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Abstract

Numerous reports indicate that African Americans and Latinos are being affected disproportionately by coronavirus disease 2019 (COVID-19). Positivity rates have not been analyzed on scale because only 4 states report race/ethnicity as part of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) testing. Previous studies also have had little ability to control for many known risk factors to better identify the effects of COVID-19 on racial and ethnic communities. Using test results from a large national reference laboratory database that included patients from all 50 states and the District of Columbia, this study compared positivity rates for SARS-CoV-2 nucleic acid amplification tests (NAAT) among various race/ethnicity groups by linking zip code-based race/ethnicity proportions from US Census data. Analysis of 2,331,175 unique patients tested March-May 2020 demonstrated an increasing trend in SARS-CoV-2 NAAT positivity across Black non-Hispanic community progressive quintiles (from 7.8% to 17.2%, $P < 0.0001$) and Hispanic community progressive quintiles (from 8.4% to 15.5%, $P < 0.0001$) and a decreasing trend across White non-Hispanic community progressive quintiles (from 17.4% to 7.1%, $P < 0.0001$). These trends in viral ribonucleic acid positivity remained in stratified analyses and in multivariable models that controlled for known risk factors including sex, population density, and the states initially hardest hit by COVID-19. These findings indicate that communities with the highest proportions of Black non-Hispanic and Hispanic populations have the highest SARS-CoV-2 NAAT positivity rates, even after controlling for other risk factors. More efforts are needed to mitigate the increased impact of COVID-19 on both the African American and Hispanic communities.

Keywords: SARS-CoV-2, COVID-19, race, ethnicity

Introduction

NUMEROUS REPORTS SUPPORT that ethnic minorities are being affected disproportionately by SARS-CoV-2 infection and COVID-19 disease.[1–6] As of June 24, 2020, there were nearly 2.4 million confirmed cases of COVID-19 in the United States and 120,000 COVID-19-related deaths.[7] In early June, the reported COVID-19 fatality rate was nearly 2.5 times higher for African Americans than for the White non-Hispanic population in the states reporting race/ethnicity data, with some states showing even larger disparities.[8] These findings are based on data analyses from the American Public Media Research Lab that indicated non-Hispanic African Americans accounted for 24% of COVID-19 deaths, despite comprising only 12% of the US population.[9] The same report noted the mortality rate per 100,000 people was similar among White (22.7), Asian (24.3), and Latino (24.9) populations.[9]

As of June 1, 2020, race/ethnicity was included as part of confirmed positive cases in 47 states and as part of COVID-19 death reports in 42 states; however, only 4 states (Delaware, Illinois, Kansas, and Nevada) report race/ethnicity testing rates,[8] making positivity rates based on race and ethnicity difficult to calculate. Even in states that have recently reported confirmed cases and deaths by race and ethnicity (eg, New York), it can be difficult to know the degree to which these racial divides are affected by large African American and Hispanic communities in some of the areas with the most COVID-19 infections (eg, New York City). Additionally, conflicting outcomes have been reported on the relationship between SARS-CoV-2 nucleic acid amplification test (NAAT) positivity and race and

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ethnicity, and most prior reports were based on a relatively small number of individuals.[10]

Positivity rates reflect positive test results among only those people who were tested. Therefore, positivity rates are greatly affected by the amount of testing and the selection of individuals tested. Laboratory test positivity rates must be distinguished from infection and disease rates. Infection rates reflect who is infected in the population; incidence is defined by the occurrence of new cases whereas prevalence is defined as the proportion of cases in the population at a given time. Positivity rates are an additional useful measurement in population disease assessment as they account for the rapidly evolving number of patients being tested. To best understand the specific contribution of SARS-CoV-2 NAAT positivity rates, this study examined differences among US Census-defined race/ethnicity groups using data from a large national reference laboratory.

Methods

All SARS-CoV-2 ribonucleic acid (RNA) molecular testing was performed by Quest Diagnostics using 4 different US Food and Drug Administration Emergency Use Authorized tests; the Quest Diagnostics laboratory-developed test (Quest SARS-CoV-2 rRT-PCR), the Roche Diagnostics cobas SARS-CoV-2 test, Hologic Panther Fusion SARS-CoV-2 assay, and Hologic Aptima SARS-CoV-2 test.

Study population

All SARS-CoV-2 NAAT test results performed by Quest Diagnostics that were stored in the Informatics Data Warehouse as of June 5, 2020 were retrieved for potential inclusion in this study. Results were obtained from tests performed from March 9, 2020 (first day of testing at Quest Diagnostics) through May 31, 2020. The study population was limited to 1 result per patient. If any patient SARS-CoV-2 NAAT test result was positive, that patient was considered positive and patients with only negative result(s) were classified as negative. Specimens with equivocal/inconclusive results were excluded because their status could not be categorized. Results from patients for whom the testing laboratory did not provide the residential zip code – essential to assigning race/ethnicity, income, and population density proportions – also were excluded.

Census estimates by zip code

To analyze race/ethnicity, patient zip code data were linked to estimated race/ethnicity proportions in each corresponding zip code as reported by the 2018 5-year American Community Survey (ACS) on the US Census data website (the most recent data available).[11] The research team used estimated proportions for single race, Black non-Hispanic, Hispanic, White non-Hispanic, and Asian non-Hispanic into categories of the same name. The team grouped all other race/ethnicities, including multiple race/ethnicities, into the ''other'' race/ethnicity categories. To determine the proportion of testing that likely came from each race/ethnicity group, the team weighted the result by the race/ethnicity proportions within that zip code. For example, if a specimen came from a community with equal race/ethnicity proportions for the 5 categories, each would be assigned a value of 0.2. These values were then summed in the full analytic data set. To analyze income, mean household income in the past 12 months (in 2018 inflation-adjusted dollars) from 2018 ACS 5-Year Estimates was used.[12] Population density data came from the 2010 Census.[13] The team analyzed positivity rates by quintiles of race/ethnicity proportion, population density, and mean income to approximate the association with each of these factors.

Statistical analyses

The research team controlled for various potentially confounding factors, such as age, sex, income, and population density to better isolate the association of COVID-19 and minority communities, as determined by SARS-CoV-2 NAAT positivity rates. The chi-square test for proportions and the t test for means were used to analyze differences between included and excluded patients. Trends in COVID-19 positivity among race/ethnicity quintiles were analyzed using the Cochran-Armitage test for trend. All variables of interest (including statistically insignificant variables) were included in the multivariable logistic regression model, given their potential as confounders. The team separately included patient residence in the 5 states with the highest confirmed COVID-19 rates per capita (New York, New Jersey, Massachusetts, Rhode Island, and Connecticut)[14] as binary variables in the multivariable model. Race/ethnicity proportions were included as continuous variables. Data analyses were performed using SAS Studio 3.6 on SAS 9.4 (SAS Institute Inc., Cary, NC, USA). This Quest Diagnostics Health Trends study was deemed exempt by the Western Institutional Review Board (Puyallup, Washington).

Results

The potential cohort included 3,134,778 SARS-CoV-2 molecular specimens from 2,935,158 unique patients representing all 50 states and the District of Columbia. Patients without valid residential zip code data (n = 600,472) were excluded followed by those with equivocal/inconclusive results (n = 3511). The final analytic cohort (N = 2,331,175) constituted 79.4% of potential patients for whom definitive SARS-CoV-2 NAAT were obtained. Included patients were younger, on average, than excluded patients (45.8 standard deviation [SD] 18.5 vs. 46.3 SD 18.1, $P < 0.0001$) and more likely to be female (56.5%, 95% confidence interval [CI] 56.5–56.5%, vs 55.7%, 95% CI 55.6–55.8%, $P < 0.0001$). The SARS-CoV-2 NAAT positivity rate was higher for the included population than the excluded population (11.6%, 95% CI 11.6–11.7%, vs 11.4%, 95% CI 11.3–11.5%, $P < 0.0001$). The study population was 12.4% Black non-Hispanic, 22.1% Hispanic, 56.1% White non-Hispanic, 5.9% Asian non-Hispanic, and 3.5% ''other'' race/ethnicities. These proportions are very close to American Community Survey 2018 estimates for the national population (12.3% Black non-Hispanic, 18.3% Hispanic, 60.2% White non-Hispanic, 5.6% Asian non-Hispanic, and 3.6% for all other ethnicities).[15]

There was a statistically significant increasing trend in SARS-CoV-2 NAAT positivity for Black non-Hispanic
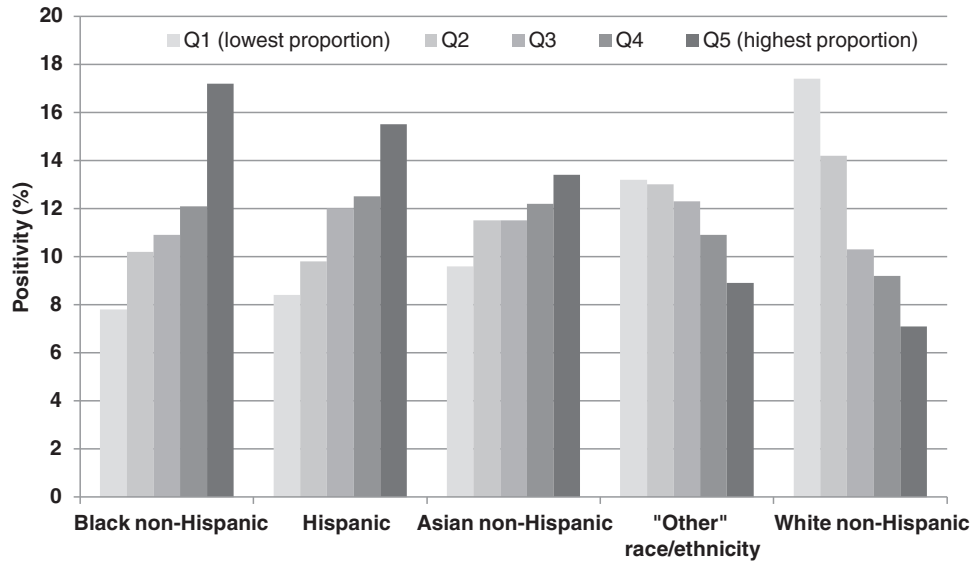
FIG. 1. COVID-19 positivity by race/ethnicity community quintiles. Quintiles were derived from analysis of race/ethnicity proportions as estimated by the US Census Bureau (2018 American Community Survey 5-Year Estimates). Cochran-Armitage test for trend, $P < 0.0001$ for each race/ethnicity group.

quintiles (from 7.8% to 17.2%, $P < 0.0001$), Hispanic quintiles (from 8.4% to 15.5%, $P < 0.0001$), and Asian non-Hispanic quintiles (from 9.6% to 13.4%, $P < 0.0001$) during the time period of March 9 through May 31, 2020. There was a statistically significant decreasing trend in SARS-CoV-2 NAAT positivity for White non-Hispanic quintiles (from 17.4% to 7.1%, $P < 0.0001$) and ''other'' race/ethnicity quintiles (from 13.2% to 8.9%, $P < 0.0001$) (Figure 1).

Progressive quintiles of population density also demonstrated a statistically significant increasing trend ($P < 0.0001$)

in SARS-CoV-2 NAAT positivity rates (quintile 1, 6.8%; quintile 2, 8.4%; quintile 3, 10.8%; quintile 4, 12.3%; quintile 5, 19.8%). Positivity rates were analyzed for race/ethnicity quintiles in the most densely populated areas (quintile 5 of population density) and the least densely populated areas (quintile 1 of population density) (Figure 2). Statistically significant increasing trends in positivity for the Black non-Hispanic and Hispanic populations were demonstrated in both the most densely populated areas ($P < 0.0001$ for all) and in the least densely populated areas

FIG. 2. COVID-19 positivity by race/ethnicity community quintiles in the most and least densely populated areas. Quintiles were derived from analysis of race/ethnicity proportions as estimated for each zip code by the US Census Bureau (2018 American Community Survey 5-Year Estimates). Population density quintiles were derived from analysis of each zip code by the US Census Bureau (2010 Census). Cochran-Armitage test for trend, $P < 0.0001$ for all groups except Asian non-Hispanic in least densely populated areas (not significant).

($P < 0.0001$ for all). Statistically significant decreasing trends in positivity for the White non-Hispanic population and the ''other'' race/ethnicity populations were demonstrated in the most and least densely populated areas ($P < 0.0001$ for both). Statistically significant decreasing trends in positivity for the Asian non-Hispanic population were demonstrated in the most densely populated areas ($P < 0.0001$) but there was no significant trend in the least densely populated areas.

Progressive quintiles of mean income demonstrated a small but statistically significant decreasing trend ($P < 0.0001$) in SARS-CoV-2 NAAT positivity rates (quintile 1, 12.7%; quintile 2, 10.9%; quintile 3, 12.1%; quintile 4, 11.5%; quintile 5, 11.0%). Positivity rates for race/ethnicity quintiles in the highest income quintile and lowest income quintile were analyzed (Figure 3). Statistically significant increasing trends in positivity for the Black non-Hispanic, Hispanic, and Asian non-Hispanic populations were demonstrated in both the highest and lowest income areas ($P < 0.0001$ for all). Statistically significant decreasing trends in positivity for the White non-Hispanic population and the ''other'' race/ethnicity populations were demonstrated in both the highest and lowest income areas ($P < 0.0001$ for all). In virtually every case, the race/ethnicity quintile differences were considerably larger in the lowest income quintile than they were in the highest income quintile.

The increases in positivity associated with increases in proportions of Black non-Hispanic and Hispanic populations also are demonstrated in multivariable models (Table 1). The model indicates significant increased risk of SARS-CoV-2 NAAT positivity for males, and patients from individual states (New York, New Jersey, Connecticut, and Massachusetts). There was a stepwise relationship between progressive population density quintiles and SARS-CoV-2 NAAT positivity and a smaller, but also stepwise relationship between progressive income quintiles and SARS-CoV-2 NAAT positivity. The association between SARS-CoV-2 NAAT positivity and increases in proportion of the Asian non-Hispanic population changed from being strongly predictive in the unadjusted model (unadjusted odds ratio 4.61, 95% CI 4.40–4.83) to slightly protective in the adjusted model (adjusted odds ratio 0.94, 95% CI 0.89–0.99).

Discussion

These findings on a national basis suggest that COVID-19 has disproportionately affected Black non-Hispanic communities, consistent in scope with previous analyses of confirmed positive cases and mortality.[1–6] The results indicate that Hispanic communities have been disproportionately affected as well, a subject that has not been thoroughly researched previously. In both populations, these results are indicated even in a multivariable model controlling for known risk factors such as sex, the hardest hit individual states, and population density.

Study data suggest that Black non-Hispanic and Hispanic communities are representative among all patients tested for SARS-CoV-2 RNA. The reasons for increased SARS-CoV-2 positivity rates in Black non-Hispanic and Hispanic communities tested are likely as complex as the communities themselves; however, population health experts have proposed several situations that could be causing these disparities. Ethnic minorities are overrepresented in essential jobs in industries including transportation, government, health care, and food supply services, which may increase their chances of being infected while at work.[16] Previous research also has shown higher rates of diseases such as diabetes, heart disease,[17] and obesity[18] in African Americans, all of which have been linked to COVID-19 mortality,[19] although the impact of these conditions on infection
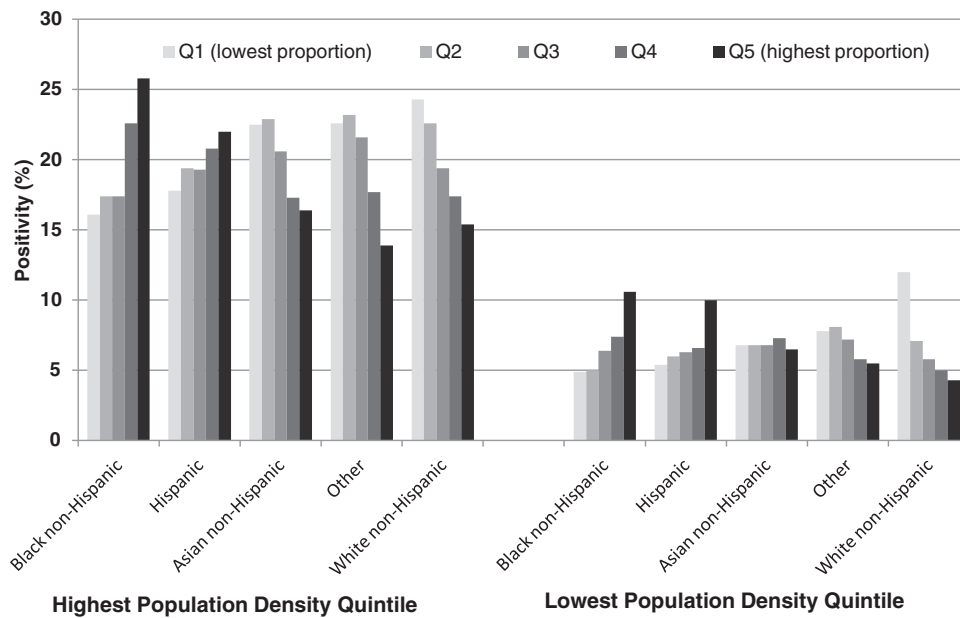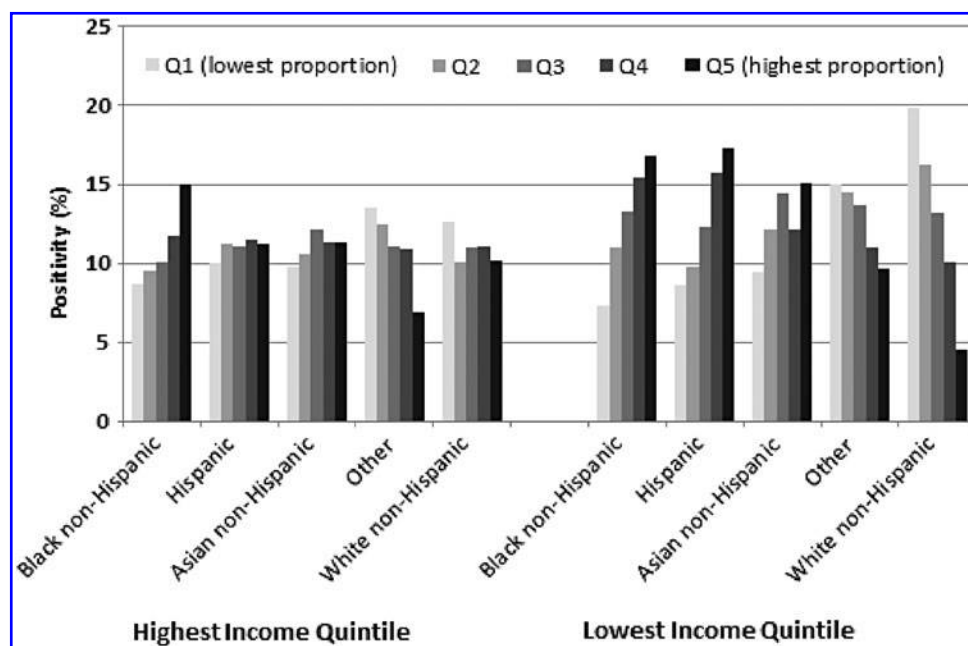

FIG. 3. COVID-19 positivity by race/ethnicity community quintiles in the highest and lowest income areas. Quintiles were derived from analysis of race/ethnicity proportions and mean income as estimated for each zip code by the US Census Bureau (2018 American Community Survey 5-Year Estimates). Cochran-Armitage test for trend, $P < 0.0001$ for all groups.

TABLE 1. FACTORS ASSOCIATED WITH COVID-19 POSITIVITY

Factors	Unadjusted odds ratio (95% Wald confidence limits)	Adjusted odds ratio (95% Wald confidence limits)
Race/ethnicity proportions		
Black non-Hispanic	5.34 (5.24–5.45)	4.60 (4.48–4.72)
Hispanic	3.10 (3.05–3.15)	3.06 (2.99–3.13)
Asian non-Hispanic	4.61 (4.40–4.83)	0.94 (0.89–0.99)
"Other" race/ethnicity	1.00 (1.00–1.00)	1.18 (1.07–1.30)
White non-Hispanic	reference	reference
Age	0.997 (0.996–0.997)	0.998 (0.998–0.998)
Sex		
Male	1.22 (1.21–1.23)	1.23 (1.22–1.24)
Female	reference	reference
Population Density		
Quintile 5 (highest density)	3.37 (3.32–3.41)	1.61 (1.59–1.64)
Quintile 4	1.91 (1.89–1.94)	1.35 (1.33–1.38)
Quintile 3	1.64 (1.62–1.67)	1.21 (1.19–1.23)
Quintile 2	1.25 (1.23–1.27)	1.01 (1.00–1.03)
Quintile 1 (lowest density)	reference	reference
Mean Income		
Quintile 5 (highest income)	0.85 (0.84–0.86)	1.23 (1.21–1.25)
Quintile 4	0.89 (0.88–0.90)	1.23 (1.21–1.24)
Quintile 3	0.94 (0.93–0.95)	1.16 (1.14–1.18)
Quintile 2	0.84 (0.83–0.85)	1.07 (1.06–1.09)
Quintile 1 (lowest income)	reference	reference
Patient State		
New York	2.81 (2.77–2.84)	2.45 (2.41–2.48)
New Jersey	3.02 (2.97–3.06)	2.63 (2.59–2.68)
Connecticut	1.72 (1.68–1.75)	1.79 (1.75–1.83)
Massachusetts	1.83 (1.80–1.85)	2.02 (1.99–2.05)
Rhode Island	0.83 (0.75–0.91)	1.01 (0.92–1.11)
All Others	reference	reference

Multivariable model included 2,261,456 of 2,331,175 (97.1%) of the study population with no missing data for any variables included in the model. Odds ratios for race/ethnicity proportions should be interpreted using the following example; a 1% increase in the Black non-Hispanic proportion within a zip code corresponds to the odds of testing positive for SARS-CoV-2 increasing by a factor of 4.6.

rates has not yet been fully explored.[20–22] In contrast, studies demonstrated that among people ages 65 years and older, African American and Latino compared to White people have lower mortality from influenza and pneumonia as causes of death.[17,23]

Public health experts also have suggested that many risk factors for COVID-19 are connected in part to socioeconomic status, collectively referred to as social determinants of health, including reliance on public transportation for those who cannot afford a car, living in densely populated areas, having jobs without paid sick leave, disparities in access to quality health care, and living in smaller multi-family (or multigenerational) homes that make social distancing inconvenient or even impossible.[24] The cumulative impact of social inequities from an early age may influence racial and ethnic disparities in both clinical and subclinical health conditions.[25] Although the research team agrees with these factors in theory, data presented in this study demonstrated higher rates of SARS-CoV-2 positivity in higher income communities, after controlling for other factors in multivariable models. This was unexpected, especially given the small but significant association of higher

income quintiles with lower SARS-CoV-2 positivity rates in unadjusted analysis. One possible explanation is that a disproportionate number of employed health care workers are being tested for SARS-CoV-2. While there is a wide range of incomes among health care workers, some, notably physicians, have higher incomes and high exposure frequency to infected patients. Moreover, COVID-19 positivity rate disparities by race/ethnicity (particularly for the Black non-Hispanic community) remained even within the highest income communities, suggesting that lower income may not play as large a role as previously assumed. It is also important to keep in mind that the income variable used was based on the mean income for a patient's zip code. The relationship between patient income and COVID-19 positivity within zip codes, unfortunately, could not be analyzed for this study. Inclusion of these additional covariates may have yielded different results.

Other results from the multivariable models were interesting as well. To the research team's knowledge, this is the first study to examine SARS-CoV-2 molecular positivity rates by population density quintiles. Unsurprisingly, higher population density rates were associated with higher

positivity rates, but the strength and stepwise nature of this association were remarkable. Although more females than males are tested, male patients were more likely to test positive than female patients, consistent with previous literature showing that male patients are associated with increased SARS-CoV-2 NAAT positivity,[26] increased hospitalization rates,[26] and mortality.[27] Four of the 5 states with the highest per capita confirmed positivity rates nationally also were strongly associated with positivity in this study, though residence in Rhode Island was not significantly associated with positivity in the adjusted multivariable model.

Limitations and strengths

A clear limitation of this study is that there were no direct patient ethnicity data, and the estimates are based on aggregate US Census race/ethnicity proportions by zip code. Other related limitations include that patients may not be tested at the same race/ethnicity mix within each zip code, some patients may reside in one zip code but became infected somewhere else, and that, historically, hospitals have been less likely to provide patient zip code information than other facility types. Further, testing was based on specimens submitted to Quest Diagnostics only; other testing sites and laboratories may have tested a different proportion of patients within each zip code. However, analysis of test share indicated the population being tested for COVID-19 by Quest Diagnostics appears to largely reflect the overall United States regarding race/ethnicity proportions, at least when analyzed by zip code. COVID-19 testing is typically not random. People with symptoms or high exposure risk (eg, health care workers) are theoretically more likely to be tested. Yet some random testing is occurring as well, such as instances of preoperation screening. The mix of these factors, and how they have changed over the time interval evaluated in this study, is unknown. Further, these results reflect the early months of COVID-19 in the United States. Data from later time periods may show different associations. Strengths included the large analytic cohort, which included patients from all 50 states and the District of Columbia, and the number of factors controlled for in multivariable models, which allowed for better isolation of the impact COVID-19 has had on racial and ethnic minority communities.

Conclusions

Communities with the highest proportions of Black non--Hispanic and Hispanic populations have the highest SARS-Cov-2 molecular positivity rates, falling in line with previous findings on confirmed COVID-19 cases and mortality. However, this study demonstrated that these higher rates exist even after controlling for many other potentially significant risk factors, including population density and income. Although, clearly, more epidemiological research is needed, the strength of these associations suggests that more efforts urgently need to be made to help mitigate the increased impact of COVID-19 and, more broadly, the health disparities affecting both African Americans and Hispanics.[28]

Author Contributions

Drs. Kaufman and Nash and Mr. Niles all contributed to writing, reviewing, and revising the manuscript for intel-lectual and technical content. Dr. Kaufman and Mr. Niles contributed to study design. Mr. Niles performed all data analyses.

Author Disclosure Statement

The authors declare that there are no conflicts of interest.

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