

Methods. From January–April 2021, we enrolled members of households in San Diego County, CA, and Denver, CO metropolitan area (Tri-County), with a confirmed SARS-CoV-2 infection in a household member with illness onset date in the previous 10 days. CDC investigators visited households at enrollment and 14 days later at closeout to obtain demographic and clinical data and nasopharyngeal (NP) samples on all consenting household members. Interim visits, with collection of NP swabs, occurred if a participant became symptomatic during follow-up. NP samples were tested for SARS-CoV-2 using TaqPath™ RT-PCR test, where failure to amplify the spike protein results in S-Gene target failure (SGTF) may indicate B.1.1.7 lineage. Demographic characteristics and SIR were compared among SGTF and non-SGTF households using two-sided p-values with chi-square tests; 95% confidence intervals (CI) were calculated with Wilson score intervals.

Results. 552 persons from 151 households were enrolled. 91 (60%) households were classified as SGTF, 57 (38%) non-SGTF, and 3 (2%) indeterminate. SGTF and non-SGTF households had similar sex distribution (49% female and 52% female, respectively; P=0.54) and age (median 30 years, interquartile range (IQR) 14–47 and 31 years (IQR 15–45), respectively). Hispanic people accounted for 24% and 32% of enrolled members of SGTF and non-SGTF households, respectively (p=0.04). At least one secondary case occurred in 61% of SGTF and 58% of non-SGTF households (P=0.66). SIR was 52% (95%[CI] 46%–59%) for SGTF and 45% (95% CI 37%–53%) for non-SGTF households (P=0.18).

Conclusion. SIRs were high in both SGTF and non-SGTF households; our findings did not support an increase in SIR for SGTF relative to non-SGTF households in this setting. Sequence confirmed SARS-CoV-2 samples will provide further information on lineage specific SIRs.

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374. Need to Improve Minority Representation through COVID-19 Community Research Partnership

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Background. Minorities are often unrepresented in research, which limits equity in healthcare advances. The racial and ethnic disparities in outcomes of individuals infected with COVID-19 highlight the importance of inclusivity in research to improve public health measures.

Methods. We performed a descriptive analysis of the racial and ethnic distribution of children enrolled in our COVID-19 Community Research Partnership (CRP) study, a syndromic and serological surveillance study of children aged 2 – 17 years receiving care at three healthcare systems spanning North and South Carolina. Syndromic surveillance involved daily symptom reporting using a web-based monitoring application. Participants consenting to serological surveillance were mailed at-home tests sampling finger prick capillary blood. In-person and electronic recruitment efforts were conducted in English and Spanish. At one of the study sites, we compared the racial/ethnic distribution of enrolled children to the racial/ethnic distribution of all children who received care at the same site during the same timeframe. We compared the racial/ethnic distribution of participants who ultimately submitted samples for serological testing compared to those who consented to serologic testing.

Results. At total of 1630 children were enrolled from April 2, 2021 – June 8, 2021. Most children were > 5 years old, 50.2% were female, and 88.5% were from mostly urban counties (Table 1). Of enrolled children, 4.2% were Hispanic, 8.2% were black, and 81.6% were white (Table 2). Among 135,355 unique children who received care at the institution during the same time, 12.4% were Hispanic, 23.0% were black, and 63.1% were white. Of 1552 participants who consented to serologic testing, 4.4% were Hispanic, 8.1% were black, and 81.8% were white (Table 3). To date, 242 children submitted serologic samples; 4.1% were Hispanic, 5.0% were black, and 85.5% were white.

Table 1. Characteristics of enrolled children in COVID-19 surveillance study

Characteristics	N (%)
Number of Atrium enrollees (N)	1630
Age (years):	
≥2 – ≤5	343 (21.0%)
>5 – ≤10	518 (31.8%)
>10 – ≤15	590 (36.2%)
>15 – ≤18	179 (11.0%)
Sex at Birth:	
Female	818 (50.2%)
Male	812 (49.8%)
Rurality of County of Residence:	
Mostly urban	1443 (88.5%)
Mostly rural	187 (11.5%)
Completely rural	0 (0%)

Table 2. Racial and Ethnic distribution of children enrolled in the study compared to target population

	Enrolled study population (N = 1630)	Enrolled healthcare system patient population (N = 135355)
Race:		
White, n (%)	1330 (81.6%)	85433 (63.1%)
Black, n (%)	133 (8.2%)	31116 (23.0%)
Native Hawaiian/Pacific Islander, n (%)	2 (0.1%)	186 (0.1%)
Asian, n (%)	54 (3.3%)	4822 (3.8%)
American Indian/Alaska Native, n (%)	7 (0.4%)	1025 (0.8%)
Middle Eastern/North African, n (%)	1 (0.1%)	260 (0.2%)
2+ Races, n (%)	33 (2.0%)	2901 (2.1%)
Do not wish to specify, n (%)	70 (4.3%)	9612 (7.1%)
Ethnicity:		
Hispanic/Latino	69 (4.2%)	16834 (12.4%)
Not Hispanic/Latino	1472 (90.3%)	111492 (82.4%)
Not Specified	89 (5.4%)	7029 (5.2%)

Table 3. Racial and ethnic distribution of children who participated in serology testing

	Serology Completed (N = 242)	Consented to serology testing (N = 1552)
Race:		
White, n (%)	207 (85.5%)	1270 (81.8%)
Black, n (%)	12 (5.0%)	125 (8.1%)
Native Hawaiian/Pacific Islander, n (%)	2 (0.8%)	2 (0.1%)
Asian, n (%)	9 (3.7%)	50 (3.2%)
American Indian/Alaska Native, n (%)	1 (0.4%)	7 (0.5%)
Middle Eastern/North African, n (%)	0 (0%)	0 (0%)
2+ Races, n (%)	3 (1.2%)	32 (2.1%)
Do not wish to specify, n (%)	8 (3.3%)	66 (4.3%)
Ethnicity:		
Hispanic/Latino	10 (4.1%)	68 (4.4%)
Not Hispanic/Latino	218 (90.1%)	1405 (90.5%)
Not Specified	14 (5.8%)	79 (5.1%)

Conclusion. Despite efforts to recruit a diverse group of children, the proportion of minorities enrolled in our COVID-19 surveillance study underrepresents the targeted population. Ongoing efforts will work to identify barriers and facilitators to research participation among minority families.

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375. High Laboratory-confirmed SARS-CoV-2 Attack Rate in Lima Health Care Personnel During August 2020-March 2021 Suggests Role for Improved Infection Control

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Background. Peru has one of the highest per capita SARS-CoV-2 death rates in Latin America. Healthcare workers (HCW) are a critical workforce during the COVID-19 pandemic but are themselves often at increased risk of infection. We evaluated SARS-CoV-2 attack rate and risk factors among frontline HCWs.

Methods. We performed a prospective cohort study of HCW serving two acute care hospitals in Lima, Peru from Aug 2020 to Mar 2021. Participants had baseline SARS-CoV-2 serology using the CDC ELISA, active symptom monitoring, and weekly respiratory specimen collection with COVID-19 exposure/risk assessment for 16-weeks regardless of symptoms. Respiratory specimens were tested by real-time reverse transcriptase PCR (rRT-PCR).

Results. Of 783 eligible, 667 (85%) HCW were enrolled (33% nurse assistants, 29% non-clinical staff, 26% nurses, 7% physicians, and 6% other). At baseline and prior to COVID-19 vaccine introduction, 214 (32.1%; 214/667) were reactive for SARS-CoV-2 antibodies. In total, 72 (10.8%; 72/667) HCWs were found to be rRT-PCR positive during weekly follow-up. Of the rRT-PCR positive HCWs, 37.5% (27/72) did not report symptoms within 1-week of specimen collection. During follow up, HCW without detectable SARS-CoV-2 antibodies at baseline were significantly more likely to be rRT-PCR positive (65/453, 14.3%) compared to those with SARS-CoV-2 antibodies at baseline (4/214, 1.9%) (p-value: < 0.001). Three HCW were both serologically reactive and rRT-PCR positive at baseline. Looking only at HCW without SARS-CoV-2 antibodies, nurse assistants (rRT-PCR positive: 18.6%; 27/141) and non-clinical healthcare workers (16.5%; 21/127) were at greater risk of infection compared to nurses (8.5%; 10/118), physicians (7.9%; 3/38), and other staff (10.3%; 4/29) (RR 1.95;95%CI 1.2,3.3; p-value: 0.01).

Conclusion. Baseline SARS-CoV-2 prevalence and 16-week cumulative incidence were substantial in this pre-vaccination Peruvian HCW cohort. Almost 40% of new infections occurred in HCW without complaint of symptoms illustrating a limitation of symptom-based HCW screening for COVID-19 prevention. Nurse assistants and non-clinical healthcare workers were at greater risk of infection indicating a role for focused infection prevention and risk reduction strategies for some groups of HCW.

Disclosures. Fernanda C. Lessa, MD, MPH, Nothing to disclose

376. Sensitivity and Specificity of the WHO Probable SARS-CoV-2 Case Definition Among Symptomatic Healthcare Personnel

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Background. SARS-CoV-2 continues to spread globally, including in limited resource settings. It is therefore important to derive general case definitions that can be useful and accurate in the absence of timely test results. We aim to validate the World Health Organization (WHO) case definition, a symptom-screening tool currently used to identify SARS-CoV-2 cases in a cohort of symptomatic health care providers (HCP) who completed a symptom survey interview and received a PCR test at Boston Medical Center (BMC) between March 13, 2020 and May 5, 2020.

Methods. We classified each HCP as a probable or not probable case of SARS-CoV-2 based on the WHO case definition. Using PCR test as gold standard, we computed the sensitivity and specificity of the WHO case definition. We used a stepwise logistic regression model on all PCR-tested HCP to identify symptoms predictive of PCR positivity.

Results. Of 328 included HCP, 109 (33.2%) were PCR positive, 213 (64.9%) negative, and 6 (1.8%) had indeterminate test result. The sensitivity and specificity of the WHO case definition were 65.1% and 74.6%, respectively. The positive predictive value was 56.8% and the negative predictive value was 80.7%. Symptoms found to be predictive of PCR positivity were fever, headache, loss of smell and/or loss of taste, and muscle ache/joint pain. Sore throat was found to be predictive of PCR negativity. The area under the curve using the final model was 0.8412. All statistically significant symptoms included in the final model, were also included in the WHO case definition.

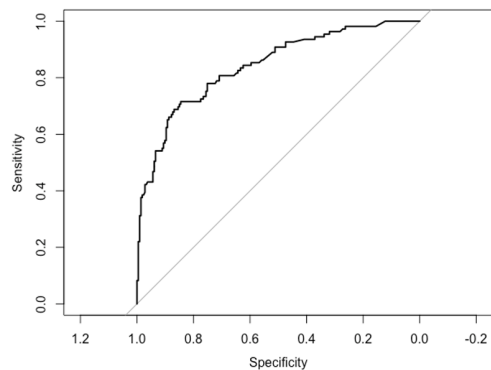
Table 1. Results for sensitivity and specificity

Result from WHO case definition	Gold Standard (test result)	
	Positive	Negative
	Positive	71
Negative	38	159

Table 2. Stepwise Logistic Regression Results

	Estimate	OR	p-value
Intercept	-1.79	0.17	<0.001
Sore Throat	-1.02	0.36	0.001
Fever	0.55	1.73	0.075
Headache	0.65	1.91	0.034
Loss of Taste and/or Loss of Smell	2.55	12.86	<0.001
Muscle Ache/Joint Pain	0.73	2.08	0.018
Rash	1.09	2.96	0.151

Figure 1. ROC curve for stepwise logistic regression model



Conclusion. In our largely symptomatic HCP cohort, our model yielded similar symptoms to those identified in the WHO probable case definition. As seen in similar studies, it is unlikely that further adjustment will improve the performance of a SARS-CoV-2 case definition. However, it is concerning that 35% (38/109) of PCR positive SARS-CoV-2 HCP would have been classified as not probable cases by the WHO definition, given that this definition does not even include asymptomatic cases. This

further evidence for global building of laboratory capacity and development of affordable diagnostics to improve global pandemic control.

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377. SARS-CoV-2 Genomic Surveillance Reveals Little Spread Between a Large University Campus and the Surrounding Community

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Background. Understanding SARS-CoV-2 transmission dynamics is critical for controlling and preventing outbreaks. The genomic epidemiology of SARS-CoV-2 on college campuses has not been comprehensively studied, and the extent to which campus-associated outbreaks lead to transmission in nearby communities is unclear. We used high-density genomic surveillance to track SARS-CoV-2 transmission across the University of Michigan-Ann Arbor campus and Washtenaw County during the Fall 2020 semester.

Methods. We retrieved all available residual diagnostic specimens from the Michigan Medicine Clinical Microbiology Laboratory and University Health Service that were positive for SARS-CoV-2 from August 16th - November 25th, 2020 (n = 2245). We extracted viral RNA, amplified the SARS-CoV-2 genome by multiplex RT-PCR, and sequenced these amplicons on an Illumina MiSeq. We applied maximum likelihood phylogenetic analysis to whole genome sequences to define and characterize transmission lineages.

Results. We assembled complete viral genomes from 1659 individual infections, representing roughly 25% of confirmed cases in Washtenaw County across the fall semester. Of these cases, 468 were University of Michigan students. Phylogenetic analysis revealed 203 genetically distinct introductions of SARS-CoV-2 into the student population, most of which were singletons (n = 171) or small clusters of 2 - 8 students. We identified two large SARS-CoV-2 transmission lineages (115 and 73 students, respectively), including individuals from multiple on-campus residences. Viral descendants of these student outbreaks were rare, constituting less than 4% of cases in the community.

Conclusion. We identified many SARS-CoV-2 transmission introductions into the University of Michigan campus in Fall 2020. While there was widespread transmission among students, there is little evidence that these outbreaks significantly contributed to the rise in COVID-19 cases that Washtenaw County experienced in November 2020.

Disclosures. Adam Lauring, MD, PhD, Roche (Advisor or Review Panel member) Sanofi (Consultant)

378. Descriptive Analysis of SARS-CoV-2 Infections Among Health System and University Employees

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Background. We aimed to describe SARS-CoV-2 (COVID-19) infections among employees in a large, academic institution.

Table 1. COVID-19 Attribution Definitions

Attribution Classification	Definition
Healthcare/workplace-acquired	
Healthcare worker or Co-worker	Exposure to a COVID-infected healthcare worker or co-worker during their infectious window
Patient	Exposure to a COVID-infected patient while not wearing adequate personal protective equipment (pre-isolation) or breach in personal protective equipment
Visitor	Exposure to a COVID-infected visitor while not wearing adequate personal protective equipment
Community-acquired	Exposure to a COVID-infected person in the community (or a co-worker outside the workplace) including non-Duke work environments during infectious window OR the employee case and their significant other/housemate/family member developed symptoms at the same time (and confirmed positive) making a community point source the most likely explanation
Unknown, likely community-acquired	Close contact with a person who has symptoms consistent with COVID (but has not been tested for COVID infection) during their infectious window; the contact occurred in the community (or a co-worker outside the workplace) including non-Duke work environments OR the employee case and their significant other/housemate/family member developed symptoms at the same time (but did not get tested for COVID) making a community point source a likely explanation
Unknown	No known contact with a COVID-infected person in the community, no known contact with a COVID-infected co-worker or visitor in the healthcare environment during their infectious window, and no breach in PPE during care of a COVID-infected patient. Alternatively, known contact with a COVID-infected person in the community AND a COVID-infected co-workers or visitor in the healthcare environment during their infectious window.