

**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**

Han Nguyen, BA<sup>1</sup>; Sarah Weber, MPH<sup>2</sup>; Yachana Kataria, PhD<sup>2</sup>; Manisha Cole, MS<sup>2</sup>; Elizabeth Duffy, MA<sup>2</sup>; Elizabeth Ragan, MPH<sup>2</sup>; Jacquelyn Turcinovic, BS<sup>3</sup>; Nancy Miller, MD<sup>2</sup>; William P. Hanage, PhD<sup>4</sup>; John Connor, PhD<sup>3</sup>; Cassandra Pierre, MD<sup>2</sup>; Karen Jacobson, MD<sup>2</sup>; Sara Lodi, PhD<sup>1</sup>; Tara Bouton, MD<sup>2</sup>; <sup>1</sup>Boston University School of Public Health, Boston, Massachusetts; <sup>2</sup>Boston Medical Center, Boston, Massachusetts; <sup>3</sup>Boston University, Boston, Massachusetts; <sup>4</sup>Harvard T.H. Chan School of Public Health, Boston, MA

**Session:** P-16. COVID-19 Epidemiology and Screening

**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.

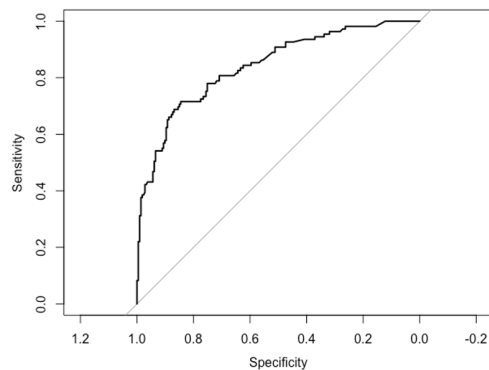
Table 1. Results for sensitivity and specificity

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.

**Disclosures.** All Authors: No reported disclosures

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

Andrew Valesano, BS<sup>1</sup>; William Fitzsimmons, MS<sup>1</sup>; Christopher Blair, BS<sup>1</sup>; Robert Woods, MD, PhD<sup>1</sup>; Julie Gilbert, MPH, MS<sup>1</sup>; Dawn Rudnik, MT(ASCP) SM<sup>1</sup>; Lindsey Mortenson, MD<sup>1</sup>; Joshua G. Petrie, PhD, MPH<sup>1</sup>; Emily T. Martin, PhD, MPH<sup>1</sup>; Adam Lauring, MD, PhD<sup>1</sup>; <sup>1</sup>University of Michigan, Ann Arbor, Michigan

**Session:** P-16. COVID-19 Epidemiology and Screening

**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 16<sup>th</sup> - November 25<sup>th</sup>, 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**

Jessica Seidelman, MD, MPH<sup>1</sup>; Ibukunoluwa Akinboyo, MD<sup>1</sup>; Maya Rinehart, n/a<sup>2</sup>; Rebekah W. Moehring, MD, MPH<sup>3</sup>; Deverick J. Anderson, MD, MPH<sup>3</sup>; Kristen Said, MD, MPH<sup>1</sup>; Carol A. Epling, MD, MSPH, MD, MSPH<sup>4</sup>; Sarah S. Lewis, MD, MPH<sup>1</sup>; Becky Smith, MD<sup>1</sup>; Matthew Stiegel, PhD<sup>1</sup>; <sup>1</sup>Duke University, Durham, NC; <sup>2</sup>Duke University Health System, Durham, NC; <sup>3</sup>Duke Center for Antimicrobial Stewardship and Infection Prevention, Durham, NC; <sup>4</sup>Duke University Medical Center, Durham, NC

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**Session:** P-16. COVID-19 Epidemiology and Screening

**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.