table 1.

Maternal race and ethnicity-adjusted state-specific cCMV prevalence

The estimated national maternal race and ethnicity-adjusted cCMV infection prevalence was 4.6 (3.0–7.3) per 1,000 live births in all years from 2018–2022, except 2020, during which it was 4.7 (3.0–7.3) per 1,000 live births (Figure 1A–E, Supplemental Table 2). Although most states had an annual maternal race and ethnicity-adjusted estimated prevalence similar to the national estimate (between 4.0–4.9 per 1,000), regional differences were observed. The estimated annual prevalence in southern states, the District of Columbia, and Alaska were consistently elevated compared to the rest of the country. The District of Columbia (DC) had the highest annual prevalence per 1,000 in all five years (ranging from 6.2–6.4), followed by Mississippi (ranging from 6.1–6.2) and Louisiana (ranging from 5.9–6.0); California had the lowest prevalence, ranging from 3.9–4.0 per 1,000. The estimated maternal race and ethnicity-adjusted cCMV prevalence per state and year are included in Supplemental Table 2.

The average, annual estimated number of cCMV infections nationally was 17,100 and the average number of disease cases was 3,090 (Supplemental Table 2). The state-specific average annual number of infections ranged from 20 (Vermont) to 1,700 (California); the average annual number of disease cases ranged from 0 (Vermont) to 300 (California).

Maternal age-adjusted state-specific cCMV prevalence

The estimated national maternal age group-adjusted cCMV infection prevalence was 4.4 (3.1–6.7) per 1,000 live births from 2018–2020 and was 4.3 (3.0–6.7) from 2021–2022 (Figure 2A–E). Most states had an estimated maternal age group-adjusted infection prevalence within the range of the national prevalence estimate (4.2–4.8 per 1,000). Mississippi, Arkansas, and West Virginia consistently had the highest maternal age group-adjusted estimated prevalence, per year (although highest prevalence among these did differ year to year). The estimated maternal age group-adjusted cCMV prevalence per state and year are included in Supplemental Table 3.

The average, annual estimated number of cCMV infections nationally was 16,100 and the average annual estimated number of disease cases was 2,900 (Supplemental Table 3). The state-specific average annual number of infections ranged from 20 (Vermont) to 18,00

(California); the average annual number of disease cases ranged from 0 (Vermont) to 320 (California).

State-specific cCMV prevalence estimates compared to study-reported prevalence

The pooled prevalence estimates were similar to study-reported prevalence for most maternal race and ethnicity and age groups in the Florida⁶ and Minnesota⁸ studies (Table 1). For infants born to non-Hispanic Black mothers, the pooled prevalence estimated in the current study was higher than the prevalence reported in the Minnesota study (9.3 vs. 5.8; Table 1).⁸ The pooled prevalence estimates in the current study were notably lower for the non-Hispanic White (3.9 vs 6.5), Hispanic (3.6 vs 7.8), and non-Hispanic Asian (2.5 vs 6.4) maternal groups compared to the prevalence per group reported in the California study.⁷

Discrepancies in reported study enrollment compared to state-specific population makeups observed in CDC WONDER were also noted (Table 2). A greater proportion of mothers aged ≤ 24 years were enrolled in the Florida study⁶ (36.1%) compared to the average Florida live birth population from 2018–2022 (21.8%), and a smaller proportion of mothers aged ≥ 30 years were enrolled (37.2% vs. 50.0%). Conversely, a smaller proportion of the youngest mothers were enrolled in the Minnesota study⁸ (9.1%) compared to the average Minnesota live birth population from 2018–2022 (15.4%), and a greater proportion of those aged ≥ 30 years were enrolled (68.7% vs. 55.8%). Maternal race and ethnicity was more consistent between study enrollment and observed populations.

DISCUSSION

This study provides an updated estimate for national cCMV infection prevalence in the United States, as well as individual, state-specific estimates for 2018–2022. Our estimates account for the demographic makeup (maternal race and ethnicity or age group) of the United States and individual states, including data from multiple studies that represent 10 geographical and economically diverse states. At the state level, these estimates may help with resource allocation, program planning, and policy- and decision-making with regards to cCMV screening, surveillance, and care for children diagnosed with cCMV. Nationally, these estimates may be useful to inform future vaccine policy, including efforts centered on improving health equity. We estimated 15,800–17,600 infants born with cCMV infection annually, approximately 2,830–3,170 of whom might present with cCMV disease at birth or related sequelae. Some studies have estimated the number of annual infections to be 40,000 with approximately 8,000 children with permanent disabilities.^{17,18} However, more recent U.S. screening studies demonstrate lower prevalence, suggesting that this number was likely an overestimate.^{5,6,8,19} Placing the burden of cCMV in context with other congenital or perinatal causes of neurodevelopmental disabilities and impairments in children is helpful to increase public awareness. It has long been stated that more children are affected by serious cCMV-related disabilities than by several better-known childhood conditions, including Down Syndrome and fetal alcohol syndrome (FAS). However, those assertions have been limited by the methods of case ascertainment for each condition (passive versus active surveillance, universal screening, analysis of hospitalization data), the case definitions or spectrum of disease captured (all disease versus severe disease), and the representativeness

of the populations studied. For example, infants born with Down Syndrome have distinctive physical characteristics that prompt immediate genetic testing. With a prevalence of 1.3 per 1,000,²⁰ Down Syndrome may lead to more cases of neurodevelopmental disabilities in U.S. children as compared to cCMV disease (assuming 18% of infections result in disease). In contrast, FAS encompasses the most severely affected cases of fetal alcohol spectrum disorder (FASD). Though FASD may not be readily identified, its prevalence ranges from 11.3–50.0 per 1,000, much higher than that of cCMV infection.^{21,22} It is therefore fair to describe cCMV infection as the leading infectious cause of neurodevelopmental disabilities and impairments in U.S. children. Future state-based surveillance will be helpful in guiding education and prevention strategies, including potential opportunities for integrated approaches to birth defect prevention.

Although most states had an annual maternal race and ethnicity-adjusted prevalence similar to the national estimate (4.6 per 1,000), there were notable regional patterns. Overall, maternal race and ethnicity-adjusted burden was disproportionately higher in southeastern parts of the country, including DC, which consistently had the highest estimated race and ethnicity-adjusted prevalence. Compared to the rest of the country, these states have large minority populations – the average proportion of infants born to non-Hispanic Black mothers from 2018–2022 was 44.3% in DC, 42.1% in Mississippi, and 36.9% in Louisiana compared to 5.0% in California (the state with the lowest prevalence) and 14.5% across the US. Disparities in cCMV burden exist among racial and ethnic minorities, as reported in all included studies in this analysis: infants born to non-Hispanic Black and non-Hispanic AI/AN mothers consistently had higher cCMV prevalence estimates compared to those born to non-Hispanic White and non-Hispanic Asian mothers (prevalence observed among Hispanic infants was inconsistent).^{5–8} Health disparities observed among racial and ethnic groups are often related to socioeconomic inequities, many of which – such as frequent and/or prolonged contact with children under six years and crowded living arrangements – directly increase the risk of cCMV infection.²³ Reasons for these disparities are likely multifactorial and should not be attributed to differential biological susceptibility. Understanding the effects of race and ethnicity and socioeconomic resources (or lack of) within the context of systemic racism and impacts on health outcomes will be important for guiding future research and developing informed prevention efforts.

In addition to disparities in disease burden, this study also demonstrated persistent inequities in the availability of public health data for racial and ethnic minorities, especially Indigenous populations such as AI/AN and HOPI persons. We were not able to estimate prevalence for infants born to HOPI mothers, and data for AI/AN infants was only available from two studies (which had to be obtained from study authors, as published data were collapsed into an “other” category – a common, albeit problematic, practice in public health research). Although pooled prevalence results in the current analysis showed increased prevalence among AI/AN infants compared to all other racial and ethnic groups, accurate enumeration of disparities among Indigenous infants is challenging because data from newborn cCMV screenings with a large proportion of Indigenous infants are lacking. One previous study reported that cCMV-coded diagnosis among AI/AN infants was significantly higher in Alaska compared to the Southern Plains region, which is consistent with our findings, but reasons for this geographic difference are unknown.²⁴ Future studies that include better (i.e.,

larger) representation of these populations will be helpful in assessing cCMV disease burden and potential health disparities.

Younger maternal age has also been shown to be associated with greater risk of cCMV. One study showed that the youngest mothers (<20 years) were the most likely to deliver an infant with cCMV (prevalence odds ratio [POR]: 4.5 per 1,000) compared to mothers aged 20–25 years (POR: 2.2 per 1,000) or mothers aged 25–29 years (POR: 1.1 per 1,000).²⁵ A more recent report from Michigan showed that approximately half of cCMV cases from 2004–2011 were born to mothers aged ≤24 years and that prevalence was highest among those born to mothers aged ≤20 years (14 per 1,000 live births).²⁶ The studies included in the pooled prevalence estimates all showed higher prevalence among infants born to the youngest mothers. However, when the pooled prevalence estimates were applied to the state-specific populations adjusted for maternal age group, prevalence was more homogenous across states compared to prevalence adjusted for race/ethnicity. Although “hot spots” were identified, differences were not as pronounced. It is likely that maternal age does not vary substantially across states and that finer scale (e.g., county-level) data are needed to identify prevalence differences by maternal age. It has been shown that maternal age at first birth is strongly driven by urbanicity²⁷ and that a larger proportion of teenage pregnancies occur in lower-income, rural settings.^{28,29} Additionally, because of limits to reported and available data, we collapsed the youngest mothers (<20 years) with mothers aged 20–24 years. Therefore, synergistic effects of teenage pregnancies and living in a rural area would have been masked, limiting the potential diversity of cCMV prevalence estimated in the current analysis.

Currently, infection with cCMV is not a nationally notifiable condition and only 12 states conduct cCMV surveillance.^{9,10} In 2023, the Council for State and Territorial Epidemiologists (CSTE) approved standardized case definitions for cCMV infection and disease, which went into effect January 2024. In August 2022, CDC began collaborating with seven jurisdictions (Illinois, Iowa, Minnesota, New Jersey, New York, Utah, and Virginia) to pilot cCMV surveillance through the Surveillance for Emerging Threats to Pregnant People and Infants Network (SET-NET).¹⁰ The ongoing pilot will inform methods for case ascertainment, as well as the feasibility of implementing the CSTE case definitions and conducting longitudinal data collection. These efforts are critical to advancing cCMV surveillance and findings from the SET-NET cCMV pilot are expected to guide the standardization of cCMV surveillance across the country. For example, Utah has conducted cCMV surveillance since 2013 and serves as a model for other jurisdictions; data collected over the past decade provides valuable insight into the impact of newborn screening protocols (hearing-targeted and later, expanded high-risk) on case ascertainment.³⁰ Surveillance in Minnesota, the first state in the U.S. to implement universal newborn cCMV screening, will provide additional information on equity in access to infant follow-up services.³¹ Across all piloting jurisdictions, a critical facilitator for collecting data has been the inclusion of cCMV in state-specific reporting rules. In the future, inclusion of cCMV in the list of nationally notifiable conditions by the CSTE may facilitate case ascertainment and data collection across the U.S. and improve representativeness. This analysis was subject to limitations. We relied on data from newborn cCMV screening studies conducted over the last two decades, representing over 15 years of data collection. However,

reported prevalence was consistent between studies, suggesting cCMV prevalence is stable. Additionally, the categorization of persons into race and ethnicity and age groups differed between the included studies, limiting the data we were able to include in the pooled prevalence estimates for some groups. Furthermore, some studies combined certain groups (e.g., non-Hispanic AI/AN and Asian into “other”), which may misrepresent minority populations. We were not able to stratify by maternal race and ethnicity and age group, both of which are known to influence the risk of cCMV and likely act synergistically. Discrepancies in maternal age were noted between reported study enrollment and state-specific makeups observed in CDC WONDER, which may have impacted the age-adjusted analysis. Finally, prevalence of cCMV in 2020 might have been impacted by the COVID-19 pandemic, as reported in recent studies.^{8,32}

CONCLUSIONS

This analysis provides updated national cCMV prevalence estimates and new state-specific, adjusted prevalence estimates over a five-year period. It demonstrated notable regional patterns in cCMV prevalence adjusted for maternal race and ethnicity, which reflect underlying health disparities. These findings highlight the need to collect more robust sociodemographic data to be able to identify groups at the greatest risk of infection, improve our understanding of specific risk factors, and develop tailored, culturally relevant education and prevention strategies. Furthermore, these data may be useful for individual jurisdictions with resource allocation, program planning, and policy- and decision-making with regards to cCMV screening, surveillance, and care for children diagnosed with cCMV.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Implications for Policy & Practice

- Estimates from this analysis underscore the need to improve collection of sociodemographic data during cCMV research to be able to identify groups at higher risk of cCMV infection, improve understanding of risk factors, and develop tailored, culturally relevant education and prevention strategies.
- These estimates may be used by individual jurisdictions to inform resource allocation, program planning, and policy- and decision-making with regards to cCMV screening, surveillance, and case management.

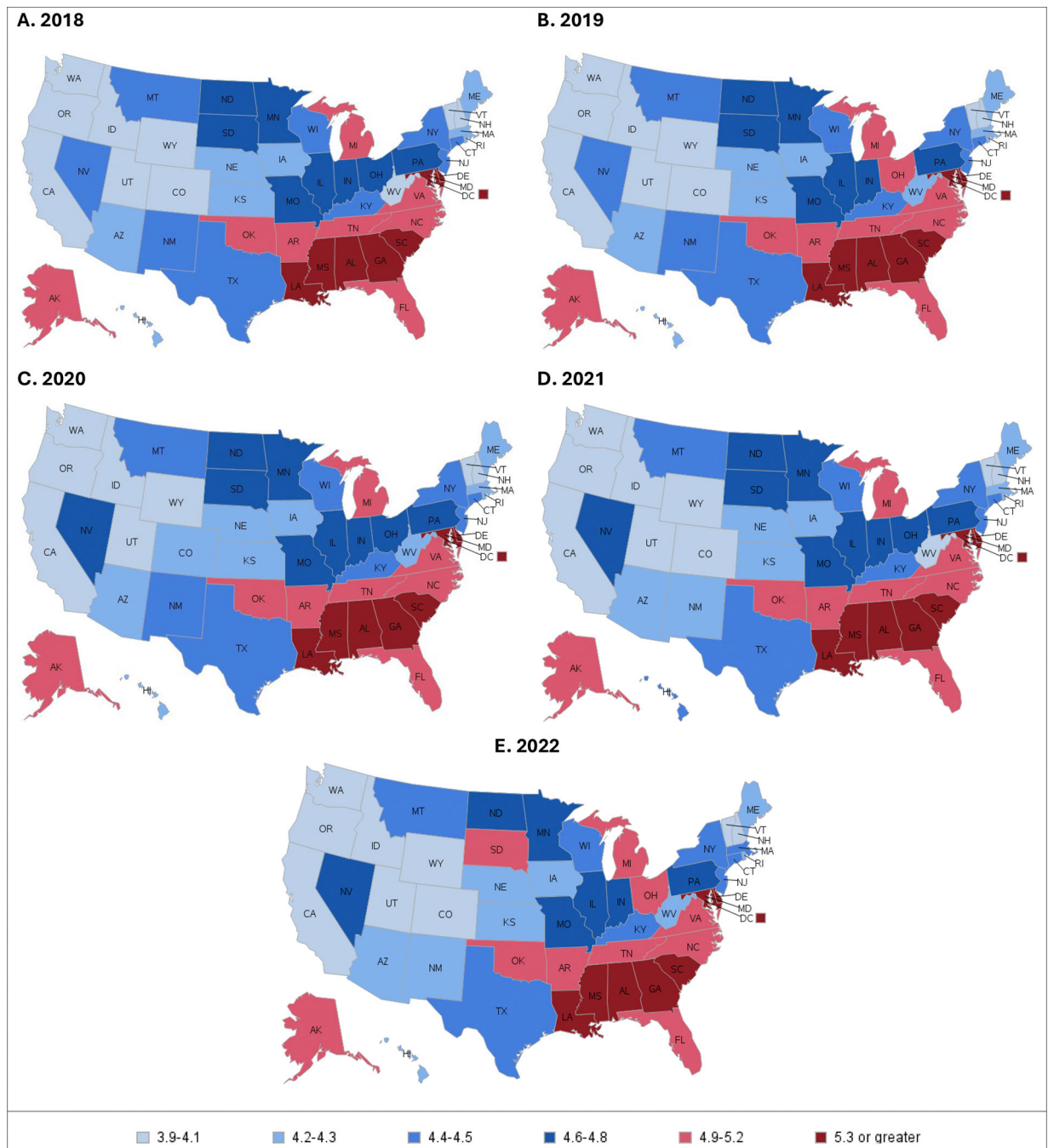


Figure 1.
Maternal race and ethnicity-adjusted cCMV infection prevalence per 1,000 live births, by year, 2018–2022

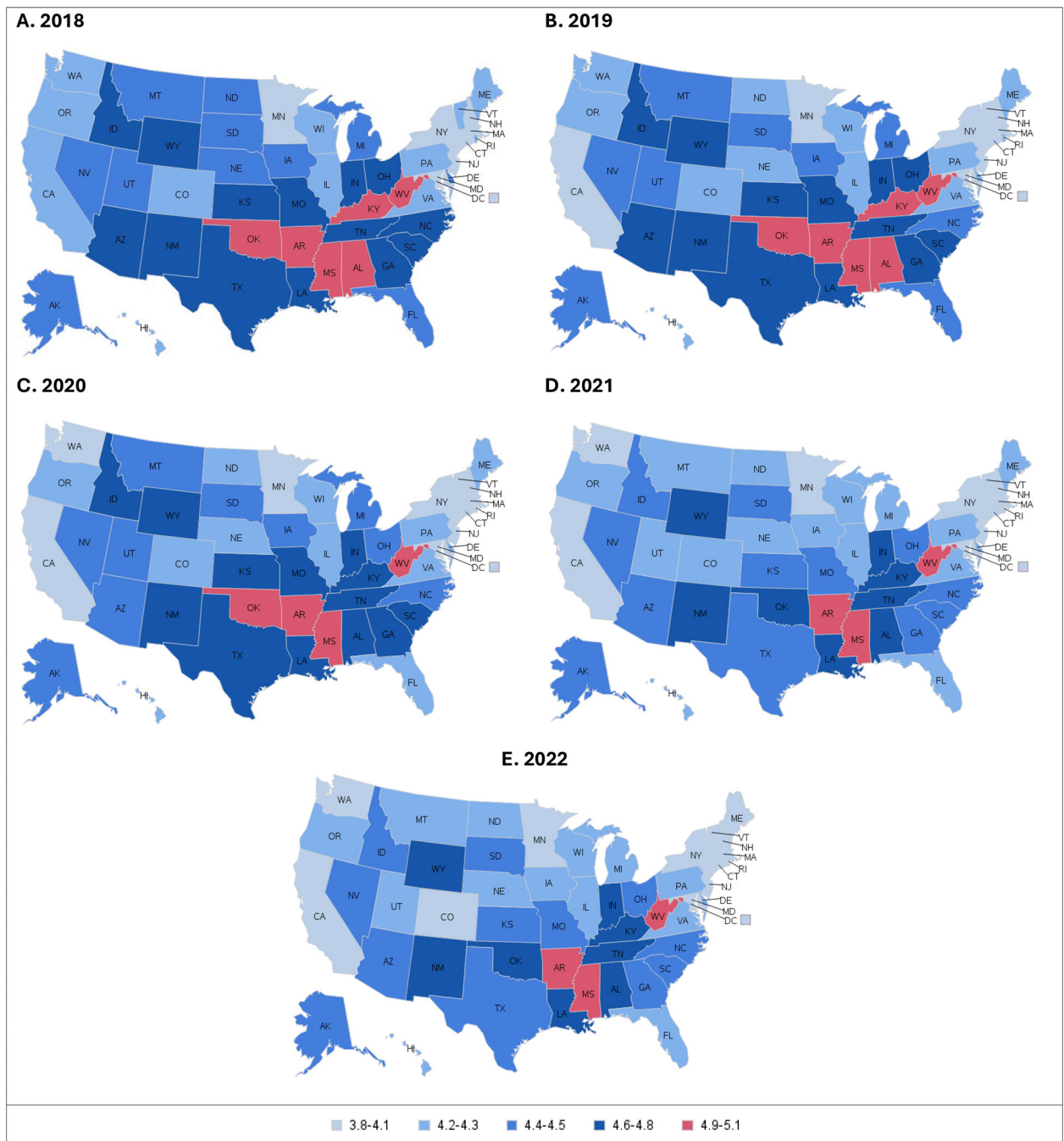


Figure 2.
Maternal age group-adjusted cCMV infection prevalence per 1,000 live births, by year,
2018–2022

Table 1.

Maternal race and ethnicity- and age group-stratified cCMV prevalence estimates reported in published screening studies and estimates from pooled prevalence analysis

	cCMV prevalence per 1,000 live births (n/N)				
Study	Kharrazi et al (CA, 2004–2005)	Fowler et al (AL, MS, NC, NJ, OH, PA, TX, 2007–2012)	DePasquale et al (FL, 2008)	Schleiss et al (MN, 2016–2021) ^d	Pooled estimate ^b (95% CI)
Overall	7.1 (28/3,927)	4.5 (449/100,332)	4.5 (14/3,101)	4.5 (70/15,697)	4.8 (4.0–5.7)
Strata					
<i>Maternal race and ethnicity</i>					
Non-Hispanic White	6.5 (7/1,077) ^c	2.7 (100/32,310)	2.7 (4/1,473)	5.1 (56/11,069)	3.9 (2.4–6.3)
Non-Hispanic Black	9.5 (2/211)	9.5 (228/24,100)	8.4 (6/716)	5.8 (8/1,389)	9.3 (8.2–10.5)
Hispanic	7.8 (16/2,053)	3.0 (96/32,310)	3.3 (3/896)	0.7 (1/1,408)	3.6 (1.7–7.4)
Non-Hispanic Asian	6.4 (3/469)	1.0 (4/4,166)	NR	2.7 (3/1,094) ^d	2.5 (0.8–7.5)
Non-Hispanic AI/AN	NR	10.0 (1/101)	NR	7.2 (1/138) ^d	8.5 (2.1–33.2)
Non-Hispanic HOPI	NR	NR	NR	0.0 (0/27) ^e	NE
Multiracial	NR	7.8 (19/2,436)	NR	0.0 (0/75) ^e	7.8 (5.0–12.2)
Non-Hispanic Other	0.0 (0/96) ^e	NR	62.5 (1/16) ^e	NR	NE
<i>Maternal age group</i>					
≤24 years	NR	8.6 (299/34,950) ^f	4.5 (5/1,120)	7.7 (11/1,435)	8.2 (6.9–9.9)
25–29 years	NR	3.0 (83/27,854) ^f	2.4 (2/828)	3.7 (13/3,480)	3.1 (2.5–3.7)
30–34 years	NR	2.0 (47/23,900) ^f	7.3 (5/682)	4.5 (30/6,667)	3.7 (1.8–7.7)
≥35 years	NR	1.5 (20/13,624) ^f	4.2 (2/471)	3.9 (16/4,115)	2.7 (1.2–5.8)

AI/AN, American Indian and Alaska Native; AL, Alabama; API, Asian and Pacific Islander; CA, California; cCMV, congenital cytomegalovirus; FL, Florida; HOPI, Hawaiian and Other Pacific Islander; MN, Minnesota; MS, Mississippi; NC, North Carolina; NE, not estimated; NJ, New Jersey; No, number; NR, not reported; OH, Ohio; PA, Pennsylvania; TX, Texas

^a Study included overall prevalence estimates and prevalence estimates stratified by pre- and during-COVID-19 pandemic. Only pre-pandemic estimates were included in the main analysis and reported in this table; overall estimates were included in secondary analyses and are reported in Supplemental Table 1. Race and ethnicity- and age group-stratified pre-pandemic estimates were obtained from study authors and were not published.

^b Pooled prevalence estimated in the current study.

^c Study authors collapsed non-Hispanic White, API, and other into one category for reported prevalence. We assumed this category comprised mostly non-Hispanic white mothers and therefore used this reported prevalence for our non-Hispanic white pooled estimate, but did not include it in the non-Hispanic Asian pooled estimate.

^d Non-Hispanic AI/AN and Non-Hispanic Asian infants collapsed into “Other” category in publication; disaggregated prevalence obtained via study authors.

^e Number of infants tested <100 and group not included in pooled prevalence calculations.

^f Study reported the following age groups: 13–19, 20–29, 30–39, and ≥40 years. Prevalence estimates for age groups used in the current study obtained from study authors and were not published.

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Table 2.

Proportion of participants enrolled in published studies (2004–2021) compared to the average live-birth proportions in California, Florida, Minnesota, and the United States (2018–2022) by maternal race and ethnicity and age group

	Kharrazi et al (CA, 2004– 2005)	Average ^a proportion of CA live births	DePasquale et al (FL, 2008)	Average ^a proportion of FL live births	Schleiss et al (MN, 2016– 2021)	Average ^a proportion of MN live births	Fowler et al (AL, MS, NC, NJ, OH, PA, TX, 2007–2012)	Average ^a proportion of national live births
	%	%	%	%	%	%	%	%
<i>Maternal race and ethnicity</i>								
Non-Hispanic White	27.0	29.4	47.5	42.2	70.5	67.4	37.1	51.7
Non-Hispanic Black	5.0	5.3	23.1	21.5	8.9	12.4	24.0	14.5
Hispanic	52.0	46.7	28.9	31.7	9.0	8.3	32.2	24.1
Non-Hispanic Asian	12.0	15.3	0.0	3.1	7.0	7.8	4.2	6.3
Non-Hispanic AI/AN	0.0	0.3	0.0	0.1	0.9	1.3	0.1	0.7
Non-Hispanic HOPI	0.0	0.4	0.0	0.1	0.2	0.1	0.0	0.3
Multiracial	0.0	2.5	0.0	1.3	0.5	2.7	2.4	2.3
Other non-Hispanic	2.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Unknown	1.0	0.0	0.5	0.0	3.2	0.0	0.0	0.0
<i>Maternal age group</i>								
≤24 years	NA ^b	17.8	36.1	21.8	9.1	15.4	34.8 ^c	22.7
25–29 years	NA ^b	25.4	26.7	28.1	22.2	28.7	27.8 ^c	28.3
30–34 years	NA ^b	31.6	22.0	29.7	42.5	35.2	23.8 ^c	29.7
≥35 years	NA ^b	25.2	15.2	20.3	26.2	20.6	13.6 ^c	19.3

AI/AN, American Indian and Alaska Native; HOPI, Hawaiian and Other Pacific Islander; NA, not applicable; NR, not reported

Note: percentages may not add to exactly 100.0 due to rounding.

^a Average from 2018–2022, as observed in CDC Wonder¹⁴

^b Study did not report maternal age groups.

^c Study reported the following age groups: 13–19, 20–29, 30–39, and ≥40 years. Study population composition according to the age groups used in the current study obtained from study authors and were not published.