Original Research

Neighborhood Characteristics and Racial Disparities in Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Seropositivity in Pregnancy

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OBJECTIVE: To quantify the extent to which neighborhood characteristics contribute to racial and ethnic disparities in severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) seropositivity in pregnancy.

METHODS: This cohort study included pregnant patients who presented for childbirth at two hospitals in Philadelphia, Pennsylvania from April 13 to December 31, 2020. Seropositivity for SARS-CoV-2 was determined by measuring immunoglobulin G and immunoglobulin M antibodies by enzyme-linked immunosorbent assay in discarded maternal serum samples obtained for clinical purposes. Race and ethnicity were self-reported and abstracted from medical records. Patients' residential addresses were geocoded to obtain three Census tract variables: community deprivation, racial segregation (Index of Concentration at the Extremes), and crowding. Multivariable mixed effects logistic regression models and causal mediation analyses were used to quantify the extent to which neighborhood variables may explain racial and ethnic disparities in seropositivity.

RESULTS: Among 5,991 pregnant patients, 562 (9.4%) were seropositive for SARS-CoV-2. Higher seropositivity rates were observed among Hispanic (19.3%, 104/538) and Black (14.0%, 373/2,658) patients, compared with Asian (3.2%, 13/406) patients, White (2.7%, 57/2,133) patients, and patients of another race or ethnicity (5.9%, 15/256) ($P<.001$). In adjusted models, per SD increase, deprivation (adjusted odds ratio [aOR] 1.16, 95% CI 1.02–1.32) and crowding (aOR 1.15, 95% CI 1.05–1.26) were associated with seropositivity, but segregation was not (aOR 0.90, 95% CI 0.78–1.04). Mediation analyses revealed that crowded housing may explain 6.7% (95% CI 2.0–14.7%) of the Hispanic–White disparity and that neighborhood deprivation may explain 10.2% (95% CI 0.5–21.1%) of the Black–White disparity.

CONCLUSION: Neighborhood deprivation and crowding were associated with SARS-CoV-2 seropositivity in

pregnancy in the prevaccination era and may partially explain high rates of SARS-CoV-2 seropositivity among Black and Hispanic patients. Investing in structural neighborhood improvements may reduce inequities in viral transmission.

The coronavirus disease 2019 (COVID-19) pandemic has disproportionately affected Hispanic and Black communities across the United States. Hispanic and Black people are 2.8 times more likely to be hospitalized and twice as likely to die from COVID-19 compared with White people.[1] These disparities have also been reported among pregnant patients, with Hispanic and Black patients more likely to have a positive test result for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection during pregnancy.[2] However, whether a patient is tested for SARS-CoV-2 clinically depends on illness presentation, patient and clinician choice, testing protocols, access, and availability. In contrast, population surveillance with antibody testing, before the availability of vaccines, enables determination of exposure and immune response to SARS-CoV-2 infection independent of health care decisions and access.

A prior study of seroprevalence in pregnancy early in the pandemic (April 4–June 3, 2020) demonstrated 5-fold higher rates of seropositivity for SARS-CoV-2 for pregnant Black (9.7%) and Hispanic (10.4%) patients, compared with pregnant White (2.0%) patients in a hospital-based cohort in Philadelphia, Pennsylvania.[3] Factors that contribute to racial and ethnic disparities in seropositivity remain incompletely understood.

Many aspects of life in the United States are racially and ethnically segregated, including residential neighborhoods[4] and workplaces.[5] Living and working conditions affect the feasibility of reducing exposure to SARS-CoV-2 through practices such as social distancing.[6] Neighborhoods affect health,[7] and outbreaks of infectious diseases can occur from differences in sanitation, ventilation, employment, and social activities.[8–12] Emerging data suggest that risk of COVID-19 may vary by neighborhood in the general population.[11,13–19] Our hypotheses were that, in the prevaccination era, neighborhood characteristics would be associated with the odds of seropositivity and might partially explain racial and ethnic disparities in seropositivity. Specifically, we assessed associations of three neighborhood characteristics (area-level community deprivation, racial segregation, and crowding) with SARS-CoV-2 seroprevalence in a pregnant population. Secondarily, we quantified the extent to which these neighborhood characteristics might explain racial and ethnic disparities in seropositivity using causal mediation analysis.[20]

METHODS

Patients who gave birth from April 13, 2020, to December 31, 2020, in two hospitals in Philadelphia, Pennsylvania, that combined account for approximately 9,000 births annually, were eligible for this study. Demographic and clinical data were obtained from the electronic health record. Limited English proficiency was assigned using the medical record indicator for the need for interpreter.[21] Race and ethnicity were also abstracted from the medical record, which is patient-identified at the time of registration for outpatient visits and inpatient hospitalizations. Patients can separately indicate race and Hispanic ethnicity, and select more than one race designation including Black, White, and Asian. We constructed mutually exclusive racial and ethnic categories including non-Hispanic Black, non-Hispanic White, non-Hispanic Asian, and Hispanic. Because there were small numbers, we combined another, multiple, and unknown racial and ethnic categories into a single group for descriptive purposes and then further added non-Hispanic Asian patients to this group when modeling disparities. For brevity, we refer to non-Hispanic Black, non-Hispanic White, and non-Hispanic Asian patients as Black, White, and Asian, respectively. Patient residential addresses at the time of the labor and delivery admission were geocoded using ArcMAP 10.8 and the ArcGIS Street Map Premium North America 2021.1 address locator, with a minimum match score of 75; 26 patients were excluded because their addresses were not matched. The resulting coordinates were mapped to the U.S. Census Bureau's 2019 cartographic boundary shapefile to assign each address a Census tract. The Institutional Review Board at the University of Pennsylvania approved this study with a waiver of consent, because there was no more than a minimal risk to participants and the protocol called for discarded samples and existing data (Protocol No. 834240). A flow chart that shows the development of the cohort is presented in Figure 1.

We chose deprivation, segregation, and crowding as potential mediators of disparities in seropositivity based on reported differences in SARS-CoV-2 infection in other U.S. nonpregnant cohorts.[16,17,19,22,23] Census tract area-level community deprivation was assigned using an index[24] that uses American Community Survey[25] 2018 indicators for the proportion of residents with income below the federal poverty line, without a high school degree, receiving federal cash
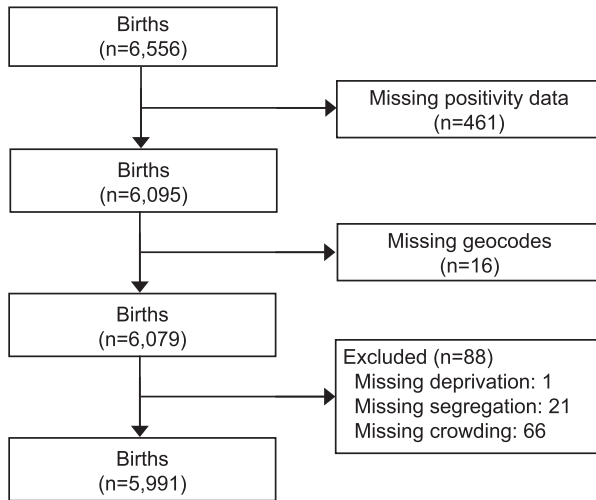
Fig. 1. Cohort development.

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assistance and lacking medical insurance, as well as median household income and proportion of vacant housing.[26] The deprivation index ranges from 0 to 1 (nationwide mean 0.35, SD 0.16), with higher values indicating more deprivation. For racial residential segregation, we used the Index of Concentration at the Extremes for Black–White segregation, which is calculated as Index of Concentration at the Extremes= (White(n)−Black(n)/(Total population(n)). The Index of Concentration at the Extremes ranges from −1 to 1, where −1 would indicate an entirely Black Census tract and 1 would indicate an entirely White Census tract. *Area-level crowded housing* was defined using American Community Survey data as the proportion of occupied housing units with more than one person per room.

Pregnant patients have blood drawn for rapid plasma reagin at the time of admission for childbirth for routine syphilis screening. Residual maternal serum from this testing was collected for study purposes at the time it would otherwise be discarded by the hospital laboratories. Sera were fully de-identified before antibody measurements; 93% had available samples for analysis of which 97% were collected during the labor and delivery admission, with 3% of those collected within the month prior. Comparisons of patients with and without sera available for testing are shown in Appendix 1, available online at http://links.lww.com/AOG/C711. Sera were tested using an enzyme-linked immunosorbent assay with plates coated with the receptor binding domain of the SARS-CoV-2 spike protein.[3] Samples with immunoglobulin G or immunoglobulin M

concentrations of more than 0.48 arbitrary units/mL were considered seropositive.[3]

Unadjusted, bivariate analyses comparing baseline characteristics among seropositive and seronegative patients were performed. Multivariable logistic regression models were used to estimate adjusted odds of seropositivity by race and ethnicity. Multivariable, mixed effects logistic regression models were used to calculate adjusted odds ratios (aORs) of seropositivity per SD increment increase of each of the neighborhood indicators in the whole cohort, as well as in race and ethnicity-stratified models. A missing indicator was used for the one variable with missingness (body mass index [BMI, calculated as weight in kilograms divided by height in meters squared], 1% missing). A random effect for Census tract was included to address geographical clustering. To assess the extent to which neighborhood characteristics might explain observed racial and ethnic disparities in seropositivity, we used two strategies. First, we added neighborhood factors into multilevel, multivariable regression models to determine whether the association between race and ethnicity and seropositivity remained after covariate adjustment or appeared to be attenuated. Second, to address the confounding structure of race and ethnicity with the potential neighborhood mediator as well as between the mediator and seropositivity, we used formal causal mediation.[27] Mediation analysis quantifies the indirect effect of race and ethnicity with seropositivity that may exist from the mediator (in this case a neighborhood factor). It also quantifies the direct effect of race and ethnicity on seropositivity, which is the remaining association after the neighborhood factor is included in the analysis. The direct effect includes all of the other potential causes of the disparity. The proportion of racial or ethnic disparity mediated by the neighborhood factor is calculated with an estimate of statistical significance and degree of uncertainty (95% CIs). Mediation models included adjustment for individual-level age, BMI, insurance type, and limited English proficiency.

Given the potential for nonrandom referral patterns leading to births in our two hospital systems, we also performed a sensitivity analysis restricted to participants who reported a home address in Philadelphia County to determine whether the results were similar to those involving the whole cohort. All tests were two-tailed, and $P<.05$ was considered statistically significant. Analyses were performed using R 4.1.1[28]

RESULTS

Of the 5,991 patients in the cohort, 562 (9.4%) were seropositive for SARS-CoV-2 at the end of pregnancy (Table 1). Comparisons of patients with and without

seropositivity data showed that patients without these data were older, less likely to be obese, more likely to be privately insured, more likely to self-identify as White, and more likely to have preterm birth (Appendix 1, http://links.lww.com/AOG/C711). In unadjusted, bivariate analyses, younger age, higher prepregnancy BMI, nulliparity, public insurance, and limited English proficiency were all associated with seropositivity ($P<.001$). Higher rates of seropositivity were present among Hispanic (19.3%, 104/538) and Black (14.0%, 373/2,658) patients, compared with Asian (3.2%, 13/406) patients, White (2.7%, 57/2,133) patients, and patients of another race (5.9%, 15/256) ($P<.001$).

Figure 2A shows a map of seropositivity rates in Census tracts with at least 20 study participants, and Figure 2B–D show maps of each neighborhood factor by Census tract. Associations of patient characteristics and neighborhood factors are shown in Appendix 2, available online at http://links.lww.com/AOG/C711. All three neighborhood factors (deprivation, segregation, and crowding) were associated with seropositivity in unadjusted models (Table 2). After adjustment for age, BMI, insurance, limited English proficiency, and race, associations were attenuated but remained statistically significant for deprivation and crowding. Higher odds of seropositivity were observed with higher levels of deprivation (aOR 1.16, 95% CI 1.02–1.32) and crowding (aOR 1.15, 95% CI 1.05–1.26), but not segregation (aOR 0.90, 95% CI 0.78–1.04), with aOR indicating increase in odds ratio per SD increase in the neighborhood factor. These effect estimates correspond to 40% and 38% increased odds of seropositivity for individuals who reside in the midpoint of the highest quartile, compared with the midpoint of the lowest quartile (2.3 SD units apart) of deprivation and crowding, respectively.

Racial and ethnic disparities persisted after adjustment for potential confounding variables including age, BMI, insurance, and limited English proficiency. Specifically, compared with White patients, Hispanic

Table 1. Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Seroprevalence Among 5,991 Patients at the End of Pregnancy in the Prevaccination Era

Characteristic	Seronegative	Seropositive	P
All	5,429 (90.6)	562 (9.4)	
Age (y)			<.001
Younger than 25	899 (84.8)	161 (15.2)	
25–younger than 35	3,143 (90.9)	316 (9.1)	
35 or older	1,387 (94.2)	85 (5.8)	
Prepregnancy BMI (kg/m²)			<.001
Lower than 25	2,542 (93.4)	180 (6.6)	
25–29.9	1,344 (89.8)	152 (10.2)	
30 or higher	1,486 (87.0)	222 (13.0)	
Missing	57 (87.7)	8 (12.3)	
Parity			<.001
0	2,471 (92.7)	194 (7.3)	
1 or more	2,958 (88.9)	368 (11.1)	
Insurance			<.001
Private	3,235 (95.1)	166 (4.9)	
Public	2,194 (84.7)	396 (15.3)	
Limited English proficiency			<.001
Yes	170 (73.3)	62 (26.7)	
No	5,259 (91.3)	500 (8.7)	
Race and ethnicity			<.001
Hispanic	434 (80.7)	104 (19.3)	
Non-Hispanic Asian	393 (96.8)	13 (3.2)	
Non-Hispanic Black	2,285 (86.0)	373 (14.0)	
Non-Hispanic White	2,076 (97.3)	57 (2.7)	
None of the above, multiple, or unknown	241 (94.1)	15 (5.9)	
Gestational age at delivery (wk)			.09
Preterm (less than 37)	477 (88.5)	62 (11.5)	
Term (37 or more)	4,952 (90.8)	500 (9.2)	

BMI, body mass index.
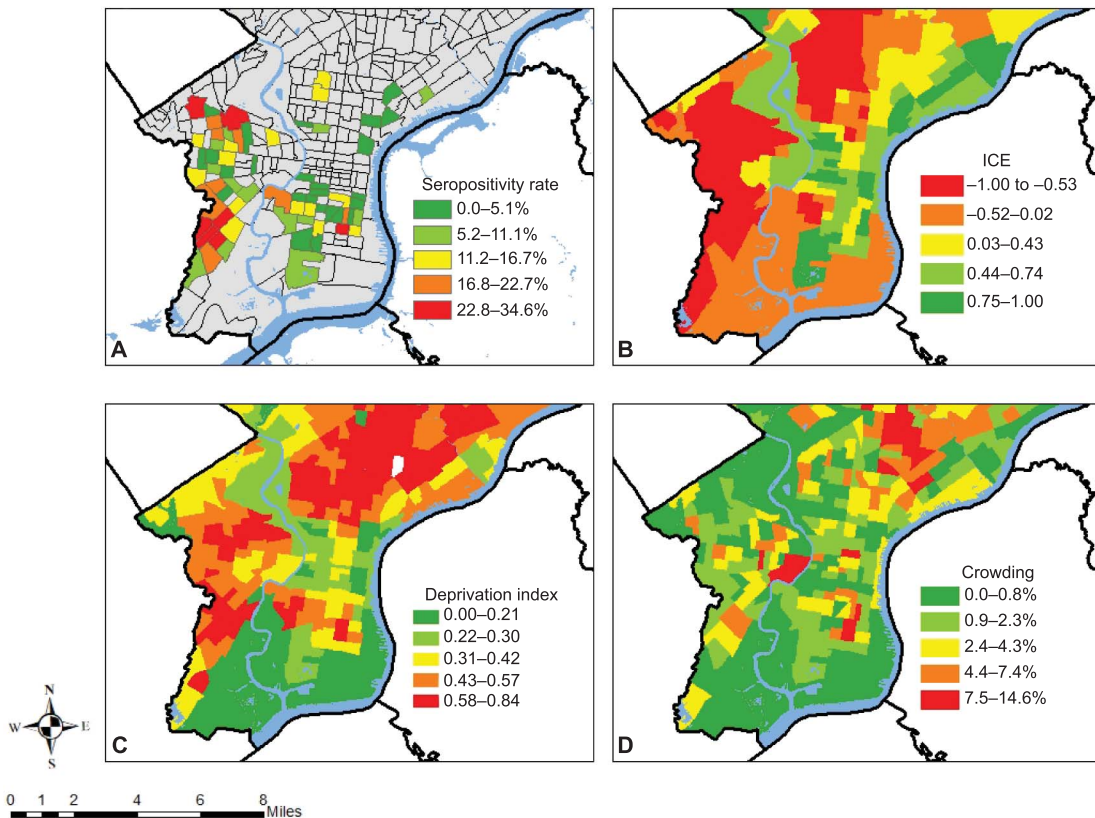Data are n (row %) unless otherwise specified.

Fig. 2. A. Map of seropositivity rates in Census tracts with at least 20 study participants. Study participants lived in other tracts, but rates would be too unstable and individuals too identifiable to depict. **B**. Map of segregation using the Index of Concentration at the Extremes (ICE). Higher values indicate higher proportion of White residents. **C**. Map of neighborhood deprivation index includes six indicators and ranges from 0 to 1, with 1 indicating more deprivation. **D**. Map of *crowding*, defined as the proportion of residences with more humans than rooms in the house. Maps created using ArcGIS software by Esri. ArcGIS and ArcMap are the intellectual property of Esri and are used herein under license. Copyright Esri. All rights reserved. For more information about Esri software, please visit www.esri.com. Census tract boundaries, water features, segregation, and crowding data are from the U.S. Census Bureau (https://www.census.gov). Neighborhood deprivation index data are from Brokamp's Nationwide Community Deprivation Index (https://github.com/geomarker-io/dep_index).

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(aOR 3.36, 95% CI 2.10–5.38) and Black patients (aOR 3.98, 95% CI 2.83–5.60) had significantly higher odds of seropositivity (Table 3). There was not a significant disparity among patients of another race (aOR 1.36, 95% CI 0.80–2.30). Additional adjustment for parity made no change to the models and was collinear with age so was not included in adjusted analyses.

Race and ethnicity were associated with differences in all three neighborhood factors (Appendix 2, http://links.lww.com/AOG/C711). Hispanic and Black patients lived in Census tracts with more deprivation, lower Index of Concentration at the Extremes values (ie, lower proportion of White residents), and higher levels of crowding. In models with race or ethnicity as the independent (predictor) variable and seropositivity as the dependent (outcome) variable, adding

individual age, BMI, insurance type, and limited English proficiency substantially attenuated Hispanic–White and Black–White disparities (Table 3). The addition of neighborhood factors appeared to attenuate disparities subtly. Formal mediation analyses, adjusted for individual-level age, BMI, insurance type, and limited English proficiency, revealed that 6.7% (95% CI 2.0–14.7%) of the disparity in seropositivity between Hispanic and White patients could be explained by differences in Census tract–level residential crowding (*P*=.01) (Fig. 3). There was no significant mediation of the Hispanic–White disparity by deprivation or segregation. With respect to the disparity in seropositivity between Black and White patients, mediation analyses revealed that 10.2% (95% CI 0.5–21.1%) could be explained by differences in deprivation (*P*=.04). A significant mediation was not detected for

Table 2. Census Tract Neighborhood Factors and Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Seroprevalence Among 5,991 Patients at the End of Pregnancy in the Prevaccination Era

Neighborhood Factor at the Census Tract Level	Seronegative (n=5,429)	Seropositive (n=562)	Associations of 1 SD Increase in the Neighborhood Factor With Seropositivity	
			Unadjusted OR (95% CI)	Adjusted OR (95% CI)*
Deprivation[†]	0.40±0.17	0.49±0.13	1.84 (1.63–2.06)	1.16 (1.02–1.32)
Segregation[‡]	0.05±0.70	−0.31±0.60	0.56 (0.49–0.63)	0.90 (0.78–1.04)
Crowding[§]	2.11±2.36	2.98±2.79	1.38 (1.24–1.55)	1.15 (1.05–1.26)

OR, odds ratio.
Data are mean±SD unless otherwise specified.
* Multilevel logistic regression models adjusted for age, body mass index, insurance, limited English proficiency, and race and ethnicity, with a random effect for Census tract. A missing indicator was used for the 65 patients missing body mass index data.
[†] Neighborhood deprivation index includes six indicators and ranges from 0 to 1, with 1 indicating more deprivation.
[‡] The Index of Concentration at the Extremes ranges from −1 to 1, with higher values indicating higher proportion of White residents.
[§] Crowding is defined as the proportion of residences with more humans than rooms in the house.

any other factor for either Hispanic–White or Black–White disparities. In analyses restricted to patients residing in Philadelphia County (n=4,436), results were similar with crowding mediating 6.8% (95% CI 1.7–14.5%) of the Hispanic–White disparity and deprivation mediating 13.8% (95% CI 2.9–27%) of the Black–White disparity in seropositivity.

DISCUSSION

In the prevaccination era of the COVID-19 pandemic, we observed large racial and ethnic disparities in SARS-CoV-2 seroprevalence. Hispanic and Black pregnant patients were more likely to be seropositive than White patients. Mediation analyses revealed that part of these disparities might be explained by

Table 3. Associations of Race and Ethnicity With Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Seropositivity at the End of Pregnancy in Unadjusted, Individual Covariate–Adjusted, and Then Neighborhood Factor–Adjusted Models

Models of the Disparity in Seropositivity	OR	95% CI
Models of the Hispanic–White disparity		
M0=unadjusted	8.48	5.91–12.2
M1=M0+individual covariates*	3.36	2.10–5.38
M2=M1+deprivation[†]	3.16	1.93–5.15
M3=M1+segregation[‡]	3.43	2.12–5.54
M4=M1+crowding[§]	3.04	1.89–4.87
Models of the Black–White disparity		
M0=unadjusted	5.84	4.35–7.84
M1=M0+individual covariates*	3.98	2.83–5.60
M2=M1+deprivation[†]	3.48	2.41–5.02
M3=M1+segregation[‡]	3.60	2.42–5.36
M4=M1+crowding[§]	3.89	2.77–5.47
Models of the another race or ethnicity–White disparity[‖]		
M0=unadjusted	1.55	0.93–2.60
M1=M0+individual covariates*	1.36	0.80–2.30
M2=M1+deprivation[†]	1.32	0.78–2.21
M3=M1+segregation[‡]	1.26	0.73–2.17
M4=M1+crowding[§]	1.35	0.79–2.28

OR, odds ratio calculated using multilevel logistic regression.
* Age, body mass index, insurance, limited English proficiency.
[†] Neighborhood deprivation index includes six indicators and ranges from 0 to 1, with 1 indicating more deprivation.
[‡] For the Index of Concentration at the Extremes, higher values indicate a higher proportion of White residents.
[§] Crowding is defined as the proportion of residences with more humans than rooms in the house.
[‖] Nine individuals with missing body mass index data were removed owing lack of convergence.
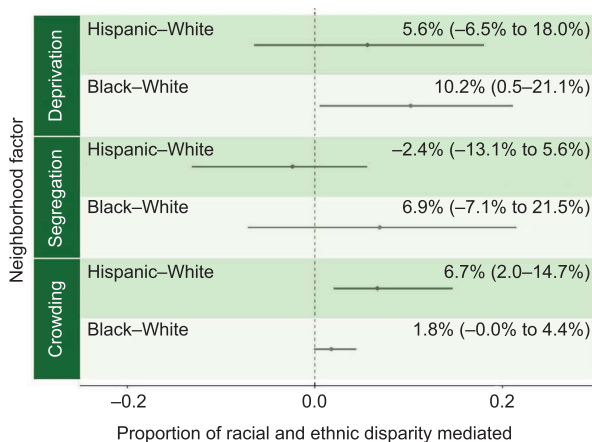
Fig. 3. Proportion (and 95% CIs) of the racial and ethnic disparity in severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) seropositivity at the end of pregnancy, mediated by neighborhood factors. Neighborhood deprivation index includes six indicators and ranges from 0 to 1, with 1 indicating more deprivation. Segregation was assigned using the Index of Concentration at the Extremes; higher values indicate a higher proportion of White residents. *Crowding* is defined as the proportion of residences with more humans than rooms in the house.

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differences in neighborhood conditions, specifically deprivation and crowding.

Although our study is novel with respect to studying neighborhood factors in association with SARS-CoV-2 seroprevalence in pregnancy as well as interrogating them as potential mediators, it is consistent with others that have reported associations of neighborhood factors with rates of SARS-CoV-2 infection and COVID-19 mortality in the United States. Carrion et al analyzed neighborhoods in New York City, in the first 9 weeks of the pandemic and found that neighborhoods with high subway ridership had a higher burden of COVID-19 mortality; these neighborhoods had a higher proportion of Hispanic and Black residents.[14] Krieger et al[16] showed that ZIP code poverty levels and crowding were significantly associated with COVID-19 mortality in Massachusetts. Chen and Krieger[17] analyzed county-level variables in association with COVID-19 in New York and Illinois and found higher rates in counties with higher poverty rates, more crowding, and lower proportion of White residents. A study of the built environment in King County, Washington, also demonstrated that fewer open spaces and more crowding were associated with COVID-19.[29] Another study demonstrated that residents living in Louisiana neighborhoods with high levels of deprivation had

40% higher risk of COVID-19.[22] Additionally a study of 434 patients admitted for labor and delivery at a New York City hospital with universal polymerase chain reaction (PCR) testing from the first month of the COVID-19 pandemic (March 22–April 21, 2020) demonstrated that lower neighborhood socioeconomic status and more household crowding were associated with SARS-CoV-2 infection.[30] Our study differs from these prior reports in that it interrogated seroprevalence, which captures information about past infections in patients who may not test positive using a PCR test at the time of admission for parturition. Furthermore, we examined the extent to which neighborhood factors might explain racial and ethnic disparities in seropositivity.

Although studies quantifying neighborhood factors' contribution to disparities are rare, the effects with respect to deprivation's contribution to the Black–White disparity (11.6% overall and 14.6% in Philadelphia County) are similar in magnitude to those in a preterm birth study in California; 16.1% of Black–White disparities were attributable to a combination of several neighborhood factors in that study.[31] Nonetheless, it is clear that unmeasured factors explain the disparity in seropositivity that persisted after adjusting for individual and neighborhood factors, with aORs of seropositivity among Hispanic and Black patients compared with White patients exceeding 3. Additional work to determine the extent to which occupational, transportation, or other socioenvironmental factors explain persistent disparities in seropositivity, and many other health outcomes, is warranted.

Although the effect estimates in models of associations of deprivation and crowding with seropositivity were substantially weakened by the addition of individual covariates, they remained significant. Potential mechanisms by which neighborhood factors such as deprivation and crowding might contribute to higher SARS-CoV-2 exposure include close quarters leading to shared ambient air, insufficient ventilation, and inability to quarantine. Such conditions can enable transmission of airborne infections such as tuberculosis.[32,33] It is also possible that neighborhood factors are markers of other exposures. The opportunity to socially distance at home and work may vary substantially by race and ethnicity. Hispanic and Black women are more likely, for example, to be essential personnel such as home health aides and nursing home workers[34]–jobs that may have placed Hispanic and Black patients at higher risk for SARS-CoV-2 exposure. Nonetheless, VoPham et al analyzed area-level indicators as potential effect modifiers of social distancing (measured with smartphone data)

on COVID-19 rates and found that social distancing was less effective in counties with lower median household incomes, larger "minority" population, and more residential crowding.[23] These findings suggest that even when residents practice social distancing, neighborhood factors may play a role in virus transmission. Furthermore, in our analysis, deprivation and crowding continued be associated with seropositivity even when controlling for insurance type (a marker of socioeconomic position) and significantly mediated disparities, suggesting they may play a causal role.

Strengths of our study include a large sample size of pregnant patients in whom we analyzed seroprevalence in an unselected population. By not relying on clinician and patient decisions regarding PCR or antigen testing, we were able to avoid selection bias. Importantly, by studying antibody levels, we could account for both symptomatic and asymptomatic SARS-CoV-2 infection, but we did not study the disease itself (COVID-19). Prior studies have found that residents in disadvantaged neighborhoods have less testing and higher positivity ratios when tested, suggesting that ascertainment bias may lead to underestimation of disparities in exposure to SARS-CoV-2 and, consequently, in COVID-19.[35] Furthermore, by testing at the time of parturition, we were able to capture exposure to the virus at any time before or during pregnancy, as opposed to the shorter time of the few weeks at the end of pregnancy during which a PCR or antigen test result would still be positive. Limitations include the possibility of unmeasured confounders such as employment and detailed socioeconomic indicators such as income or education. Although diverse, our study population had few cases of seropositivity among Asian patients (n=13) and patients self-designated as another, multiple, or unknown race or ethnicity (n=15), which necessitated combining this group for modeling and likely resulted in lack of power to rule out disparities. There were some differences between patients with and without seropositivity data, which could affect generalizability of findings. Specifically, patients without available samples were more likely to be older, White, privately insured, and have preterm birth. We suspect that this population may have been transferred into our hospitals from other hospitals where the blood sample had already been drawn or was so sick that add-on tests used up the sample and there was no volume left for our assay. We used Census tract variables, which may misclassify exposures of individual patients whose local neighborhood environment may differ from the Census tract indicator.

There are other measures of neighborhood deprivation in the literature. We chose to use a specific material community deprivation index[26] because it did not have an indicator for the proportion of "minority" residents as the Centers for Disease Control and Prevention Social Vulnerability Index[36] does, nor an indicator for "crowding," which is included in the Area Deprivation Index.[37,38] We wanted to assess segregation and crowding separately. Nonetheless, findings might vary with the choice of neighborhood deprivation index. Although the method we used is often called "causal mediation," this study was observational and, thus, cannot prove causal effects.[39]

In conclusion, we found that neighborhood factors such as deprivation and crowding likely explain a portion of the racial and ethnic disparities observed in SARS-CoV-2 seropositivity in pregnancy in the prevaccination era. Addressing the structural racism that has led to persistently different living conditions by race and ethnicity in the United States, and investing in residential communities, will be key to advancing health equity.

REFERENCES

1. Centers for Disease Control and Prevention. Risk for COVID-19 infection, hospitalization, and death by race/ethnicity. Accessed September 28, 2021. https://www.cdc.gov/coronavirus/2019-ncov/covid-data/investigations-discovery/hospitalization-death-by-race-ethnicity.html

2. Son M, Gallagher K, Lo JY, Lindgren E, Burris HH, Dysart K, et al. Coronavirus disease 2019 (COVID-19) pandemic and pregnancy outcomes in a U.S. population. Obstet Gynecol 2021;138:542–51. doi: 10.1097/AOG.0000000000004547

3. Flannery DD, Gouma S, Dhudasia MB, Mukhopadhyay S, Pfeifer MR, Woodford EC, et al. SARS-CoV-2 seroprevalence among parturient women in Philadelphia. Sci Immunol 2020; 5:eabd5709. doi: 10.1126/sciimmunol.abd5709

4. Nardone A, Chiang J, Corburn J. Historic redlining and urban health today in U.S. cities. Environ Justice 2020;13:109–19. doi: 10.1089/env.2020.0011

5. Lowe TS, Wallace M. Occupational race segregation, globalization, and White advantage: White-Black earnings inequality in U.S. metropolitan areas. Sociological Spectr 2017;37:353–70. doi: 10.1080/02732173.2017.1365028

6. Hawkins D. Differential occupational risk for COVID-19 and other infection exposure according to race and ethnicity. Am J Ind Med 2020;63:817–20. doi: 10.1002/ajim.23145

7. Diez Roux AV, Mair C. Neighborhoods and health. Ann N Y Acad Sci 2010;1186:125–45. doi: 10.1111/j.1749-6632.2009.05333.x

8. Snow J. On the mode of communication of cholera. John Churchill; 1855.

9. Kline SE, Hedemark LL, Davies SF. Outbreak of tuberculosis among regular patrons of a neighborhood bar. New Engl J Med 1995;333:222–7. doi: 10.1056/NEJM199507273330404

10. Zhang Z, Wang H, Wang C, Fang H. Modeling epidemics spreading on social contact networks. IEEE Trans Emerging Top Comput 2015;3:410–9. doi: 10.1109/TETC.2015.2398353

11. Mylona EK, Shehadeh F, Kalligeros M, Benitez G, Chan PA, Mylonakis E. Real-time spatiotemporal analysis of microepidemics of influenza and COVID-19 based on hospital network data: colocalization of neighborhood-level hotspots. Am J Public Health 2020;110:1817–24. doi: 10.2105/AJPH.2020.305911

12. Nwanaji-Enwerem JC, Allen JG, Beamer PI. Another invisible enemy indoors: COVID-19, human health, the home, and United States indoor air policy. J Expo Sci Environ Epidemiol 2020;30:773–5. doi: 10.1038/s41370-020-0247-x

13. Hong B, Bonczak BJ, Gupta A, Thorpe LE, Kontokosta CE. Exposure density and neighborhood disparities in COVID-19 infection risk. Proc Natl Acad Sci U S A 2021;118: e2021258118. doi: 10.1073/pnas.2021258118

14. Carrión D, Colicino E, Pedretti NF, Arfer KB, Rush J, DeFelice N, et al. Neighborhood-level disparities and subway utilization during the COVID-19 pandemic in New York City. Nat Commun 2021;12:3692. doi: 10.1038/s41467-021-24088-7

15. Hatef E, Chang HY, Kitchen C, Weiner JP, Kharrazi H. Assessing the impact of neighborhood socioeconomic characteristics on COVID-19 prevalence across seven States in the United States. Front Public Health 2020;8:571808. doi: 10. 3389/fpubh.2020.571808

16. Krieger N, Waterman PD, Chen JT. COVID-19 and overall mortality inequities in the surge in death rates by ZIP code characteristics: Massachusetts, January 1 to May 19, 2020. Am J Public Health 2020;110:1850–2. doi: 10.2105/AJPH. 2020.305913

17. Chen JT, Krieger N. Revealing the unequal burden of COVID-19 by income, race/ethnicity, and household crowding: US county versus ZIP code analyses. J Public Health Manage Pract 2021;27:S43–56. doi: 10.1097/PHH.0000000000001263

18. Kashem SB, Baker DM, González SR, Lee CA. Exploring the nexus between social vulnerability, built environment, and the prevalence of COVID-19: a case study of Chicago. Sustain Cities Soc 2021;75:103261. doi: 10.1016/j.scs.2021.103261

19. Morrissey K, Spooner F, Salter J, Shaddick G. Area level deprivation and monthly COVID-19 cases: the impact of government policy in England. Soc Sci Med 2021;289:114413. doi: 10. 1016/j.socscimed.2021.114413

20. VanderWeele TJ. Explanation in causal inference: developments in mediation and interaction. Int J Epidemiol 2016;45: 1904–8. doi: 10.1093/ije/dyw277

21. Montoya-Williams D, Mullin AM, Handley SC, Flannery DD, Lorch SA, Elovitz MA, et al. Disparities in SARS-CoV-2 positivity among pregnant patients with limited English proficiency. J Perinatol 2021;41:2564–5. doi: 10.1038/s41372-021-01148-w

22. KC M, Oral E, Straif-Bourgeois S, Rung AL, Peters ES. The effect of area deprivation on COVID-19 risk in Louisiana. PLoS One 2020;15:e0243028. doi: 10.1371/journal.pone. 0243028

23. VoPham T, Weaver MD, Adamkiewicz G, Hart JE. Social distancing associations with COVID-19 infection and mortality are modified by crowding and socioeconomic status. Int J Environ Res Public Health 2021;18:4680. doi: 10. 3390/ijerph18094680

24. A nationwide community deprivation index. Accessed October 1, 2021. https://github.com/geomarker-io/dep_index

25. United States Census Bureau. American Community Survey data. Accessed September 30, 2021. https://www.census.gov/programs-surveys/acs/data.html

26. Brokamp C, Beck AF, Goyal NK, Ryan P, Greenberg JM, Hall ES. Material community deprivation and hospital utilization during the first year of life: an urban population-based cohort study. Ann Epidemiol 2019;30:37–43. doi: 10.1016/j.annepidem.2018.11.008

27. Tingley D, Yamamoto T, Hirose K, Keele L, Imai K. Mediation: R package for causal mediation analysis. J Stat Soft 2014; 59. doi: 10.18637/jss.v059.i05

28. R. The R project for statistical computing. Accessed October 11, 2021. https://www.r-project.org/

29. Liu C, Liu Z, Guan C. The impacts of the built environment on the incidence rate of COVID-19: a case study of King County, Washington. Sustain Cities Soc 2021;74:103144. doi: 10.1016/j. scs.2021.103144

30. Emeruwa UN, Ona S, Shaman JL, Turitz A, Wright JD, Gyamfi-Bannerman C, et al. Associations between built environment, neighborhood socioeconomic status, and SARS-CoV-2 infection among pregnant women in New York city. JAMA 2020; 324:390–2. doi: 10.1001/jama.2020.11370

31. Benmarhnia T, Huang J, Basu R, Wu J, Bruckner TA. Decomposition analysis of Black-White disparities in birth outcomes: the relative contribution of air pollution and social factors in California. Environ Health Perspect 2017;125:107003. doi: 10. 1289/EHP490

32. Centers for Disease Control (CDC). Transmission of multidrug-resistant tuberculosis among immunocompromised persons in a correctional system–New York, 1991. MMWR Morb Mortal Wkly Rep 1992;41:507–9.

33. Nardell E, McInnis B, Thomas B, Weidhaas S. Exogenous reinfection with tuberculosis in a shelter for the homeless. N Engl J Med 1986;315:1570–5. doi: 10.1056/NEJM198612183152502

34. U.S. Bureau of Labor Statistics. Labor force statistics from the current population survey. Household data annual averages. 18. Employed persons by detailed industry, sex, race, and Hispanic or Latino ethnicity. Accessed April 8, 2022. https://www. bls.gov/cps/cpsaat18.htm

35. Bilal U, Tabb LP, Barber S, Diez Roux AV. Spatial inequities in COVID-19 testing, positivity, confirmed cases, and mortality in 3 U.S. cities: an ecological study. Ann Intern Med 2021;174: 936–44. doi: 10.7326/M20-3936

36. Agency for Toxic Substances and Disease Registry. At a glance: CDC/ATSDR Social Vulnerability Index. Accessed February 15, 2022. https://www.atsdr.cdc.gov/placeandhealth/svi/at-a-glance_svi.html

37. Kind AJ, Jencks S, Brock J, Yu M, Bartels C, Ehlenbach W, et al. Neighborhood socioeconomic disadvantage and 30 day rehospitalizations: an analysis of Medicare data. Ann Intern Med 2014;161:765–74. doi: 10.7326/M13-2946

38. Kind AJH, Buckingham WR. Making neighborhood-disadvantage metrics accessible–the neighborhood atlas. New Engl J Med 2018;378:2456–8. doi: 10.1056/NEJMp1802313

39. Keele L. Causal mediation analysis: warning! Assumptions ahead. Am J Eval 2015;36:500–13. doi: 10. 1177/1098214015594689

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