King County, Washington Anti-SARS-CoV-2 Seroprevalence Survey, August 2020

Karen D. Cowgill, PhD, MSc, University of Washington Departments of Global Health and Health Services, School of Public Health

Elena A. Erosheva, PhD, University of Washington, Department of Statistics, School of Social Work, and the Center for Statistics and the Social Sciences

Adam Elder, PhD student, Department of Biostatistics, University of Washington, School of Public Health

Susan Buskin, PhD, Public Health – Seattle & King County and University of Washington, Department of Epidemiology, School of Public Health

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Introduction

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the virus that causes COVID-19, has been circulating in western Washington state since at least late January 2020.[1] Polymerase chain reaction (PCR) testing to detect active infection was limited in the early months of the outbreak, and access to and use of testing has been uneven around King County, with lower rates of testing among underrepresented racial and ethnic groups and in the southern part of the county through July 2020.[2] The true number of infections in King County residents since late January 2020 is unknown. Mathematical models based on detected cases of active infection along with other sources of data have produced estimates that are 10 or more times higher than reported cases in other parts of the United States (US).[3,4] This seroprevalence survey aimed to help understand the true number of infections in King County as of August 2020 by measuring the proportion of residents who had evidence of past infection with SARS-CoV-2.

OBJECTIVES

The primary objectives of this survey were to:

1) Estimate the prevalence of antibody to SARS-CoV-2 among the 2.2 million residents of King County, Washington and

2) Explore which groups bear a higher burden of disease by estimating cumulative incidence in subgroups of the population stratified by, e.g., age, sex, and race/ethnicity.

Secondary objectives were to:

3) Identify modifiable risk factors using a social seroepidemiologic approach, and

4) Assess virulence by calculating the symptomatic proportion of cases and ratio of severe disease among those with evidence of past infection with SARS-CoV-2.

Methods

Survey design

A cross-sectional address-based household survey with random and non-random (convenience) samples to measure anti-SARS-CoV-2 prevalence at a single time.

Sample size

We anticipated a seroprevalence of about 2.5%, so we aimed to complete surveys from 800 households to obtain a reasonably precise estimate.

Sampling methodology

Participating households were recruited via two strategies: a random sample and a non-random sample. The random sample was a stratified probability sample of 5,000 households with an oversampling of households from selected census block groups (CBGs) with a high density (30% or more) of households where at least one member identified as Black/African American or, separately, Hispanic/Latinx. This random sample was supplemented by a non-random sample to aim for a target of at least 50 households with at least one member who identified as Native Hawaiian/Pacific Islander and 50 households with at least one member who identified as American Indian/Alaska Native.

For the random samples, we contracted with a survey firm (Marketing Systems Group, www.M-S-G.com) to pull an address-based sample (ABS) that met these requirements and then sent postcards in English and Spanish inviting 2,500 randomly sampled households from targeted CBGs for African American and Hispanic households (1,250 each) and 2,500 randomly sampled households from the remaining CBGs to participate in our study; the postcards also had short messages in Korean, Simplified Chinese, Amharic, Somali, and Vietnamese, languages identified by the Public Health Seattle & King County (PHSKC) Language Liaison to be the most relevant for recruiting a representative sample. For the additional non-random sample of households from underrepresented groups, we enlisted the help of community-based organizations (CBOs), including Community Health Centers and other participants in the weekly PHSKC Community Health Services COVID-19 and Racial Equity call and the PHSKC Community Mitigation Response Group, for recruitment.

Survey location

Households in King County, Washington were eligible for the survey. King County includes the city of Seattle and other large cities, as well as smaller cities and towns and unincorporated and rural areas, across an area of 2,307 square miles.

For the address-based random sample, fixed specimen collection sites were in north Seattle (Aurora) on August 9th and 16th, south Seattle (SoDo) on August 9th, south King County (Federal Way) on August 8th, and on the east side of the county (Eastgate) on August 15th. Mobile teams wearing personal protective equipment collected specimens outdoors at the homes of participants not able to attend the fixed sites during the weeks of August 10th-14th and 17th-21st.

For the non-random sample, there were two fixed-site events: a small-scale one in Seattle on August 26th, and a large-scale one at Tyee High School south of Seattle (SeaTac) on August 29th.

Survey population

King County's total population in 2020 was about 2.26 million,[5] nearly one quarter of Washington State's population. The address-based sample included residents living at selected non-institutional addresses; households of any size, including single people, were eligible to participate.

We received a list of addresses of 5,000 households to which we mailed postcards. Landline and/or cell phone numbers were appended to just over half the postal addresses, and 22% had email addresses as well. We sent text messages to cell phones and email messages to email addresses inviting participation. A professional call center called the landline numbers and volunteer callers from the Public Health Reserve Corps (PHRC) called cell phone numbers. If the person at the cell or landline phone number answered and lived in King County, they were considered eligible to participate whether or not they lived at the address associated with that number or were the person named in the address-based sample list.

Community outreach and engagement

The survey page on the PHSKC website had information about the survey, a link to the online questionnaire, and Frequently Asked Questions in English, Spanish, Amharic, Simplified and Traditional Chinese, Korean, and Vietnamese. Survey organizers reached out to organizations representing individual American Indian tribes in King County as well as to the Urban Indian Health Initiative and the Seattle Indian Health Board in an effort to oversample this population.[6] A member of the Pacific Islander community spread word about the survey through social networks and on the Radio Tonga livestream show (https://www.facebook.com/RadioTongaSeattle). The PHSKC Equity Response Team gave feedback on the draft questionnaire. The survey was featured in a weekly Spanish livestream on COVID-19 and in email information and/or presentations to community health boards, community navigators, participants in the weekly PHSKC Community Health Services COVID-19 and Racial Equity call, and members of the PHSKC Community Mitigation and Response Group. PHSKC Communications advertised the August 29th event on social media and in the PHSKC Public Health Insider blog.

Data collection

The questionnaire collected information on demographics, COVID-19 symptoms and illness episodes, medical history, and social risk factors for COVID-19 illness and was available online in English and Spanish. It was based on a survey instrument from the Centers for Disease Control and Prevention's COVID-19 Community Seroepidemiological Investigation[7] and on the first version the Social Risk Factors for COVID-19 Exposure Survey, posted May 21, 2020. This latter was designed by "researchers from the Harvard T.H. Chan School of Public Health interested in understanding in what settings people are exposed to SARS-CoV-2 (the virus causing COVID-19), especially as it relates to racial, ethnic and socioeconomic disparities in infection risk. [They] designed a survey to measure SARS-CoV-2 exposure risk in the household, on transportation, and at the workplace that can be used in conjunction with serological testing to identify risk factors for and modifiers of exposure," and adapted questions from the American Community Survey, U.S. Census Bureau 2020 COVID-19 Household Pulse Survey, and the John Hopkins University COVID-19 Community Response Survey.[8]

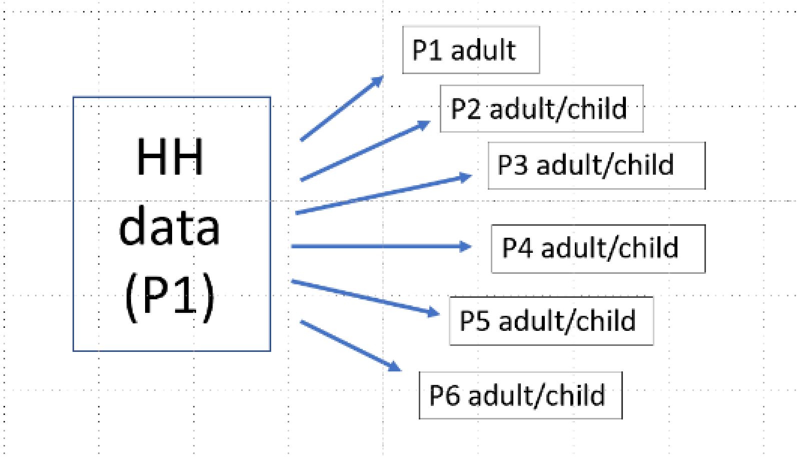


Figure 1. Database architecture, King County, WA COVID-19 Antibody Testing Survey, August 2020

The questionnaire was designed to allow for responses from up to six members of participating households, with the first adult member (Person 1, or P1) completing an initial household questionnaire and an individual questionnaire and up to five other adult or child members (P2-P6) completing individual questionnaires (see Figure 1). Each consenting adult HH member was to complete an individual questionnaire or have one completed for them if they were unable to complete it themselves. Adolescents (ages 13-17) who gave assent and whose parents or guardians consented were to either complete an individual questionnaire themselves or have one completed for them, and parents or guardians who consented were to complete one for their children younger than 13.

The survey questionnaire was entered into REDCap (Institute of Translational Health Sciences, Seattle, WA, USA), with a link via the PHSKC website for participants to complete the survey on a mobile device or computer. For participants who were not able to or who chose not to complete the survey themselves, there was a back-up option to complete it by phone. For the address-based sample, the first adult member of the household completed a household questionnaire and scheduled an appointment at one of the fixed sites or requested a visit from a mobile team for collection of blood specimens from consenting/assenting household members or children. The process was the same for the non-random sample, except that instead of requesting appointments, participants were invited to attend one of the two fixed sites on specified dates, and no home visits were offered.

Phone interpretation services were available for those who spoke a language other than English or Spanish.

Accessibility

Participants from the address-based sample had the option to provide blood specimens by fingerstick at either a fixed site or by a mobile team, so those who were unable to get to a fixed site on the designated dates or times could still arrange to participate.

Survey materials were available in English and Spanish; speakers of other languages and those who are visually impaired, do not have Internet access, or have low literacy had the option to participate by phone with the help of an interviewer and interpreter, as needed.

Data management

All data generated from this survey were managed and stored according to established data management principles. Confidentiality and security methods included confirming that all project staff and PHRC volunteers had been trained in protecting participant confidentiality and had signed a workforce agreement laying out the best practices for security and confidentiality and the consequences for data breaches. All electronic data are stored in password-protected locations and stored on a HIPAA-compliant site at the University of Washington's Institute of Translational Health Sciences (www.iths.org).

Ethical considerations

This survey was a public health activity per the King County Health Officer and as such was not subject to institutional review board review or oversight. Nonetheless, human subjects protections were implemented, including consent from all adult participants and assent from minors, the right to refuse or withdraw from participation, and protection of confidential health information. Each household that completed the survey (including providing a blood specimen) received a $20 grocery gift card to acknowledge the time and inconvenience of participating.

Specimen collection and storage

Survey staff collected blood specimens from participants via fingerstick. Four to five blood spots (a total of 240-350 microliters) were collected on a filter-paper card and dried and shipped overnight to the testing laboratory, Molecular Testing Labs (MTL) in Vancouver, Washington. Some 142, or 10%, of the dried blood spot specimens collected could not be tested by the lab because the quantity of blood collected was insufficient. We were able to re-contact and collect second specimens from 63 people, but there were 79 participants whose specimens could not be tested.

Specimen testing

Upon receipt at MTL, the DBS were eluted and tested via a validated in-house adaptation of the Bio-Rad Platelia qualitative ELISA for total antibody (IgG, IgA, IgM) against the nucleocapsid protein of SARS-CoV-2.[9] All samples that were positive by this first assay were then tested using a validated in-house adaptation of the EuroImmun qualitative ELISA for IgG against the spike protein of SARS-CoV-2.[10] The unweighted count of participants positive for antibody to SARS-CoV-2 was 33; an additional nine were positive only on the first assay.

Results sharing and use

Individual participants received a printed report of their test results by postal mail. The lab notified Washington State Department of Health of positive antibody test results, including identifying information as required by Washington Administrative Code.

Data analysis

We extracted demographic variables for each responding household member and sent a cleaned, de-identified version of this dataset to M-S-G, where a weighted sequential hot-deck procedure was used to impute missing values for the demographic variables (age group, race, ethnicity, education, income, and household size). The random and non-random samples were combined for the analysis. M-S-G used the dual frame where the random (address-based) sample and the non-random sample were assigned initial uniform weights to generate adjusted sampling weights for each household and individual participant via raking. Specifically, raking was done to King County's population data on sex, age group, income, race, and Hispanic status distributions. The weights adjusted for non-response and under-coverage.

The weighted data were used to obtain seroprevalence estimates. Only individuals who tested positive on both tests were counted as positive. This combination assumes that the tests are independent conditional on each individual's true status and allows us to treat this sequential testing procedure as a single test (see Table 1). These estimates were adjusted for missingness on the response variable – as noted above, 79 participants' blood specimens were insufficient for testing –-- and the combined sensitivity and specificity of the sequential antibody assays. In addition, statistical adjustments were considered to correct for the fact that individuals in the non-random sample were more likely to have had a COVID-19-like illness; however, these adjustments are not included in our best estimate due to the lack of suitable population benchmarks. Detailed statistical methods are presented in Appendix 2.

Table 1 Performance of Serial Antibody Assays, King County, Washington anti-SARS-CoV-2 seroprevalence survey, August 2020

Test	**Negative percent agreement (specificity)**	**Positive percent agreement (sensitivity)**
Bio-Rad Ab test[9]	99.56%	92.16%
EuroImmun ELISA (IgG)[10]	100%	90%
Sequential Test[11]	100%	82.94%

Results

Our best overall estimate of anti-SARS-CoV-2 prevalence in King County as of August 2020 is 3.9% (95% confidence interval (CI) 2.4%-6.0%). Based on our analyses comparing the random and the non-random samples, it is likely that our best estimates are slightly biased upward. See Appendix 2 for details.

Subgroup analysis by race, sex, income, and age group are calculated using the adjustments described in Appendix 2 and are based on a single imputation of missing values. In the original dataset, the proportion of missing values among key demographic variables ranged from 0-46% (see Table 2) due to errors in the design of the online questionnaire that allowed respondents to skip some demographic information questions that were intended to be required.

Table 2. Percent of Missing Values, King County, Washington anti-SARS-CoV-2 seroprevalence survey, August 2020 (n = 1,364)

Variable	Percent Missing
Sex	0*
Age Category	3.15
Income	9.09
Race	11.00
Ethnicity	45.53

**Sex was a required field for laboratory testing*

During the initial survey phase through August 16th, 860 households from the address-based sample initiated the online questionnaire, of which 417 (48.5%) completed the survey (i.e., completed the questionnaire and provided a blood specimen). After August 16th, 844 households in the non-random sample initiated the questionnaire, of which 310 (36.7%) completed the survey. Overall, there was a total of 727 participating households with an average of 1.88 participating individuals per household. There were 3,163 individual questionnaire starts online, of which 1,364 (43.1%) are associated with laboratory results. Taking into account missingness and household clustering, the effective sample size was 589.

Race

The number of participants identifying as Native Hawaiian or Other Pacific Islanders and American Indian or Alaska Natives and the number of participants for whom information about Hispanic ethnicity was available were too low to generate separate estimates for these groups. Thus, people of Hispanic ethnicity are represented only by race, and those who identified as Native Hawaiian or Pacific Islander and American Indian or Alaska Native are subsumed in the ‘Other’ category. The unweighted proportion of participants by race after imputation compared to the proportions in King County are shown in Table 3.

Table 3: Proportion of participants by race, King County, Washington anti-SARS-CoV-2 seroprevalence survey, August 2020

Race	King County 2020	Unweighted Survey Sample
White	66.1%	69.9%
Black or African-American	7.2%	6.0%
American Indian or Alaska Native	1.0%	--*
Asian	19.3%	20.5%
Native Hawaiian or Other Pacific Islander	0.9%	--
Two or more races	5.5%	--
Other	-	3.7%

**numbers in these categories were small and were collapsed into the 'Other' category before imputation of missing values*

Prevalence estimates and the associated 95% confidence intervals for participants identifying as White, Black, and Asian are shown in Table 4 and in the accompanying plot (Figure 2). Prevalence point estimates were approximately seven times higher in those identifying as Black and Other than in those identifying as White, though due to the small sample sizes in these groups, the confidence intervals are wide. Estimated point prevalence was slightly higher in those reporting male sex than in females (Table 4 and Figure 3), although more females participated. Estimated point prevalence was more than four and a half times higher in those who reported their 2019 household income was at or below $100,000 as in those with incomes above $100,000 (Table 4 and Figure 4). Finally, point prevalence estimates varied substantially by age group and suggest that seroprevalence was highest in the 16-25-year age group (Table 4 and Figure 5).

Table 4 Weighted Prevalence Estimates for anti-SARS-CoV-2, King County, Washington anti-SARS-CoV-2 seroprevalence survey, August 2020

	Unweighted Number (*number missing and imputed*)	Unweighted Percentage	**Weighted Prevalence Estimate (95% CI)**
Total	1364	100%	**3.91 (2.35-5.96)**
Race			
White	953 (*110*)	69.9%	**1.74 (1.02-3.57)**
Black	82 (*6*)	6.0%	**11.78 (7.25-24.77)**
Asian	279 (*25*)	20.5%	**2.35 (1.05-7.41)**
Other	50 (*9*)	3.7%	**12.96 (7.53-33.10)**
Sex			
Male	650 (*0*)	47.7%	**4.39 (2.99-8.50)**
Female	714 (*0*)	52.3%	**3.42 (2.37-7.38)**
Income[1]			
At or below $100,000	585 (*57*)	42.9%	**7.34 (4.96-13.99)**
Above $100,000	779 (*67*)	57.1%	**1.57 (0.94-3.48)**
Age Group			
65 - < 100	206 (*8*)	15.1%	**3.01 (1.32-9.31)**
45 - < 65	391 (*10*)	28.7%	**4.87 (3.03-11.14)**
25 - < 45	488 (*12*)	35.8%	**2.21 (1.19-5.25)**
16 - < 25	108 (*4*)	7.9%	**12.89 (6.42-32.74)**
0 - <16	171 (*9*)	12.5%	**1.59 (0.28-5.85)**

Figure 2

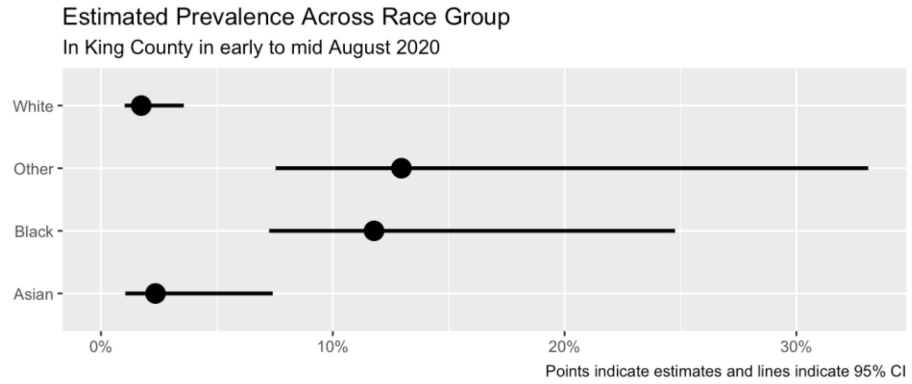


Figure 3

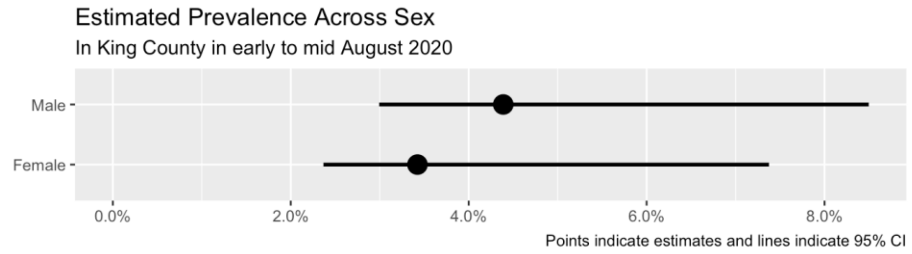


Figure 4

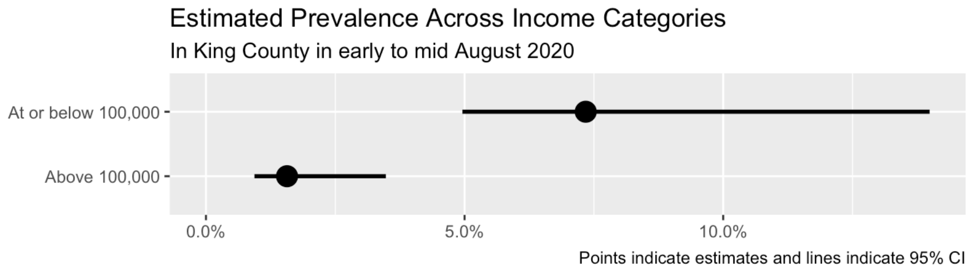
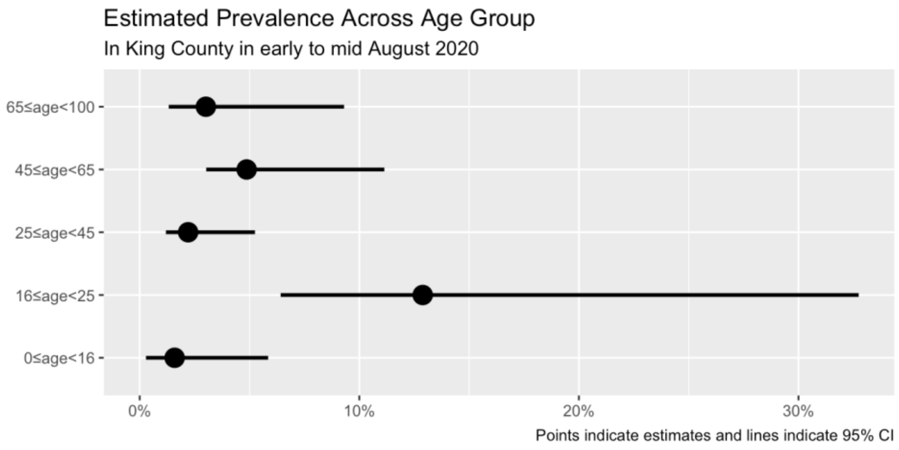


Figure 5



Discussion

Our best estimate of the proportion of King County residents with antibodies against SARS-CoV-2, the virus that causes COVID-19, in August 2020 is about 4%, or 90,000 people. Based on our analyses from comparing the random and the non-random samples, it is likely that our best estimates are slightly biased upward. However, this correction is not presented in the main analysis since the extent of this bias is uncertain. Vaccines were still in clinical trials at the time of this survey and therefore none of the participants would have received a vaccine against COVID-19 unless they were participants in a clinical trial. The first antibody assay in the serial testing algorithm detected total antibody to the nucleocapsid protein, which is generated by natural infection, but not by vaccination, so we are confident that this estimate reflects natural infection and not vaccine-induced immune response.

A total of 18,060 positive test results for SARS-CoV-2 had been reported to King County through August 15, 2020, the midpoint of our survey.[2] Assuming each of these represented a unique test result of a King County resident, the reported period prevalence of infection up until that date was at most 0.8% of the county's population; our survey thus suggests that viral testing was underestimating incidence by a factor of about five. There were 2,192 hospitalizations and 698 deaths through August 15th,[2] suggesting the proportion of cases that were serious (based on hospitalization) or fatal was 2.4% and 0.8%, respectively.

As expected, prevalence varied by subgroup. We saw that households reporting incomes at or below $100,000 in 2019 had nearly five times higher estimated antibody prevalence than those with incomes above $100,000. Data on race and ethnicity were limited but indicated that those reporting non-White race had roughly seven times higher estimated antibody prevalence than those reporting White race. This survey was noteworthy for including people of all ages; our data suggest that older teens and young adults in King County had higher antibody prevalence at the time of this survey than did people of other ages, and younger children had the lowest prevalence. Note that the goal of the subgroup analysis was to explore which groups bear a higher burden of disease, but these group-to-group comparisons are purely exploratory and thus these analyses do not contain statistical significance statements that would support cross-group comparisons.

This is the first data-based local estimate of anti-SARS-CoV-2 seroprevalence for King County. Our estimate is somewhat higher than those from others generated around the same time. National commercial laboratory seroprevalence data show that in the latter half of August 2020, the seroprevalence for Washington State as a whole was estimated at 3.0% (95% CI 1.8-4.5%).[12] Data from the 10-Site Commercial Laboratory Seroprevalence Survey show a considerably lower estimated seroprevalence for the Western Washington Region at the end of July 2020 of just 1.3% (95% CI 0.9-2.4%).[13,14] An unpublished mathematical model from the Institute for Disease Modeling (IDM, www.idmod.org) estimated seroprevalence to be 2% (95% CI 1%-3%) in King County for August 2020 (unpublished data; Mike Famulare, personal communication, March 23, 2021).

Seroprevalence surveys in other US jurisdictions in April and May of 2020 reported 2.5% (Georgia),[7] 2.8% (Santa Clara County, CA),[15], and 4.7% (Los Angeles County, CA).[16] In Indiana, seroprevalence was 1.09% in a mostly White random sample and 5.8% in a mostly Black and other people of color non-random sample.[17] It is difficult to compare results across surveys because of different sampling and analysis strategies and survey timing.

We conducted our study three to four months later than these others and when the county and country were in the midst of a then-unprecedented surge in cases. For both these reasons, it is expected that more cases would have accumulated and seroprevalence would be higher than in April or May. At the same time, there is evidence to suggest that antibody levels may fall below detectable limits after three to four months,[18] so participants in our survey who were infected in the early months of the epidemic may no longer have had detectable levels of antibody. It is important to note that antibody status alone does not predict immunity to COVID-19; strong evidence exists that T-cell memory persists over the long term.[19] Still, people with documented antibody should still get vaccinated, continue to wear masks and maintain appropriate distance in public.

As noted above, nine participants had results positive only for the first of the two sequential assays. These may represent either false positives on the first assay or, what is more likely based on the sensitivity of the assays, false negatives on the second test. However, if the test results are accurate, these may have been individuals who were infected with SARS-CoV-2 too short a time prior to the test to have developed a detectable IgG response, or who generated a response to the nucleocapsid but not the spike protein, or whose response was atypical (either weak overall or deficient in the IgG isotype[20]).

The estimated underreporting multiplier for infection based on this survey – 5 -- is lower than the estimates of 8.3 to 33.2 based on community serosurveys from April and May 2020 in Los Angeles, California, Miami-Dade County, Florida, Dekalb-Fulton counties, Georgia, and the states of Indiana and New York,[3] and also lower than a published estimate of 7 infections per confirmed case in Washington State as of April 20, 2020.[4] These discrepancies may reflect in part the timing of our survey in August; the pace of viral testing increased across the country in summer 2020, which would tend to close the gap between reported cases and actual infections.

In fact, our estimate of an underreporting multiplier of 5 aligns well with a mathematical model from IDM, which estimated on average 4.3 infections for every reported case in King County through mid-August.[21] Of note, the IDM model estimated that in the early part of the outbreak, from mid-March to June, there were about 8.3 infections for every case, but that by mid-July, this ratio had dropped to about 3.4 – coinciding "with the June 5 roll-out of free, drive-thru testing sites in King County, suggesting that changes in testing strategy significantly improved the infection-detection system."[21]

Goals for this survey were ambitious – we hoped to quickly generate a seroprevalence estimate for King County that would include large enough numbers of people to be able to estimate seroprevalence in all age, income, race, and ethnicity groups as well as information about social risk factors for COVID-19 that might be modifiable through behavior or policy changes.

Unfortunately, we encountered serious limitations that affected timeliness and quality of the data. This report addresses only three of the survey's four stated objectives; it does not address the third objective, which was to identify modifiable risk factors. Early in the COVID-19 epidemic in the US, it was clear that it brought into focus existing inequities related to racial, ethnic, income, employment, geography, and immigration status.[22–26] In this analysis, we did not cross-tabulate data to look at the relationships among income, age, and race, but these characteristics are known to be related to each other and to employment in jobs considered essential or without telecommuting options that would increase risk for exposure to the coronavirus.[22,25] Additional data on social risk factors and geographic distribution from this survey remain to be analyzed and can help move beyond simply describing inequities to inform action to address them.

In addition to these and other implementation challenges, we faced more general limitations, such as differential participation by class, race, sex, and age – participants were disproportionately wealthy, White, female, and older compared to the King County population. In both the random and non-random samples, there was participation bias that worked in both directions: we were aware both of people who were ill at the time they were scheduled to be tested who did not attend and provide a blood specimen as well as people who had had an illness they suspected was COVID-19 and made a special effort to get tested.

Limitations included:

- Resources: this effort was under-resourced, with only one regular full-time PHSKC employee and one full-time consultant. The survey was accomplished due to the huge efforts of at least 138 clinical and non-clinical Public Health Reserve Corps (PHRC) volunteers who dedicated well over 2,000 hours to this project building the data capture system, setting up and staffing fixed sites, visiting homes to collect blood specimens, and phoning to recruit participants from households in the address-based sample.
- Questionnaire: the questionnaire was long and the framing for some of the questions was inadequate, both of which may have discouraged participants from completing it. The sequencing of some potentially intrusive questions (e.g., about household income) was poor, some skip patterns and required questions were incorrectly implemented and/or inconsistent across the different versions of the questionnaire (e.g., race wasn't initially a required field so there was quite a bit of missing race data), and email and text message reminders to complete the questionnaire or to attend blood specimen collection appointments were not correctly automated. Because this was a federally funded project, we were required to use federal language on race and ethnicity as well as on sexual orientation and gender identity. However, we know that these categories are not sufficiently nuanced to describe participants' identities; [27] in particular, participants who identified as Hispanic ethnicity frequently chose "Prefer not to say" for race.
- Quality Control: About 10% of dried blood spot specimens did not have sufficient quantity of blood to be tested by the lab.
- Assay performance: The use of dried blood spots rather than serum may have caused some decline in assay performance.
- Reagent shortages: After the lab had received all our specimens and assayed and reported results from many of them, they experienced a shortage of Bio-Rad total antibody kits. Delays in lab testing due to kit shortages resulted in delays in return of results, data cleaning, and analysis, especially since COVID-delegated staff had returned to other duties by the time the final lab results were received in late September.
- Community outreach and engagement: We did not attain our goal of oversampling members of the American Indian[6] and Pacific Islander populations despite efforts to reach out to and engage with them in conjunction with leaders from within those communities. This was due in part to the lack of existing community relationships and the short lead time for the survey as well as to challenges in conveying the value of participation to community members.

Despite these limitations, we believe these data provide important point estimates of SARS COV-2 seroprevalence in the community, which we were able to disaggregate by race, income, age, and sex assigned at birth. Similar to reported case counts, seroprevalence estimates are notably higher among those with lower incomes, people of color, and –something not widely demonstrated at the time of this survey -- young adults. Unlike case counts, our findings are less likely to be biased by differential testing rates and allow for more accurate estimates of the proportion of severe cases and of the infection fatality ratio.

Of course, many more cases have occurred in King County since the time of this survey; in December 2020, the average number of reported daily cases rose to 7 times the level of August 2020.[2] As of mid-January 2021, the National Commercial Laboratory Seroprevalence Study estimate for Washington State had risen to 9.1% (95% CI 7.0%-11.2%).[12] Seattle, which accounts for one third of King County's population, so far has one of the lowest incidence rates of COVID-19 of any major metropolitan area in the country.[28] The relatively low underreporting factor revealed by this survey suggests that King County was testing and detecting a relatively high proportion of COVID-19 cases.

Results from this survey, combined with those of surveillance systems and other researchers, provide documentation of the extent and differential spread of SARS-CoV-2 in King County. Additional analyses may provide further insights to support messaging and policies to reduce risks.

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Eastgate Public Health Clinic

References

1. Jorden MA, Rudman SL, Villarina E, et al. Evidence for Limited Early Spread of COVID-19 Within the United States, January–February 2020. *MMWR Morb Mortal Wkly Rep*. 2020;69:680-684.
2. Public Health - Seattle & King County COVID-19 Outbreak Summary: Testing volume and percent positive by Geography over Time. https://www.kingcounty.gov/depts/health/covid-19/data/daily-summary.aspx. Accessed March 19, 2021.
3. Angulo FJ, Finelli L, Swerdlow DL. Estimation of US SARS-CoV-2 Infections, Symptomatic Infections, Hospitalizations, and Deaths Using Seroprevalence Surveys. *JAMA Netw open*. 2021;4(1):e2033706. doi:10.1001/jamanetworkopen.2020.33706
4. Wu SL, Mertens AN, Crider YS, et al. Substantial underestimation of SARS-CoV-2 infection in the United States. *Nat Commun*. 2020;11. doi:10.1038/s41467-020-18272-4
5. Washington State Office of Financial Management. Estimates of April 1 population by age, sex, race and Hispanic origin. https://ofm.wa.gov/washington-data-research/population-demographics/population-estimates/estimates-april-1-population-age-sex-race-and-hispanic-origin. Published 2021. Accessed March 19, 2021.
6. Urban Indian Health Institute. *Best Practices for American Indian and Alaska Native Data Collection*. Seattle; 2020. www.uihi.org.
7. Biggs HM, Harris JB, Breakwell L, Dahlgren FS, Abedi GR, Szablewski CM. Estimated Community Seroprevalence of SARS-CoV-2 Antibodies — Two Georgia Counties, April 28-May 3, 2020. 2020;69(29):965-970.
8. Accorsi EK, Cowger T, Lipsitch M. Social Risk Factors for COVID-19 Exposure Questionnaire, v1. 2020. https://osf.io/a9xpd/wiki/home/.
9. Bio-Rad Laboratories. Platelia SARS-CoV-2 Total Ab Instructions for Use. 2020. www.bio-rad.com.
10. EuroImmun. Anti-SARS-CoV-2 ELISA (IgG) Instruction for use. 2020. www.euroimmun.us.
11. AusVet. Sensitivity and specificity of two tests used in parallel or series. EpiTools. https://epitools.ausvet.com.au/twoteststwo. Published 2021.
12. Centers for Disease Control and Prevention. COVID Data Tracker: Nationwide Commercial Laboratory Seroprevalence Survey. https://covid.cdc.gov/covid-data-tracker/#national-lab. Accessed March 28, 2021.
13. Centers for Disease Control and Prevention. COVID Data Tracker: Commercial Laboratory Seroprevalence Survey Data. https://covid.cdc.gov/covid-data-tracker/#serology-surveillance. Accessed March 28, 2021.
14. Havers FP, Reed C, Lim T, et al. Seroprevalence of Antibodies to SARS-CoV-2 in 10 Sites in the United States, March 23-May 12, 2020. *JAMA Intern Med*. 2020;180(12):1776-1786. doi:10.1001/jamainternmed.2020.4130
15. Bendavid E, Mulaney B, Sood N, et al. COVID-19 antibody seroprevalence in Santa Clara County, California. *medRxiv*. 2020. doi:10.1101/2020.04.14.20062463
16. Sood N, Simon P, Ebner P, et al. Seroprevalence of SARS-CoV-2-Specific Antibodies Among Adults in Los Angeles County, California, on April 10-11, 2020. *JAMA - J Am Med Assoc*. 2020;323(23):2425-2427. doi:10.1002/cpmc.100
17. Menachemi N, Yiannoutsos CT, Dixon BE, et al. Population Point Prevalence of SARS-CoV-2

Infection Based on a Statewide Random Sample — Indiana, April 25–29, 2020. *MMWR Morb Mortal Wkly Rep*. 2020;69(29):960-964. doi:10.15585/mmwr.mm6929e1

18. Shioda K, Lau MSY, Kraay ANM, et al. Estimating the cumulative incidence of SARS-CoV-2 infection and the infection fatality ratio in light of waning antibodies. *medRxiv*. 2020:1-28. doi:10.1101/2020.11.13.20231266

19. Le Bert N, Tan AT, Kunasegaran K, et al. SARS-CoV-2-specific T cell immunity in cases of COVID-19 and SARS, and uninfected controls. *Nature*. 2020;584(7821):457-462. doi:10.1038/s41586-020-2550-z

20. Melgaço JG, Azamor T, Ano Bom APD. Protective immunity after COVID-19 has been questioned: What can we do without SARS-CoV-2-IgG detection? *Cell Immunol*. 2020;353(April):104114. doi:10.1016/j.cellimm.2020.104114

21. Thakkar N, Famulare M. *One State , Many Outbreaks: A Transmission Modeling Perspective on Current COVID-19 Trends in King , Pierce , and Yakima Counties*. Institute for Disease Modeling:Seattle; 2020.

22. Mahajan U V., Larkins-Pettigrew M. Racial demographics and COVID-19 confirmed cases and deaths: A correlational analysis of 2886 US counties. *J Public Heal (United Kingdom)*. 2020;42(3):445-447. doi:10.1093/pubmed/fdaa070

23. Tai DBG, Shah A, Doubeni CA, Sia IG, Wieland ML. The Disproportionate Impact of COVID-19 on Racial and Ethnic Minorities in the United States. *Clin Infect Dis*. 2020;72:705-708. doi:10.1093/cid/ciaa815

24. Williams DR, Cooper LA. COVID-19 and Health Equity - A New Kind of “herd Immunity.” *JAMA - J Am Med Assoc*. 2020;323(24):2478-2480. doi:10.1001/jama.2020.8051

25. Mackey K, Ayers CK, Kondo KK, et al. Racial and Ethnic Disparities in COVID-19–Related Infections, Hospitalizations, and Deaths. *Ann Intern Med*. 2020;174(3). doi:10.7326/m20-6306

26. Gray DM, Anyane-Yeboa A, Balzora S, Issaka RB, May FP. COVID-19 and the other pandemic: populations made vulnerable by systemic inequity. *Nat Rev Gastroenterol Hepatol*. 2020;17(9):520-522. doi:10.1038/s41575-020-0330-8

27. Pew Research Center. *Multiracial in America: Proud, Diverse and Growing in Numbers*. Washington, DC; 2015. doi:10.1111/j.1813-6982.1967.tb01936.x

28. Baker M. Seattle’s Virus Success Shows What Could Have Been. *The New York Times*. https://www.nytimes.com/2021/03/11/us/coronavirus-seattle-success.html. Published 2021.

29. Harris P, Taylor R, Thielke R, Payne J, Gonzalez N, Conde J. Research electronic data capture (REDCap) -- A metadata-driven methodology and workflow process for providing translational research informatics support. *J Biomed Inf*. 2009;42(2):377-381.

30. Harris P, Taylor R, Minor B, et al. The REDCap consortium: Building an international community of software partners. *J Biomed Inf*. 2019. doi:10.1016/j.jbi.2019.103208

Appendix 1. Questionnaire

Link to PDF of English P1 Questionnaire

- Note that PDF doesn't capture skip patterns – most respondents would answer only a subset of questions. Likewise, the PDF does not indicate which questions were required. It turned out that there were inconsistencies across the 22 versions (11 English and 11 Spanish, one each for the first person in the household and adolescent/adult and child versions of the five other surveys).

Appendix 2. Detailed statistical methods

Link to Prevalence Estimation file