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Temporal Variations in Seroprevalence of Severe Acute Respiratory Syndrome Coronavirus 2 Infections by Race and Ethnicity in Arkansas

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Background. The aim of this study was to estimate severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection rates in the small rural state of Arkansas, using SARS-CoV-2 antibody prevalence as an indicator of infection.

Methods. We collected residual serum samples from adult outpatients seen at hospitals or clinics in Arkansas for non–coronavirus disease 2019 (COVID-19)–related reasons. A total of 5804 samples were identified over 3 time periods: 15 August–5 September 2020 (time period 1), 12 September–24 October 2020 (time period 2), and 7 November–19 December 2020 (time period 3).

Results. The age-, sex-, race-, and ethnicity-standardized SARS-CoV-2 seroprevalence during each period, from 2.6% in time period 1 to 4.1% in time period 2 and 7.4% in time period 3. No statistically significant difference in seroprevalence was found based on age, sex, or residence (urban vs rural). However, we found higher seroprevalence rates in each time period for Hispanics (17.6%, 20.6%, and 23.4%, respectively) and non-Hispanic Blacks (4.8%, 5.4%, and 8.9%, respectively) relative to non-Hispanic Whites (1.1%, 2.6%, and 5.5%, respectively).

Conclusions. Our data imply that the number of Arkansas residents infected with SARS-CoV-2 rose steadily from 2.6% in August to 7.4% in December 2020. There was no statistical difference in seroprevalence between rural and urban locales. Hispanics and Blacks had higher rates of SARS-CoV-2 antibodies than Whites, indicating that SARS-CoV-2 spread disproportionately in racial and ethnic minorities during the first year of the COVID-19 pandemic.

Keywords. antibodies; COVID-19; health disparities; SARS-CoV-2; seroprevalence; temporal variation.

Since emerging in 2019, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has spread around the world, causing high morbidity and mortality [1–4]. SARS-CoV-2 infections in the United States (US) were initially concentrated in cities but subsequently spread to rural areas [5–7]. Determining how much of the population has been infected with SARS-CoV-2 is critical for national, state, and local officials as they consider measures to contain the virus and manage the pandemic. Limited testing in the initial stages of the pandemic, coupled with the potential for asymptomatic spread, made it difficult to determine the true prevalence of SARS-CoV-2 infections in the population. Some reports estimate that 40%–45% of cases of SARS-CoV-2 were asymptomatic [8–11]. A more effective way to quantify infection rates and include a more representative group is population-based seroprevalence surveys [5, 12, 13]. Antibodies generated in response to SARS-CoV-2 infections, even asymptomatic ones, can remain in the blood for months to years [14–16]. Consequently, determining the number of people with SARS-CoV-2–specific antibodies can serve as a surrogate for determining SARS-CoV-2 infection rates.

Arkansas is a rural state with an ethnically and racially diverse population of approximately 3.2 million. The following manuscript reports our work to prospectively compare SARS-CoV-2

seroprevalence in a convenience sample of remnant sera from subjects in urban and rural settings and across age, racial, and ethnic groups in the early stages of the pandemic from August through December 2020.

MATERIALS AND METHODS

Human Specimens

Remnant serum samples collected for routine, non–coronavirus disease 2019 (COVID-19)–related outpatient clinical laboratory tests were obtained from the University of Arkansas for Medical Sciences (UAMS) in Little Rock, Arkansas; family medicine clinics in Springdale, Fort Smith, and Pine Bluff, Arkansas; and the Arkansas Department of Health (ADH) with locations across the state. These locations were selected to provide broad geographic coverage across the state. Many of the ADH samples were obtained for evaluation of sexually transmitted infections, while the hospital/regional clinic samples had a multitude of reasons for collection. Every serum sample obtained from an ADH site and sent to the central laboratory in Little Rock was procured for this study during the appropriate time period listed below. Samples were collected across 3 time periods: 15 August–5 September 2020 (time period 1), 12 September–24 October 2020 (time period 2), and 7 November–19 December 2020 (time period 3). Time period 1 was used as a proof of concept and was shorter in duration than time periods 2 or 3. These time periods were chosen to provide ample time to obtain sample numbers and give a broad sampling across the state.

Patient Consent Statement

The study was reviewed and approved by the UAMS Institutional Review Board (IRB numbers 261232 and 260916) as an exempt study with waivers for consent and the Health Insurance Portability and Accountability Act of 1996 (HIPAA).

Patient Inclusion and Exclusion Criteria

Inclusion criteria for serum collection were age ≥18 years, Arkansas residency, and a specimen collected at one of the study sites. Samples were excluded with the following diagnosis codes: immunodeficiency (primary immunodeficiency [D80–D89], transplant recipient [all codes beginning with Z94], and cancer [C00–D49]). Samples from patients receiving chemotherapy (prior 2 months), steroids (prior 30 days), and/or intravenous immunoglobulin (prior 6 months) were also excluded. These criteria were meant to exclude potential false-positive serological testing or testing those patients with immunosuppression.

Data Collection and Storage

At UAMS, electronic health record data contained within the Arkansas Central Data Repository were examined by an honest broker according to the study inclusion criteria to identify study samples. A similar procedure was followed for ADH samples. Remnant samples were defined as clinical samples requiring no additional testing 5–7 days after a clinical visit. Remnant samples have been widely used for studies in special populations [17–19], such as premature infants where extensive blood sampling is a safety concern, or in resource-constrained environments. All samples were stored at 4°C until shipment to the research laboratory. All clinical and demographic variables were stored in a protected REDCap database [20, 21] and included patient age, sex, race, ethnicity, ZIP code, and county of residence. Urban vs rural determination was made by cross-referencing patient zip codes with the Federal Office of Rural Health Policy's data files identifying nonmetropolitan counties and rural census tracts [22].

Laboratory Methods

SARS-CoV-2 antibody positivity was determined using a 2-step process, consistent with the US Centers for Disease Control and Prevention (CDC) guidelines [23]. Serum was inactivated at 56°C for 1 hour prior to testing. All sera were tested for SARS-CoV-2 receptor-binding domain immunoglobulin G (IgG) antibodies using the Beckman Coulter Access SARS-CoV-2 IgG (Brea, California) in the Clinical Laboratory at UAMS. The Access SARS-CoV-2 IgG assay in the UAMS Clinical Laboratory had a positive percent agreement of 74%, 94%, and 100% with reference samples collected 0–7, 8–14, and ≥15 days, respectively, after a positive SARS-CoV-2 reverse-transcription polymerase chain reaction (PCR) test. The negative percent agreement was 100% for samples collected prior to the SARS-CoV-2 pandemic.

Confirmation of specimens that scored as reactive by the Access SARS-CoV-2 IgG assay was performed using a 4-antigen confirmation test enzyme-linked immunosorbent assay (ELISA) as described previously [24]. An additional 5% of negative sera were randomly selected and tested in parallel. Approximately 44 samples in duplicate were tested on each run to diminish intrarun variability. To decrease interrun variability, negative pre–COVID-19 samples and samples with known positive SARS-CoV-2 antibodies were included in each ELISA.

Statistical Analyses

The prevalence of SARS-CoV-2 antibodies in the sample was reported with 95% confidence intervals (CIs) obtained using exact binomial distributions. Age-, sex-, and race/ethnicity-standardized prevalence rates were calculated using 2019 US Census Bureau Arkansas state adult population estimates [25]. Separate univariable and multivariable logistic regressions were employed to determine associations between variables and SARS-CoV-2 antibody positivity for each time period.

The significance of a monotone trend of the positivity to SARS-CoV-2 was tested by the Cochran-Armitage method. A multivariable logistic regression using the backward selection algorithm was employed to test the trend effect of race/ethnicity by the time period, starting with main effects and 2-way

interaction terms, and in each step retaining only the factors showing significant associations ($P < .2$). The final model included sex, race/ethnicity, sample collection site, time period, and the 2-way interaction terms: time period with race/ethnicity and time period with the site.

Because the outcome rate was <10%, a bias-reducing penalized likelihood optimization was applied for all of the logistic regression fittings [26]. Goodness-of-fit was examined by the deviance test results, which did not indicate model-fitting concerns. Statistical significance was set at .05. All analyses were conducted using SAS (version 9.4) and graphics were created using R (version 4.0.2) and ArcGIS Pro (version 2.7.3).

RESULTS

Cohort Characteristics

Table 1 provides the demographic characteristics for each time period. We collected 1301 serum samples in time period 1, 2098 in time period 2, and 2405 in time period 3, for a total of 5804 samples. In terms of age distribution, the age groups 40–49 years and ≥70 years had the smallest number of samples (834 [14.4%] and 839 [14.5%], respectively), and the age group 18–29 years comprised the highest number of samples (1225 [21.1%]). The age distribution was generally consistent across each collection period, with a mean age of 47.8 years for time period 1, 48.6 years for time period 2, and 47.2 for time period 3. More

Table 1. Demographics of Sampled Populations in Arkansas Over 3 Collection Periods, August–December 2020

Characteristic[a]	Time Period 1 (n = 1301)	Time Period 2 (n = 2098)	Time Period 3 (n = 2405)	Total (N = 5804)	Arkansas (n = 2 282 191)
Age group					
18-29 y	257 (19.8)	406 (19.4)	562 (23.4)	1225 (21.1)	471 866 (20.7)
30-39 y	244 (18.8)	394 (18.8)	428 (17.8)	1066 (18.4)	377 230 (16.5)
40-49 y	205 (15.8)	294 (14.0)	335 (13.9)	834 (14.4)	355 760 (15.6)
50-59 y	211 (16.2)	335 (16.0)	358 (14.9)	904 (15.6)	373 048 (16.3)
60-69 y	209 (16.1)	349 (16.6)	377 (15.7)	935 (16.1)	349 101 (15.3)
≥70 y	175 (13.5)	319 (15.2)	345 (14.4)	839 (14.5)	355 186 (15.6)
Missing	0	1	0	1	…
Sex					
Female	898 (69.3)	1430 (68.2)	1661 (69.1)	3989 (68.8)	1 176 416 (51.5)
Male	398 (30.7)	668 (31.8)	742 (30.9)	1808 (31.2)	1 105 775 (48.5)
Missing	5	0	2	7	…
Race/ethnicity					
White	565 (45.7)	937 (47.6)	1120 (47.0)	2622 (46.9)	1 733 824 (76.0)
Black	558 (45.2)	831 (42.2)	1026 (43.1)	2415 (43.2)	341 540 (15.0)
Hispanic	74 (6.0)	126 (6.4)	137 (5.8)	337 (6.0)	144 447 (6.3)
Other	39 (3.2)	75 (3.8)	99 (4.2)	213 (3.8)	62 380 (2.7)
Missing	65	129	23	217	…
Area					
Urban	1126 (86.8)	1838 (87.6)	1990 (82.8)	4954 (85.4)	1 816 489 (60.4)[b]
Rural	171 (13.2)	260 (12.4)	413 (17.2)	844 (14.6)	1 189 468 (39.6)[b]
Missing	4	0	2	6	…
Collection site					
UAMS	981 (75.4)	1338 (63.8)	1485 (61.8)	3804 (65.5)	…
Pine Bluff	266 (20.5)	403 (19.2)	319 (13.3)	988 (17.0)	…
Fort Smith	…	206 (9.8)	131 (5.5)	337 (5.8)	…
Springdale	54 (4.2)	151 (7.2)	220 (9.2)	425 (7.3)	…
ADH	…	…	250 (10.4)	250 (4.3)	…
SARS-CoV-2 test performed					
Yes	139 (11.4)	271 (12.9)	437 (20.3)	847 (15.5)	…
No	1078 (88.6)	1827 (87.1)	1717 (79.7)	4622 (84.5)	…
Missing	84	0	251	335	…
SARS-CoV-2 test result					
Positive	12 (9.1)	17 (6.3)	8 (8.3)	37 (7.4)	…
Negative	120 (90.9)	253 (93.7)	89 (91.8)	462 (92.6)	…
Missing	1169	1828	2308	5305	…

Data are presented as No. (%) unless otherwise indicated.

Abbreviations: ADH, Arkansas Department of Health; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2; UAMS, University of Arkansas for Medical Sciences.

[a]Missing data are not included in the analysis for a variable.

[b]The Arkansas rural/urban population is total population (N = 3 005 957) rather than adults only.

specimens were collected from females (n = 3989 [68.8%]) than from males (n = 1808 [31.2%]). The racial and ethnic distribution of the study population was 46.9% non-Hispanic White (n = 2622), 43.2% non-Hispanic Black (n = 2415), and 6.0% Hispanic (n = 337). A total of 213 specimens (3.8%) were collected from patients who did not identify as White, Black, or Hispanic. Most specimens were collected from patients living in urban areas (n = 4954 [85.4%]) compared to rural areas (n = 844 [14.6%]). Samples were obtained from 74 of 75 counties in the state (Supplementary Figure 1).

Extrapolated Seroprevalence Estimates
The observed seroprevalence rates were 3.8%, 4.9%, and 8.1% for time periods 1, 2, and 3, respectively (Supplementary Table 1). After standardizing by age, sex, and race/ethnicity for the Arkansas general population, the seroprevalence rate for time period 1 was 2.6% (95% CI, 1.7%–3.5%), 4.1% (95% CI, 3.1%–5.1%) for time period 2, and 7.4% (95% CI, 6.0%–8.7%) for time period 3 (Figure 1A).

Demographic Differences in Seroprevalence
The percentage of Hispanic patients with SARS-CoV-2 antibodies was substantially higher in all 3 time periods compared to White patients (time period 1, 17.6% vs 1.1%; time period 2, 20.6% vs 2.6%; time period 3, 23.4% vs 5.5%) (Supplementary Table 1, Figure 1B). A similar trend was observed for Black patients compared to White patients (time period 1, 4.8% vs 1.1%; time period 2, 5.4% vs 2.6%; time period 3, 8.9% vs 5.5%). Consistent with the increased percentages of SARS-CoV-2 seropositivity in Hispanic and Black patients, the adjusted odds ratios (ORs) comparing the racial and ethnic groups also were statistically significant (Table 2).

Over the course of the study, we observed a consistent increase in seroprevalence, including seroprevalence by racial/ethnic group. During all time periods, Blacks and Hispanics were more likely to be seropositive when adjusted for other variables (Table 3). However, a logistic regression fitting model showed that the increasing slope of seroprevalence by time period for Hispanics was significantly lower compared to the slope for Whites (OR, 0.49 [95% CI, .3–.78]) (Supplementary Table 2). Thus, although the positivity to SARS-CoV-2 was higher in Hispanics compared to Whites, the additive infection rate to Hispanics was smaller than to Whites over the time course of the study. The same finding was observed for Blacks, but there was not a statistical difference for Blacks compared to Whites (OR, 0.75 [95% CI, .5–1.12]) (Supplementary Table 2).

We observed a statistically significant association with positive antibody tests for 2 age groups in 2 separate time periods (Supplementary Table 1). In time period 1, individuals aged 18–29 years were more likely to have antibodies than those aged >70 years (OR, 3.59 [95% CI, 1.12–11.52]). Individuals aged 30–39 years were more likely to have antibodies than those aged ≥70 years age group in time period 2 (crude OR, 2.17 [95% CI, 1.08–4.36]) and time period 3 (crude OR, 1.85 [95% CI, 1.00–3.06]). However, no difference in the likelihood of testing positive for SARS-CoV-2 antibodies was observed for any age group when the data was adjusted by age, sex, and area (Table 2). Together, these data indicate that age did not affect the likelihood of testing positive for SARS-CoV-2 antibodies in our study. Similarly, there was no statistically significant association between sex or area of residence (rural vs urban) and having SARS-CoV-2 antibodies during any time period.
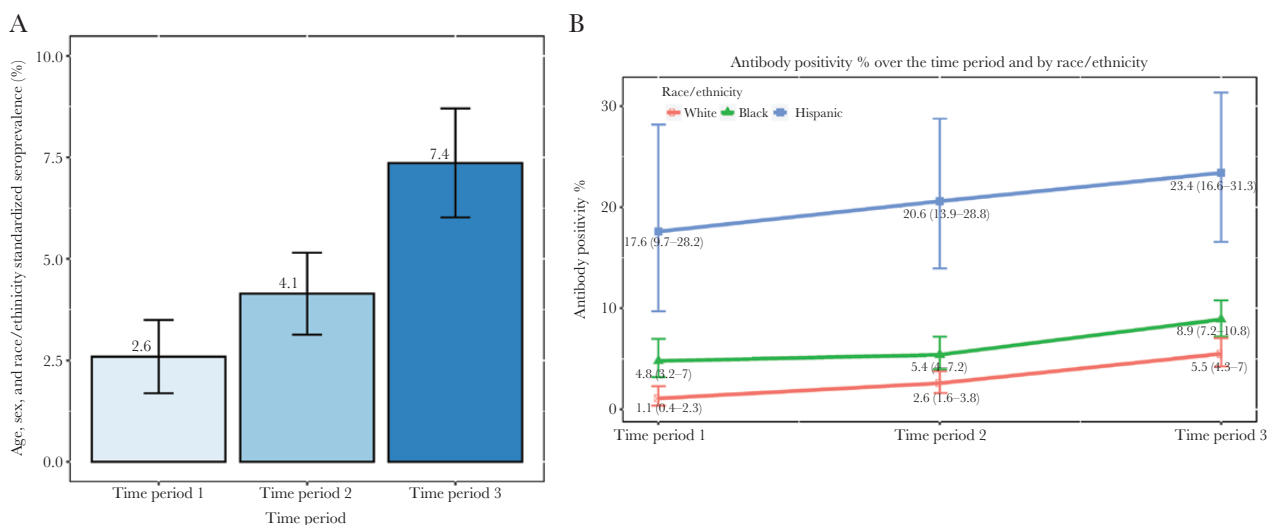

Figure 1. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) seropositivity rate. *A*, Age-, sex-, race-, and ethnicity-adjusted seroprevalence rates are shown for each time period. *B*, The percentage of samples with positive SARS-CoV-2 antibody tests is shown for each race/ethnicity group for each time period. Error bars indicate the 95% confidence interval.

Table 2. Adjusted Association With Severe Acute Respiratory Syndrome Coronavirus 2 Antibody Positivity by Time Period

Effect	Time Period 1 (n = 1301) OR (95% CI)	P Value[a]	Time Period 2 (n = 2098) OR (95% CI)	P Value[a]	Time Period 3 (n = 2405) OR (95% CI)	P Value[a]
Age, y		.4392		.6390		.8960
18–29 vs ≥70	2.04 (.62–6.65)		1.09 (.51–2.3)		1.14 (.64–2.04)	
30–39 vs ≥70	1.84 (.55–6.14)		1.66 (.8–3.42)		1.29 (.71–2.31)	
40–49 vs ≥70	1.08 (.28–4.16)		1.13 (.51–2.54)		0.95 (.51–1.79)	
50–59 vs ≥70	1.4 (.38–5.14)		1.17 (.53–2.58)		1.19 (.65–2.17)	
60–69 vs ≥70	0.71 (.16–3.09)		1.01 (.45–2.26)		1.21 (.67–2.21)	
Sex		.3658		.9875		.1131
Female vs male	1.39 (.68–2.83)		1 (.63–1.57)		0.77 (.56–1.06)	
Race/ethnicity		<.0001		<.0001		<.0001
Black vs White	**3.9 (1.66–9.19)**		**1.93 (1.14–3.26)**		**2.03 (1.41–2.92)**	
Hispanic vs White	**15.06 (5.59–40.6)**		**9.83 (5.32–18.14)**		**4.42 (2.71–7.23)**	
Others vs White	0.91 (.05–15.63)		2.55 (.98–6.65)		1.43 (.64–3.17)	
Area		.5473		.8258		.1481
Urban vs rural	0.75 (.3–1.9)		0.93 (.47–1.81)		0.73 (.47–1.12)	
Collection site		.5701		.4906		<.0001
Pine Bluff vs UAMS	1.49 (.71–3.14)		1.49 (.87–2.54)		0.8 (.47–1.37)	
Fort Smith vs UAMS	…		0.85 (.41–1.79)		**3.37 (1.99–5.71)**	
Springdale vs UAMS	0.89 (.21–3.78)		1.01 (.42–2.43)		**1.73 (1.01–2.97)**	
ADH vs UAMS	…		…		**1.75 (1.07–2.85)**	

Bold text indicates a statistically significant difference in antibody positivity between the indicated groups. Abbreviations: ADH, Arkansas Department of Health; CI, confidence interval; OR, odds ratio; UAMS, University of Arkansas for Medical Sciences.

[a]P value indicates whether the positivity differs between the category of a respective variable.

Temporal Variations in SARS-CoV-2 Seroprevalence

Examination of weekly changes in seroprevalence showed a gradual increase throughout the study. The peak of seroprevalence occurred in time period 3 where rates increased from 5.3% to 13.7% (Figure 2). Rates across race and ethnicity also increased accordingly with time. Seroprevalence of SARS-CoV-2 antibodies in Blacks and Hispanics were consistently higher throughout the course of the study as compared to Whites. The trend test showed that the seroprevalence significantly increased from time period 1 to time period 3 among Whites (P for trend < .0001) and Blacks (P for trend = .0009) (Table 3). Hispanics had a higher seroprevalence across 3 time periods (P for trend = .3409). In the trend of adjusted effect for race/ethnicity, the likelihood of antibody positivity for Hispanics decreased compared with non-Hispanic Whites in the later time period (OR, 0.49 [95% CI, .3–.78]) (Supplementary Table 2).

DISCUSSION

Our study using remnant samples found that the SARS-CoV-2 seroprevalence rate in Arkansas increased from 2.6% to 7.4% from August to December 2020. During the last week of the study, the raw seroprevalence rate approached 14%. The seroprevalence we observed is consistent with both reported infections and data from American Red Cross blood donations in southern US states [27] and the CDC Multi-State Assessment of SARS-CoV-2 Seroprevalence (MASS-C) [5]. The American Red Cross blood study found only 2.9% seroprevalence from August to September in southern states, while the MASS-C data revealed 9.2% seroprevalence in December in Arkansas. It should be noted that these earlier studies had no [28] or low [5] representation from Arkansas.

For comparison, ADH reported a total of 213 267 confirmed or suspected SARS-CoV-2 infections as of 25 December

Table 3. Temporal Trends of Severe Acute Respiratory Syndrome Coronavirus 2 Antibody Seroprevalence in Relationship to Race/Ethnicity

Characteristic	Time Period 1 Positivity	Time Period 2 Positivity	Time Period 3 Positivity	Time Period 2 vs 1 Difference	Time Period 3 vs 2 Difference	Trend Test P Value
Overall	3.77 (2.8–4.95)	4.91 (4.02–5.92)	8.07 (7.01–9.23)	1.14 (–.24 to 2.53)	3.16 (1.73–4.59)	<.0001
Race/ethnicity						
White	1.06 (.39–2.3)	2.56 (1.65–3.79)	5.54 (4.27–7.04)	1.5 (.18–2.82)	2.97 (1.3–4.65)	<.0001
Black	4.84 (3.21–6.96)	5.42 (3.98–7.18)	8.87 (7.2–10.78)	0.58 (–1.78 to 2.93)	3.45 (1.13–5.78)	.0009
Hispanic	17.57 (9.7–28.17)	20.63 (13.94–28.75)	23.36 (16.56–31.34)	3.07 (–8.12 to 14.04)	2.72 (–7.28 to 12.73)	.3409

Data are presented as percentage (95% confidence interval) unless otherwise indicated.
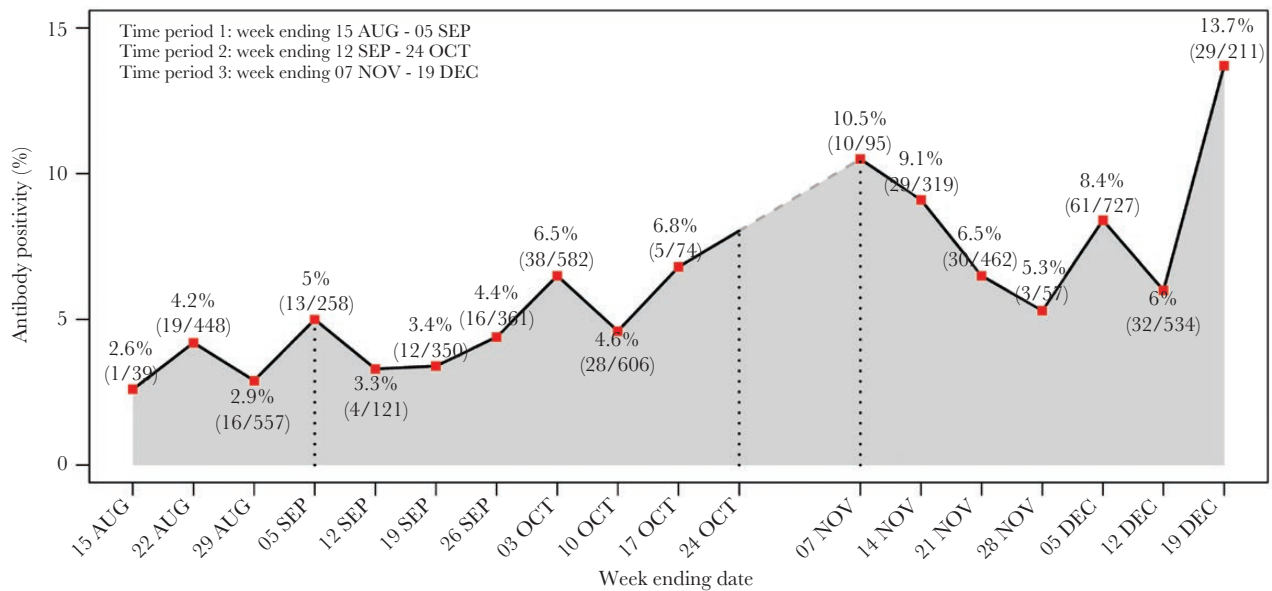
Figure 2. Seroprevalence in Arkansas by week. There was a gradual increase in seroprevalence of severe acute respiratory syndrome coronavirus 2 antibodies over the course of the study with a peak in December 2020. Error bars indicate the 95% confidence interval.

2020—roughly equivalent to 7% of the Arkansas population. Based on these numbers, our sampling potentially detected asymptomatic and untested people who were previously infected with SARS-CoV-2 in the state. Taken together, the data support the conclusion that more Arkansans had been infected with SARS-CoV-2 than previously recognized. The low seroprevalence rate in combination with slow vaccine uptake despite rapid distribution of vaccinations across the state left many people vulnerable to SARS-CoV-2 infection with variants of concern. In fact, in the spring of 2021, Arkansas experienced an uptick in cases due to the Delta variant, causing the state to rank as one of the worst for number of cases per 100 000 people during that time [29, 30].

We found higher seroprevalence of SARS-CoV-2 antibodies in Hispanics and Blacks compared to Whites throughout the study. Our data align with an earlier report that examined samples obtained from the American Red Cross for PCR testing across the US (4.11% African American, 4.35% Hispanic, and 1.65% White) [27]. In fact, CDC data from our state also noted higher rates of PCR-positive tests in Hispanics and Blacks early during our study. According to CDC data of PCR testing from the August 2020 to December 2020 time period, Hispanics had 600 incident cases per 100 000 that dropped to 388 incident cases per 100 000, while Blacks had 238 incident cases per 100 000 that increased to 385 incident cases per 100 000. In comparison, Whites had 69 incident cases per 100 000, which increased to 308 incident cases per 100 000. These numbers are consistent with our seroprevalence findings within these groups. While any attempt to explain the observed racial/ethnic disparities would be speculative, the data are consistent with a

broader theme highlighting the need to understand biologic, social, and demographic factors that impact health in underrepresented minority populations.

The temporal trend of the data showed that the increase rate of infection in Whites was more than that of Hispanics or Blacks during the same time period. Hispanics and Blacks in our state were noted to have higher rates of PCR-positive tests early in the course of the time periods. Ultimately, the rates of Hispanics and Blacks who had positive PCR tests leveled over the course of our study, as shown in the previous paragraph, which explains the lower ORs and change in effect size associated with these groups.

Contrary to our expectations, SARS-CoV-2 spread uniformly across urban and rural areas of Arkansas. This finding differs from reports from the northeastern and northwestern US, and in southern cities such as Houston and New Orleans [31, 32]. However, it is worth noting that Arkansas was home to a rural super-spreader event in March 2020 [33]. These data suggest that those in rural areas of the state are just as likely to have been infected with SARS-CoV-2 as those in urban population centers.

The benefits and limitations of convenience sampling techniques have been discussed elsewhere [13]. The limitations include but are not limited to (1) the variable entry of cases from participating sites; (2) the nonrandom nature of sampling; and (3) the association of sampling with preexisting health-seeking behavior. More specific to this study, we were limited by the higher proportion of urban individuals compared to rural individuals and the higher proportion of females and Blacks compared to the Arkansas population

([Table 1](#)). It is also possible that our sampling method could favor subjects who were more ill (eg, individuals who were hospitalized) or more willing to leave their homes (eg, individuals who were evaluated in clinics). Therefore, these data do not portend representativeness of the state; rather, the data only provide the seroprevalence within this specific population. Another limitation of this study was disparate participation from some sites across the 3 time periods of the study. For example, some sites did not provide samples until time period 3. To address this limitation, logistic regressions were fitted for each time period separately and the site factor was included as an adjusted effect ([Table 2](#)). While these 2 sites (Fort Smith and ADH; [Table 3](#)) had higher odds of infection (OR, 3.37 and 1.75, respectively; [Table 2](#)), the number of samples contributed from these sites was much less than the other 3 sites, minimizing this bias.

CONCLUSIONS

Seroprevalence studies play a critical role in defining the scope of the SARS-CoV-2 pandemic. In a state with a large rural populace, our serologic analysis of remnant samples demonstrates that SARS-CoV-2 infection was more widespread than reflected by acute testing. Additionally, Hispanics and Blacks had disproportionately higher rates of SARS-CoV-2 infections. This study highlights the need to understand factors that impact health in underrepresented minority populations and the contributory role of seroprevalence in understanding the SARS-CoV-2 pandemic.

Supplementary Data

Supplementary materials are available at *Open Forum Infectious Diseases* online. Consisting of data provided by the authors to benefit the reader, the posted materials are not copyedited and are the sole responsibility of the authors, so questions or comments should be addressed to the corresponding author.

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