Population-Based Estimates of SARS-CoV-2 Seroprevalence in Houston, TX as of September 2020

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Main Point: In a population-based investigation, SARS-CoV-2 seroprevalence in Houston, TX was nearly 14% as of September 2020 with a near two-fold difference in areas with high versus low RT-PCR positivity rates and was four times higher compared to case-based surveillance data.

Abstract

Background: In contrast to studies that relied on volunteers or convenience sampling, there are few population-based SARS-CoV-2 seroprevalence investigations and most were conducted early in the pandemic. The health department of the fourth largest city in the U.S. recognized that sound estimates of viral impact were needed to inform decision-making.

Methods: Adapting standardized disaster research methodology in September 2020, the city was divided into high and low strata based on RT-PCR positivity rates, and census block groups within each stratum were randomly selected with probability proportional to size, followed by random selection of households within each group. Using two immunoassays, the proportion of infected individuals was estimated for the city, as well as by positivity rate and by sociodemographic and other characteristics. The degree of under ascertainment of seroprevalence was estimated based on RT-PCR positive cases.

Results: Seroprevalence was estimated to be 14% with a near two-fold difference in areas with high (18%) versus low (10%) RT-PCR positivity rates and was four times higher compared to case-based surveillance data.

Conclusions: Seroprevalence was higher than previously reported and is greater than that estimated from RT-PCR data. Results will be used to inform public health decisions about testing, outreach, and vaccine rollout.

Keywords: Coronavirus, SARS-CoV-2, Epidemiology, Seroprevalence, Seroepidemiologic studies, Public Health, Infectious Diseases

Introduction

The Coronavirus Disease 2019 (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection, has led to significant morbidity and mortality worldwide.[1] Real-time reverse-transcriptase polymerase chain reaction (RT-PCR) testing measures viral RNA during an acute infection. It is critically important for diagnosing individuals with acute SARS-CoV-2 infection but provides limited information about the extent of infection in a population because testing protocols are highly variable over time[2] and RT-PCR positivity generally declines a few weeks after the onset of symptoms as viral RNA is cleared.[3, 4] In contrast, serologic testing measures antibodies against the infection, but requires 7-14 days post-infection to generate a measurable antibody response.[5] Further, for identifying acute infection, it also suffers from testing protocols that are highly variable and, if performed too early into the infection, can yield false negative results.[5] On the other hand, serological testing for SARS-CoV-2 has advantages for estimating cumulative prevalence of infection (but not for identifying acute infection) because it captures infected individuals who were tested, as well as those who were not because they had mild symptoms or were asymptomatic. Owing to the potential for underestimating infection based on case-based surveillance, seroprevalence surveys can inform both the epidemiology of SARS-CoV-2 and future actions of public health officials. Further, they may provide information on the proportion of the population that remains susceptible to the virus should antibodies provide immunity.[6]

Estimates of SARS-CoV-2 infection in the U.S. using antibody testing have varied widely, due to differences in study design (e.g., employing random or convenience sampling) and locale, and were largely conducted early in the pandemic. A key advantage of random sampling is that meaningful inferences can be made about the target population, whereas studies that rely on convenience sampling are often less expensive and easier to implement but suffer potentially from selection bias. In a statewide study that used convenience sampling of New Yorkers visiting grocery stores in April 19-28, 2020, the estimated seroprevalence was 14.0% (95% confidence interval (CI): 13.3-14.7%)[7], following post-stratification weighting by demographic characteristics of the New York state population. Innovative studies that relied on residual sera from commercial laboratories across the U.S. have also been used to estimate SARS CoV-2 seroprevalence for the early months (March-May) of the pandemic[8] and through September, 2020[9], although these estimates are not necessarily generalizable to the populations in the areas where the laboratories were located. Comparatively, investigations that employed random sampling in April and/or May of 2020 reported population-based seroprevalence estimates of 4.7% in Los Angeles County, California [4.65%; bootstrap 95% CI, 2.52-7.07%][10], 1.1% in Indiana (1.09%; 95% CI: 0.76-1.45%)[11], 2.5% in the greater Atlanta metropolitan area (2.5%, 95% CI: 1.4-4.5%)[12] and 6.9% in Orleans and Jefferson Parishes, Louisiana (6.9%, 95% CI: 6.8–6.9%)[13]. Population-based studies with random sampling of participants were also conducted in Europe around the same time as the U.S. investigations. For example, in Geneva, Switzerland during April 6 to May 9, 2020, seroprevalence ranged by week of sampling from 4.8% (95% CI 2.4–8.0%) in the first week to 10.8% (8.2–13.9%) in the fifth week.[14]

In Spain, seroprevalence during April 27 to May 11, 2020 was 4.6% (95% CI: 4.3%-5.0%).[6]

Based on estimates from PCR testing results in July 2020, Houston, the most populous city in Texas and the fourth largest city in the U.S., had reached a test positivity rate of 28% and, by September 1, 2020, had 75,207 RT-PCR-confirmed cases (3,241 cases per 100,000 population). Given the absence of population-level estimates of SARS-CoV-2 infection in the city, the Houston Health Department (HHD) in collaboration with academic partners at Baylor College of Medicine (BCM) and Rice University designed a population-based seroprevalence investigation and, herein, we report on the results of seroprevalence data that were collected on a representative sample of Houstonians in September 2020.

Methods

Study design

This investigation was determined by HHD to be a public health surveillance activity and was exempted from human subjects review.

The Community Assessment for Public Health Emergency Response (CASPER) methodology,[15] which applies a two-stage clustered sampling design, was adapted to estimate seroprevalence in the city. In total, 1,109 census block groups that fell within HHD's jurisdiction comprised the sampling frame. Data on occupied households within each block group were obtained from the 2010 U.S. Census;[16] where necessary, contiguous block groups were combined so that each group contained a minimum of 15 occupied households. Nasal swab RT-PCR results as of July 20, 2020, available at the address level, were used to compute the cumulative

positivity rate by block group and then two strata were created based on the median value (20.4%). For each stratum separately, 30 block groups were randomly selected with a probability proportional to the number of occupied households and with replacement (see Figure 1). The targeted enrollment was 7 households per census block group (420 households across the 60 block groups). Initially, a listing of 21 households was randomly generated for each census block group to be visited in order. If the initial list of 21 households was exhausted because individuals were not at home or were not interested in participating, another listing of households was randomly generated until the target number of 7 households in each census block group was met. In each household, all residents, ages 5 years and older, were invited to participate.

A 35-item survey was developed, in English and Spanish, for participants that included questions on sociodemographic characteristics, employment, medical history, RT-PCR testing history, symptoms and illnesses, SARS-CoV-2 exposure history, and masking behaviors in outside venues. Another survey gathered data on the age, sex, race/ethnicity, and RT-PCR testing history of household members.

On September 1 and 2, 2020, HHD went door to door in each block group to inform residents living in the randomly selected households of the seroprevalence investigation. HHD also distributed yard signs, posted information about the project on the City's website and social media channels, and reached out to news media with press releases about the investigation. Field staff re-visited neighborhoods and door-knocked again during September 8-19, 2020 in teams of three persons, which consisted of two HHD staff and one Houston Fire Department (HFD) Emergency Medical Technician/Paramedic. Each household was approached up to three times. For all eligible and interested individuals in the household, field staff obtained written

consent and administered the survey. The paramedics collected a 5 mL blood sample. Blood samples were stored in a cooler and transported to the HHD laboratory. Each participant received a $25 gift card and was entered into a raffle for a $500 gift card. Participants were later notified of their serological testing results via phone and in a letter, if requested.

Laboratory Methods

At the HHD laboratory, samples were centrifuged, and serum was poured into 12x75mm polypropylene tubes, refrigerated, and tested within 72 hours of collection. Samples were analyzed for the presence of COVID-19 antibodies using the Platelia SARS-CoV-2 Total Ab assay (BioRad© Laboratories, Inc., Hercules, California),[17] which is a qualitative Enzyme-linked Immunoassay (ELISA) that detects the presence of IgM, IgA, and IgG antibodies to SARS-CoV-2 (Immunoassay 1). The assay uses a recombinant SARS nucleocapsid protein and employs the principle of one-step antigen capture. The assay was performed on the EVOLIS© automated analyzer according to the manufacturer's package insert. Remnant samples were separated into two aliquots and frozen at -20^{0}C. The sensitivity and specificity of the test, respectively, are 100% and 98.9%.[17]

The sample aliquots analyzed by the BCM laboratory were tested using an in-house optimized IgG anti-S ELISA (Immunoassay 2). In brief, SARS-CoV-2 full S glycoprotein (Novavax, Gaithersburg, MD) was coated onto Immulon 2HB 96-well plates, and the plates were kept moist at 4°C overnight. The following day, the plates were washed and blocked with 5% milk in 1X KPL for one hour in the incubator at 36°C. A standard curve was generated with rabbit SARS-CoV-2-S1 IgG monoclonal antibody in each test plate. Three test samples were added to each plate in

duplicates and, diluted two-fold across the plate and incubated for one-hour. The plates were washed with KPL wash solution and the appropriate horseradish peroxidase (HRP) - conjugated anti-rabbit IgG streptavidin and HRP conjugated anti-human IgG were added at a 1/2000 dilution in 1X KPL to the standard control wells and test sample wells, respectively. After a 1 one-hour incubation period, the plates were washed in KPL wash, followed by addition of substrate (TMB: 3,3′,5,5′-tetramethylbenzidine) for 20 minutes, and the reaction was stopped with 0.16M sulfuric acid. The plates were read at wavelength 450 nm. A four-parameter logistic regression model was used to calculate the relative binding antibody concentrations (µg/mL). The lower limit of detection was 1 µg/mL. The sensitivity and specificity of the assay are 94% and 99%, respectively.

Statistical Analyses

The age, sex, and racial/ethnic distributions of participants were compared with those of the target population using chi-squared tests. The overall estimate was a weighted average of the within stratum estimates, with weights determined by the number of census block groups within each one. Sample strata weights[18-20] were further adjusted to match population demographic characteristics,[21] by gender, race/ethnicity, and age group, and for multiple observations per household. Two immunoassays were used to capture unique (one test was positive) and overlapping (both tests were positive) immune responses following SARS-CoV-2 infection. Immunoassay 1 detected antibody responses to the nucleocapsid protein, the major structural protein of SARS-CoV-2, while Immunoassay 2 measured antibody response to the spike protein, the major surface glycoprotein that induces protective neutralizing antibody. The use of both assays provides a more complete assessment of the population-based seroprevalence.[6] The prevalence of SARS-CoV-2 infection

in the population was estimated using the results from Immunoassay 1 and 2, separately, as well as combined (i.e., if at least one test was positive and then if both tests were positive). Seroprevalence estimates were also computed by sex, age group, and race/ethnicity, as well as by selected variables from the survey (i.e., history of RT-PCR testing, illness episodes, presence of comorbidities, current occupation, and frequency of visits to outside venues).

Applying previous methodology,[8] the number of infections based on the immunoassay results was divided by the cumulative number of positive RT-PCR tests to obtain the degree of under ascertainment of SARS-CoV-2 infection. Counts of infection for the period from January 1 through September 1, 2020 (7 days prior to start of specimen collection for the seroprevalence investigation), restricted to exclude individuals under the age of 5 years, from the HHD electronic disease surveillance system were used in this calculation.

The statistical software R (version 3.6.1, R Foundation for Statistical Computing) and SAS Enterprise Guide (version 7.1, Cary, NC) were used to perform statistical analyses. Two-sided *P* values less than 0.05 were considered statistically significant.

Results

Recruitment and Participant Characteristics

In total, 678 residents living in 428 households were enrolled after visiting on average, 53 households per block group. For both strata combined and for residents living in census block groups in the low positivity stratum, based on chi-squared goodness of fit tests, the sample and target populations had similar age, race/ethnicity, and sex profiles (see Table 1) ($p > 0.05$). In the high positivity stratum,

there was a greater proportion of individuals ages 5 to17 in the target population as compared to the sample population (p=0.04).

Serological Testing

Of the 678 residents on whom venipuncture was performed, blood samples for 6 residents could not be tested using either immunoassay; another 6 individuals had a result from just one of the two antibody tests. In total, 89 individuals tested positive based on Immunoassay 1 (27 in the low positivity stratum and 62 in the high positivity stratum), and 84 individuals tested positive based on Immunoassay 2 (26 in the low positivity stratum and 58 in the high positivity stratum). There was good agreement (96%) between Immunoassay 1 and Immunoassay 2 (see Supplementary Table 1).

Population-based estimates of seroprevalence for SARS-CoV-2 in Houston for individuals ages 5 years and older were 13.5% (95% CI: 9.0%-18.1%) and 12.9% (95% CI: 8.0%-17.7%) using Immunoassays 1 and 2, respectively (Table 2). Differences were detected between the low and high positivity strata: 9.6% (95% CI: 3.6%-15.7%) and 17.7% (95% CI: 10.9%-24.6%), respectively based on Immunoassay 1 and 9.1% (95% CI: 2.5%-15.6%) and 17.0% (95% CI: 9.8%-24.1%) for Immunoassay 2. Higher seroprevalence was observed among females, Hispanic Whites, and non-Hispanic Blacks as compared to other racial ethnic groups and among individuals under the age of 40. Supplementary Table 2 reports on seroprevalence estimates on the basis of history of RT-PCR testing, illness episodes, presence of comorbidities, occupation, and venues visited outside the home. Seroprevalence was 31.8% (95% CI:20.3-43.2) among individuals reporting at least one illness from January 15, 2020 to the time of blood sampling as compared

to 10.0% (95% CI: 3.9-16.2) who had no illnesses. Differences in seroprevalence were also noted for individuals who received a RT-PCR test, 26.1% (95% CI: 15.0-37.2), as compared to those who did not, 8.2% (95% CI:1.5-15.0). Finally, in analyses when results for both tests were combined in computing seroprevalence, estimates were slightly higher (14.2%, 95% CI: 9.4%-19.0%) assuming seropositivity if at least one test produced a positive result and slightly lower (12.3%; 95% CI: 8.1%-16.5%) assuming seropositivity only when both test results were positive. See Supplementary Table 3 for a breakdown of these results.

Under ascertainment in Seroprevalence based on RT-PCR Testing Results

Figure 2, adapted from Havers et al,[8] provides the time course of SARS-CoV-2 Infection (RT-PCR testing results) in Houston from January – November 4. There was over a four-fold increase in prevalence of infection when comparing the testing results from Immunoassays 1 and 2 to the surveillance of reported cases from RT-PCR testing results (see Figure 3 and Supplementary Table 4).

Discussion

This investigation was undertaken on behest of local public health officials to estimate the proportion of residents living in the fourth largest city of the U.S. who had been infected with SARS-CoV-2. Using a two-stage complex sampling design, a random sample of individuals living in households in Houston, stratified into areas with low- and high positivity rates, completed questionnaires and provided blood samples between September 8 and September 19, 2020. Blood samples were assayed using two different antibody tests, one targeting the nucleocapsid protein and the other the full S glycoprotein, both of which have excellent performance

characteristics. During this period, seroprevalence was estimated around 14% with similar results from the two serological assays that were performed.

Our community-based seroprevalence findings calculated an under ascertainment in SARS-CoV-2 cases based on RT-PCR testing results. For each RT-PCR positive SARS-CoV-2 case there were approximately 3 additional cases that were under reported based on the number of infections identified using the two immunoassays. Although RT-PCR testing is the gold standard for identifying an acute SARS-CoV-2 infection based on the detection of viral RNA, an immunoassay can provide a more comprehensive assessment of past and recent infections. This is because it relies on measuring the host antibody response that remains detectable for a prolonged period of time rather than viral RNA that is cleared rapidly during the acute infection. The under- ascertainment case ratio can provide a valuable tool for estimating the overall prevalence of SARS-CoV-2 infection based on the cumulative number of RT-PCR positive cases in the community.

Our findings confirm a two-fold difference in infection in areas with high (17.7%) versus low (9.6%) RT-PCR positivity rates. This is consistent with the persistent spatial variation in positivity rates that the HHD observed across the city since the start of the pandemic. Findings also indicate that case-based surveillance that relies on RT-PCR tests underestimates the level of SARS-CoV-2 infectivity in the city, as has been reported in a previous investigation that relied on residual sera collected in 10 sites across the U.S.[8]

The sampling design employed, based on disaster research principles[15], has advantages in providing methodology for a rapid public health response in the face of an emergency and results that allow for inferences to the target population.[22] In

Houston, considerably higher seroprevalence estimates were observed as compared to investigations conducted earlier in the pandemic both in and outside of the U.S. that employed a similar design, e.g., in Atlanta[12] or Spain.[6] The only investigation to report a greater proportion (22.7%) of individuals with SARS-CoV-2 infection was in a convenience sample in New York in April 2020,[7] which may not have been representative of the general population.

While other studies have reported geographic variation within a state[7] or across regions of the U.S,[8] this investigation reported different levels of seroprevalence within a single urban area, stratified by positivity rate. This difference is similar to a previous study conducted in May 2020 that found varying levels of current and active infection by zip code in two parishes in Louisiana.[13] Similar to investigations elsewhere in the U.S.,[7, 11-13] there were significant disparities in SARS-CoV-2 infection with approximately 3.4 and 2.9 fold-increases in estimated SARS-CoV-2 seroprevalence among Hispanics and non-Hispanic blacks as compared to non-Hispanic whites. In contrast, seroprevalence was considerably higher among females and among younger age groups than reported in an investigation in Atlanta, Georgia in spring 2020.[12] These findings suggest important groups for outreach to mitigate infection and its spread. As expected, we also found higher seroprevalence among individuals who received RT-PCR testing and among persons who reported at least one illness during the period, January 15, 2020 to the time of the blood draw.

Limitations

While we employed a stratified two-stage clustered sampling strategy to collect a random sample, the sampling frame did not extend to hospitalized patients or residents of nursing homes, group homes, or prisoners where outbreaks have occurred[23] [24] and, hence, inferences are restricted to non-hospitalized individuals living in non-congregate settings. Owing to the cross-sectional nature of the investigation, the degree to which antibodies persist could not be evaluated. However a follow-up study is planned with participants who tested positive for antibodies in the first wave, which should inform questions about the persistence of antibodies following SARS-CoV-2 infection.

Conclusions

In September 2020, approximately 14% of individuals living in the fourth largest city in the U.S. have been infected with SARS-CoV-2. The estimated seroprevalence is greater than that estimated based on RT-PCR data. Results highlight the importance of public health measures like physical distancing, wearing of face coverings, and hand hygiene to mitigate future transmission of SARS-CoV-2. Taken together, HHD's programs for both RT-PCR and antibody testing, will provide them with tools to continue to monitor and mitigate risks of the COVID-19 pandemic in Houston and inform plans for vaccine distribution.

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Footnote Page

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Table 1. Characteristics of the Sample and Target Populations, SARS-CoV-2 Seroprevalence Investigation, Houston, TX, September 2020.

	Participants			Target Population[a]		
	Overall	Low Positivity Rate Stratum	High Positivity Rate Stratum	Overall	Low Positivity Rate Stratum	High Positivity Rate Stratum
No. of households	428	214	214	783,740	429,769	353,971
Demographic Data						
No. (%) of individuals	678	319 (47.1)	359 (52.9)	1,711,199	852,827 (49.8)	858,372 (50.2)
Sex, No. (%)[b]						
Female	376 (55.5)	169 (53.0)	207 (57.7)	850,286 (49.7)	432,985 (50.8)	417,301 (48.6)
Male	302 (44.5)	150 (47.0)	152 (42.3)	860,913 (50.3)	419,842 (49.2)	441,071 (51.4)
Race/Ethnicity, No. (%)						
Hispanic	304 (44.8)	77 (24.1)	227 (63.2)	839,271 (45.3)	260,935 (28.5)	578,336 (61.7)
Non-Hispanic White	203 (29.9)	160 (50.2)	43 (12.0)	467,688 (25.2)	386,550 (42.2)	81,138 (8.7)
Non-Hispanic Black	108 (15.9)	45 (14.1)	63 (17.5)	383,953 (20.7)	162,802 (17.8)	221,151 (23.6)
Other	63 (9.3)	37 (11.6)	26 (7.2)	161,944 (8.7)	104,768 (11.4)	57,176 (6.1)
Age group (y), No. (%)[b]						
5-17	62 (9.1)	23 (7.2)	39 (10.9)	314,034 (18.4)	130,831 (15.3)	183,203 (21.3)
18-39	214 (31.6)	104 (32.6)	110 (30.6)	667,621 (39.0)	333,843 (39.1)	333,778 (38.9)
40-59	227 (33.5)	102 (32.0)	125 (34.8)	446,600 (26.1)	226,079 (26.5)	220,521 (25.7)
60 and older	175 (25.8)	90 (28.2)	85 (23.7)	282,944 (16.5)	162,074 (19.0)	120,870 (14.1)
Median MHI, $[c]	50,225	69,354	39,937	47,780	73,750	36,943
Mean MHI, $[c]	67,397	90,700	44,093	64,322	87,090	39,683

Median, % of households living below poverty level[c]	15.2	11.4	19.4	17.3	9.3	24.9
Mean, % of households living below poverty level[c]	18.1	13.3	22.9	19.1	12.8	25.9

[a] Individuals living in the sampling frame of 1,109 Census block groups that fell within the jurisdiction of the HHD.
[b] Age restricted to population 5 years and older.
[c] MHI: Median Household Income, values specific to the sample of 60 block groups, taken from 2018 American Community Survey (ACS) 5-year estimates.[15]

Table 2. Estimated Prevalence of SARS-CoV-2 Infection, by Sociodemographic Characteristics, Houston, Texas, September 2020.

	Participants, % Seropositive[a]			Prevalence Estimates, Immunoassay 1 % (95% CI)[b,c]			Prevalence Estimates, Immunoassay 2 % (95% CI)[b,c,d]		
	Overall	**Low Positivity Rate Stratum**	**High Positivity Rate Stratum**	**Overall**	**Low Positivity Rate Stratum**	**High Positivity Rate Stratum**	**Overall**	**Low Positivity Rate Stratum**	**High Positivity Rate Stratum**
Overall	13.1	8.5	17.3	13.5 (9.0-18.1)	9.6 (3.6-15.7)	17.7 (10.9-24.6)	12.9 (8.0-17.7)	9.1 (2.5-15.6)	17.0 (9.8-24.1)
Sex									
Female	14.1	8.9	18.4	16.9 (10.4-23.5)	9.4 (2.5-16.4)	25.1 (13.7-36.5)	17.0 (9.8-24.2)	9.0 (1.3-16.8)	25.6 (13.2-37.9)
Male	11.9	8.0	15.8	10.3 (6.0-14.5)	9.8 (2.9-16.8)	10.7 (5.9-15.5)	8.9 (4.9-12.9)	9.1 (2.8-15.4)	8.8 (4.0-13.5)
Race/Ethnicity									
Hispanic	20.7	16.9	22.0	18.4 (8.3-28.6)	14.6 (0.0-31.6)	22.6 (12.1-33.1)	18.1 (8.1-28.1)	13.5 (0.0-29.7)	23.1 (12.0-34.2)
Non-Hispanic White	3.9	3.1	7.0	5.4 (0.0-10.7)	4.4 (0.0-10.0)	6.5 (0.0-15.8)	4.5 (0.0-10.4)	4.5 (0.0-12.0)	4.4 (0.0-13.8)
Non-Hispanic Black	14.8	17.8	12.7	15.4 (4.6-26.2)	17.7 (0.0-36.2)	12.8 (2.6-23.0)	13.3 (2.2-24.5)	16.2 (0.0-35.7)	10.2 (0.4-20.0)
Other	3.2	2.7	3.8	3.8 (0.0-9.6)	4.1 (0.0-11.9)	3.5 (0.0-12.0)	1.3 (0.0-5.9)	3.5 (0.0-12.3)	-
Age group (y)									
5-17	19.4	17.4	20.5	17.7 (5.3-	14.1 (0.0-	21.6 (8.1-	18.0 (4.6-	14.1 (0.0-	22.2 (7.6-

				30.1)	34.4)	35.2)	31.3)	35.9)	36.8)
18-39	16.4	12.5	20.0	15.8 (9.0-22.6)	13.2 (3.6-22.8)	18.6 (8.9-28.4)	14.6 (7.8-21.4)	12.4 (3.0-21.7)	17.0 (7.0-27.0)
40-59	13.2	6.9	18.4	10.7 (5.4-15.9)	4.9 (0.0-11.0)	16.9 (8.1-25.7)	9.3 (4.1-14.5)	3.8 (0.0-9.9)	15.3 (6.7-24.0)
60 and older	6.9	3.3	10.6	8.0 (2.0-13.9)	5.4 (0.0-13.9)	10.7 (2.4-19.1)	8.5 (1.6-15.4)	5.5 (0.0-15.9)	11.7 (2.8-20.7)

[a] Based on Immunoassay 1 results.
[b] All prevalence estimates adjusted to the age, sex, and race/ethnicity distributions of the target population and for multiple observations per household.
[c] Lower confidence limits with negative values are truncated to 0.0.
[d] Prevalence estimates obtained using Immunoassay 2 are further adjusted for test performance characteristics (sensitivity, 94%; specificity 99%).

Figure Titles

Figure 1. Map of Sample and Target Population (Census Block Groups), Seroprevalence Investigation, Houston, Texas, September 2020.

Figure 2. Time course of SARS-CoV-2 Infection (RT-PCR testing results), January 1-November 4, 2020, Houston, Texas (figure adapted from Havers et al[8]).

Figure 3. Estimated Degree of Under Ascertainment in SARS-CoV-2 Infection based on Case Surveillance[a].

[a] Degree of under ascertainment is computed by dividing the population-based estimates of SARS-CoV-2 infection divided by the number of cumulative positive RT-PCR tests, January-September 2020.

[b] Both: analysis conducted for when both immunoassay results were positive. Either: analysis conducted for when either immunoassay results were positive.

Figure 1

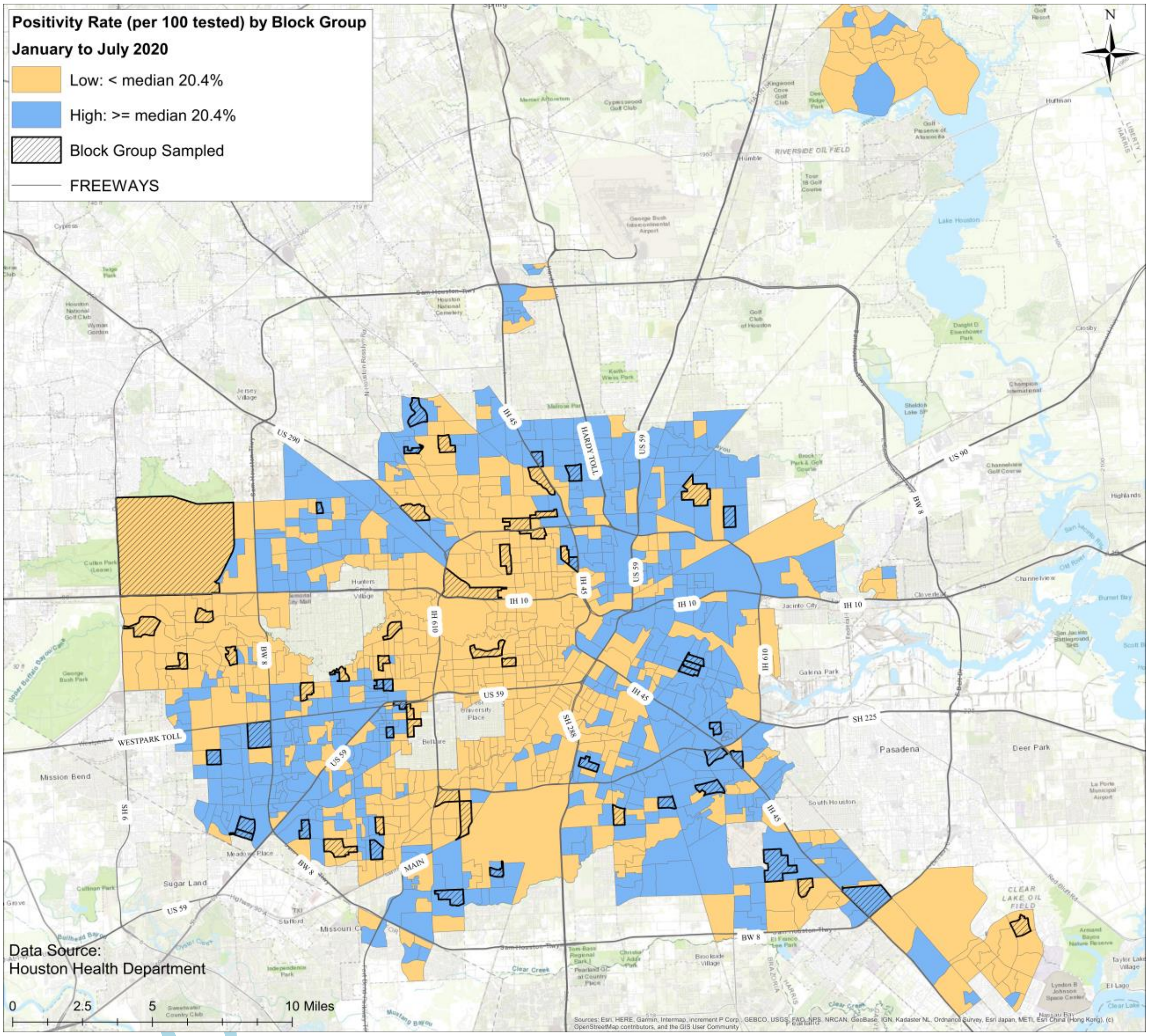

Positivity Rate (per 100 tested) by Block Group
January to July 2020
Low: < median 20.4%
High: >= median 20.4%
Block Group Sampled
FREEWAYS
Data Source:
Houston Health Department
0
2.5
5
10 Miles
N
US 290
IH 45
HARDY TOLL
US 59
IH 10
IH 610
BW 8
WESTPARK TOLL
SH 288
SH 225
MAIN
US 90
SH 6
Pasadena
Deer Park
Mission Bend
Sugar Land
Bellaire

Figure 2

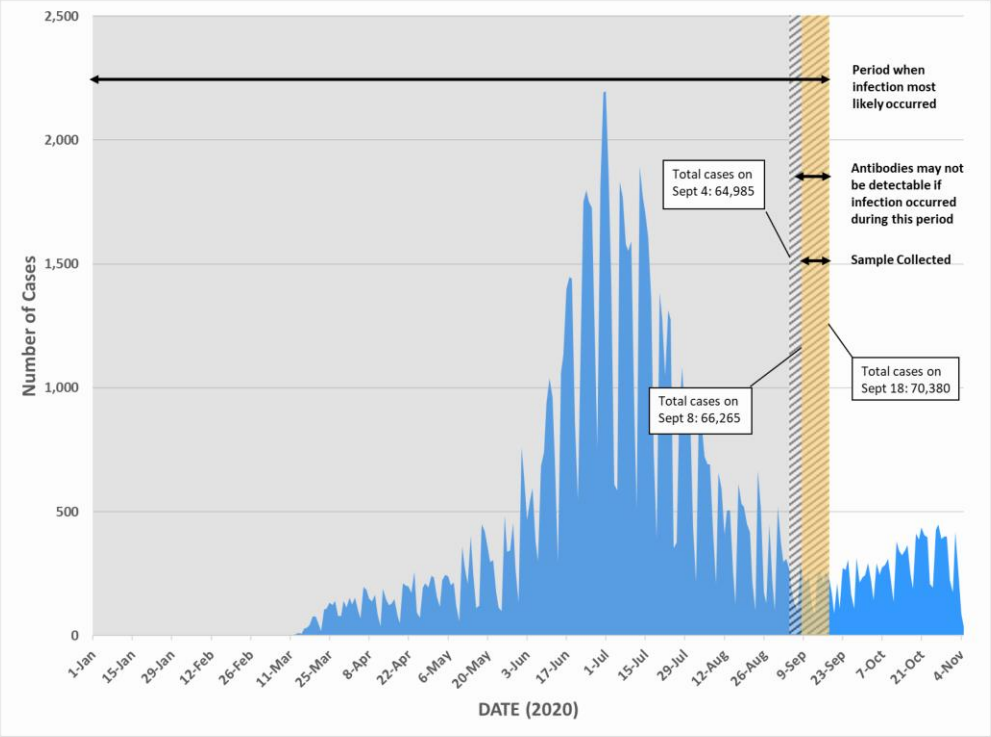
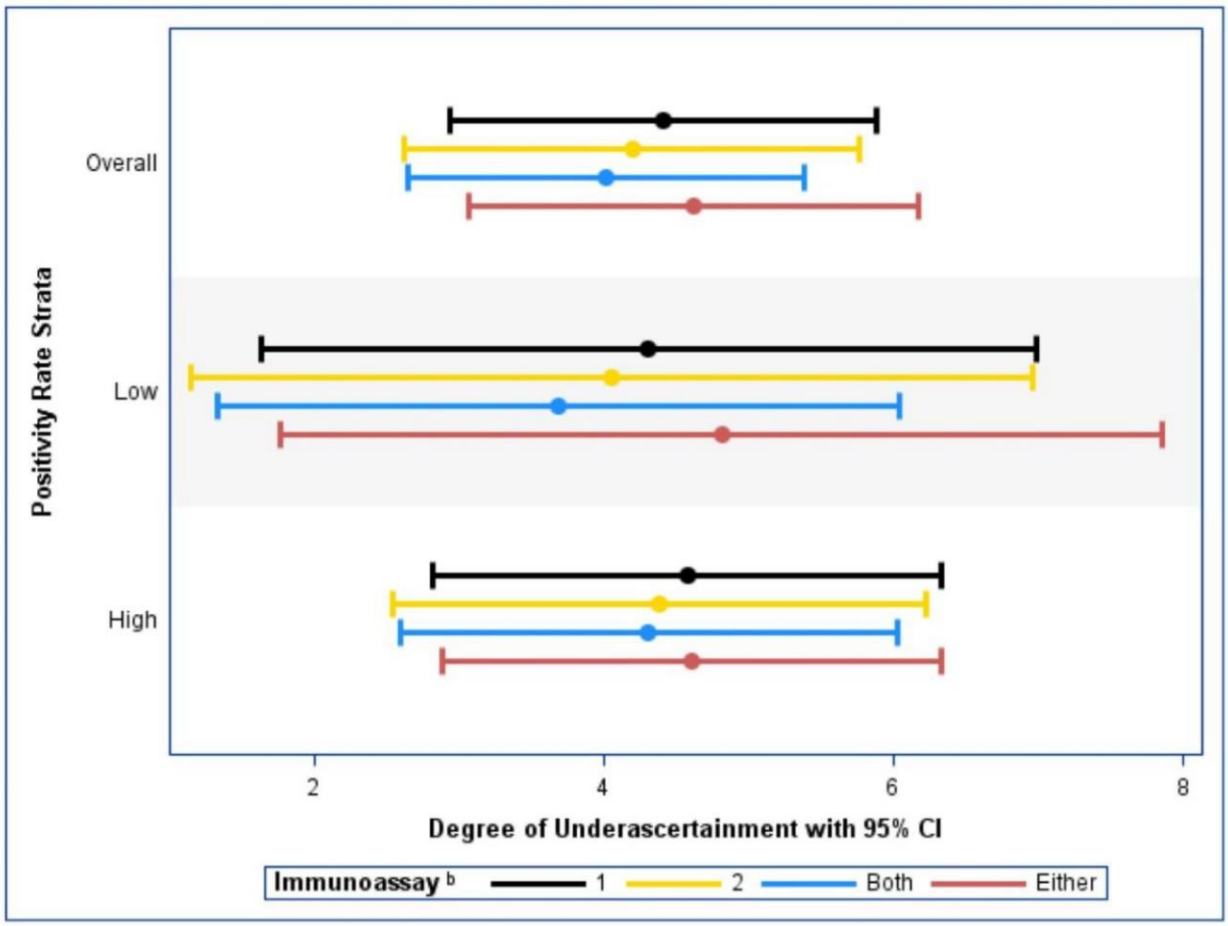


Figure 3



[a] Degree of under ascertainment is computed by dividing the population-based estimates of SARS-CoV-2 infection divided by the number of cumulative positive RT-PCR tests, January-September 2020.

[b] Both: analysis conducted for when both immunoassay results were positive. Either: analysis conducted for when either immunoassay results were positive.