Associations Between Built Environment, Neighborhood Socioeconomic Status, and SARS-CoV-2 Infection Among Pregnant Women in New York City

The built environment is associated with infectious disease dynamics, particularly in diseases transmitted by contact, aerosols, or droplets.1,2 A recent study of the ongoing severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) epidemic in New York revealed significant differences in hospitalization and death rates among the city’s boroughs, with the highest rates in Queens and the Bronx.3 To our knowledge, no studies have investigated associations between the built environment, markers of neighborhood socioeconomic status, and SARS-CoV-2 transmission. We leveraged a universal testing program for SARS-CoV-2 in pregnant women to examine associations between these factors and SARS-CoV-2 prevalence.

Methods | We conducted a cross-sectional study of New York City residents delivering at New York-Presbyterian/Columbia University Irving Medical Center or Allen Hospital after implementation of universal SARS-CoV-2 nasopharyngeal quantitative reverse transcriptase–polymerase chain reaction testing at the time of admission to the labor and delivery unit from March 22 through April 21, 2020. We linked patients to demographic and socioeconomic data from the US Census Bureau’s American Community Survey,4 a national survey with detailed demographic, socioeconomic, and housing data, and to real estate tax data from New York’s Department of City Planning.5 We abstracted building-level variables, including number of residential units per building and mean assessed value (per square foot), and neighborhood-level variables, including median household income, poverty rate, unemployment rate, population density, household membership (persons per household), and household crowding (percentage of households with >1 person per room). Neighborhood was defined using New York City neighborhood tabulation areas, which divide the city into 195 districts, with at least 15 000 residents each.4

We fit bivariable logistic regression models with cluster robust standard errors, modeling exposures as continuous independent variables. Because odds ratios (ORs) associated with a 1-unit change in independent variables can be difficult to interpret, we used these models both to estimate interdecile ORs—ie, the relative odds of SARS-CoV-2 infection for individuals at the 90th percentile of an independent variable relative to those at the 10th percentile—and to predict probabilities (and 95% CIs) of SARS-CoV-2 infection at the 10th and 90th percentiles of the independent variable distribution. Analysis was performed using Stata/MP version 16.0 (StataCorp). Two-sided P < .05 was considered significant. This study was exempted from informed consent and approved by the Columbia University institutional review board.

Results | We identified 434 New York City residents who were tested for SARS-CoV-2. Of the 396 patients (91%) linked to buildings and neighborhoods in the city, 71 (17.9%) were infected with SARS-CoV-2. Cohort characteristics are tabulated in the Table. The likelihood of SARS-CoV-2 varied substantially across measures of built environment and

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Table. Cohort Characteristics

<table>
<thead>
<tr>
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<th>SARS-CoV-2 status</th>
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<tbody>
<tr>
<td></td>
<td>Negative (n = 325)</td>
<td>Positive (n = 71)</td>
<td>P value</td>
</tr>
<tr>
<td>Maternal age, median (IQR), y</td>
<td>31.0 (27.0-35.0)</td>
<td>27.0 (24.0-32.0)</td>
<td>&lt;.001*</td>
</tr>
<tr>
<td>Gestational age, median (IQR), wk</td>
<td>39.0 (38.1-39.7)</td>
<td>39.0 (37.4-39.7)</td>
<td>.63*</td>
</tr>
<tr>
<td>Gravidity (IQR)</td>
<td>2 (1-4)</td>
<td>2 (1-3)</td>
<td>.04*</td>
</tr>
<tr>
<td>Parity (IQR)</td>
<td>1 (0-1)</td>
<td>0 (0-1)</td>
<td>.37*</td>
</tr>
<tr>
<td>Hypertension, No. (%)</td>
<td>26 (8.0)</td>
<td>7 (9.9)</td>
<td>.61*</td>
</tr>
<tr>
<td>Diabetes, No. (%)</td>
<td>18 (5.5)</td>
<td>2 (2.8)</td>
<td>.34*</td>
</tr>
</tbody>
</table>

Abbreviations: IQR, interquartile range; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

*P value based on linear regression with cluster robust standard errors.

* Both pregestational and gestational conditions included.

* P value based on logistic regression with cluster robust standard errors.
The lowest probability of infection was estimated for women living in buildings with very high assessed values (8.2% [95% CI, 1.2%-15.2%]) and the highest was for those residing in neighborhoods with high household membership (23.9% [95% CI, 18.4%-29.4%]). Odds of infection were lower among women living in buildings with more residential units (interdecile OR, 0.34 [95% CI, 0.16-0.72]) and higher assessed values (interdecile OR, 0.29 [95% CI, 0.10-0.89]) and in neighborhoods with higher median incomes (interdecile OR, 0.32 [95% CI, 0.12-0.83]). Odds of infection were higher among women residing in neighborhoods with high unemployment rates (interdecile OR, 2.13 [95 CI, 1.18-3.83]), large household membership (interdecile OR, 3.16 [95% CI, 1.58-6.37]), and greater household crowding (interdecile OR, 2.27 [95% CI, 1.12-4.61]). There was no statistically significant association between SARS-CoV-2 infection and neighborhood socioeconomic status (Figure). 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and population density (interdecile OR, 0.70 [95% CI, 0.32-1.51]) or poverty rate (interdecile OR, 2.03 [95% CI, 0.97-4.25]). Neighborhood-level variables were moderately to highly correlated ($r = 0.66-0.83$).

**Discussion** | In this study, SARS-CoV-2 transmission among pregnant women in New York City was associated with neighborhood- and building-level markers of large household membership, household crowding, and low socioeconomic status. These data may aid policy makers in the design of interventions to reduce the spread of SARS-CoV-2. A key strength of this study was the use of a universally tested population, which allowed for ascertainment of asymptomatic cases among a defined at-risk population. Limitations of the study include that the findings may not apply to other populations given the unique demographic, physiologic, and social features of pregnant women. Additionally, the small sample size and high degree of correlation between neighborhood-level variables precluded multivariable analysis. Nonetheless, this study provides empirical support for the hypothesis that variation in the urban environment may be an important social determinant of SARS-CoV-2 transmission.

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**Author Contributions:** Dr Melamed had full access to all of the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis. Drs Emeruwa and Ona contributed equally. Concept and design: Shaman, Turitz, Gyamfi-Bannerman, Melamed. Acquisition, analysis, or interpretation of data: Emeruwa, Ona, Gyamfi-Bannerman, Wright, Melamed. Drafting of the manuscript: Emeruwa, Ona, Melamed. Critical revision of the manuscript for important intellectual content: Emeruwa, Ona, Shaman, Turitz, Gyamfi-Bannerman, Wright. Statistical analysis: Melamed. Administrative, technical, or material support: Shaman, Turitz, Gyamfi-Bannerman. Supervision: Turitz, Melamed.

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**SARS-CoV-2 Positivity Rate for Latinos in the Baltimore–Washington, DC Region**

The black community has been disproportionately affected by the coronavirus disease 2019 (COVID-19) pandemic in the US. Emerging data highlight sharp increases in COVID-19 cases within the Latino community. We analyzed temporal trends in positivity rates for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in the Baltimore-Washington, DC region by race/ethnicity.

**Methods** | Samples were collected between March 11, 2020, and May 25, 2020, from 5 hospitals, including emergency departments, and 30 outpatient clinics that are part of the Johns Hopkins Health System (JHHS). SARS-CoV-2 testing inclusion criteria broadened over time (ie, initially high-risk individuals only and then all symptomatic patients) as local capacity increased but was standardized across JHHS sites. Samples collected via nasopharyngeal swabs were analyzed using SARS-CoV-2 reverse transcriptase-polymerase chain reaction data. On patient demographics, comorbidities, SARS-CoV-2 status, and hospitalization were extracted from the integrated electronic health record system.

Patients self-identified race/ethnicity from fixed categories. Racial/ethnic groups were considered mutually exclusive; ie, Latinos were excluded from other groups (white, black, other) regardless of reported race. Those who self-reported American Indian, Alaska Native, Asian American, Native Hawaiian, Pacific Islander, or multiracial were grouped as “other.” Temporal trends in daily positivity rates (7-day moving average; number positive/number tested over the date and preceding 6 days) and testing volumes stratified by race/ethnicity were evaluated. Total rates of SARS-CoV-2 positivity, hospitalization, and categorical patient characteristics were...