measures. The study illustrates that in times of crisis, such as the COVID-19 pandemic, the burden of effective infection control requires much more multidisciplinary efforts to prevent unintentional lapses in patient safety. A swift response by the state and local health departments at a tertiary-care healthcare center conveyed a positive mitigation of the highest clinical threats and decreased horizontal transmission of disease.

Funding: No

Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2021;1(Suppl. S1): doi:10.1017/ash.2021.17

## **Presentation Type:**

Poster Presentation - Top Poster Award Subject Category: COVID-19

A Cluster of Aspergillosis Associated with SARS-CoV-2

Kerrie VerLee; Jim Codman; Russell Lampen; Chau Nguyen; Tunisia Peters; Greg Kruse; Derek VanderHorst; Doreen Marcinek and Molly Kane-Carbone

Background: Coronavirus disease 2019 (COVID-19) has demonstrated a variety of presentations and clinical complications, among them coinfection of pneumonia with the mold Aspergillus spp. Patients at risk for invasive disease include transplant recipients and those with prolonged neutropenia, immune disorders, cystic fibrosis, and steroid use. There have been recent descriptions of coronavirus disease-associated pulmonary aspergillosis (CAPA). An outbreak investigation into a cluster of Aspergillus fumigatus infections in a health system intensive care unit uncovered a community-onset (CO) increase in CAPA. Methods: A multidisciplinary outbreak investigation was conducted evaluating sources of contamination, completion of construction projects, and changes in clinical processes. Retrospective chart review was done for the prior 18 months and incidence density rates for Aspergillus infections from June 2019 through December 2020 were calculated per 10,000 patient days, stratified by unit, specimen source, and coinfection with COVID-19. Data were linked with all positive and negative COVID-19 tests performed by the health system's regional laboratory from March to December 2020. Healthcare-onset (HO) classification was based on infections identified ≥7 days after admission. Statistical analysis was calculated with significance at p < 0.05. Results: Over the last 18 months, 82 patients were identified positive with Aspergillus cultures; of which 10 (12%) met CAPA definitions. Aspergillus fumigatus was the most common species and accounted for 62% of samples, followed by Aspergillus niger (17%). Median rates of HO Aspergillosis were 0.45 cases per 10,000 patient days, whereas the median total rates of infection were 1.97 cases per 10,000 patient days. Rates of CAPA coincided with COVID-19 hospitalization rates. In the spring and fall, surges of COVID-19, the rate ratio of CAPA to COVID hospitalized infections per 10,000 patient days, ranged from 0.006 to 0.015. Once CAPA infections were adjusted for, rates of CO Aspergillus remained high, whereas HO cases suggested baseline acquisition. Conclusion: This study outlines rates of CO aspergillosis as well as CAPA rates coinciding with the healthcare system's spring and fall surges of COVID-19 hospitalizations. Despite the determination that this was not a hospital-acquired cluster, the investigation revealed some areas for



## Figure 1.

Figure 1.

 
 0
 0.5
 CAPA rate system wide
 24

 25
 26

 26
 27

opportunity in construction processes along with maintaining coverage of all patient supplies to reduce the risk of contamination. **Funding:** No

## Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2021;1(Suppl. S1):s10 doi:10.1017/ash.2021.18

Presentation Type:

Poster Presentation - Top Poster Award

Subject Category: COVID-19

## Molecular Epidemiology of Large COVID-19 Clusters at an Academic Medical Center, March-October 2020

Takaaki Kobayashi; Miguel Ortiz; Stephanie Holley; William Etienne; Kyle Jenn; Oluchi Abosi; Holly Meacham; Lorinda Sheeler; Angie Dains; Mary Kukla; Alexandra Trannel; Alexandre Marra; Mohammed Alsuhaibani; Paul McCray; Stanley Perlman; Bradley Ford; Daniel Diekema; Melanie Wellington; Alejandro Pezzulo and Jorge Salinas

Background: COVID-19 in hospitalized patients may be the result of community acquisition or in-hospital transmission. Molecular epidemiology can help confirm hospital COVID-19 transmission and outbreaks. We describe large COVID-19 clusters identified in our hospital and apply molecular epidemiology to confirm outbreaks. Methods: The University of Iowa Hospitals and Clinics is an 811-bed academic medical center. We identified large clusters involving patients with hospital onset COVID-19 detected during March-October 2020. Large clusters included ≥10 individuals (patients, visitors, or HCWs) with a laboratory confirmed COVID-19 diagnosis (RT-PCR) and an epidemiologic link. Epidemiologic links were defined as hospitalization, work, or visiting in the same unit during the incubation or infectious period for the index case. Hospital onset was defined as a COVID-19 diagnosis ≥14 days from admission date. Admission screening has been conducted since May 2020 and serial testing (every 5 days) since July 2020. Nasopharyngeal swab specimens were retrieved for viral whole-genome sequencing (WGS). Cluster patients with a pairwise difference in  $\leq 5$  mutations were considered part of an outbreak. WGS was performed using Oxford Nanopore Technology and protocols from the ARTIC network. Results: We identified 2 large clusters involving patients with hospital-onset COVID-19. Cluster 1: 2 hospital-onset cases were identified in a medical-surgical unit in June 2020. Source and contact tracing revealed 4 additional patients, 1 visitor, and 13 employees with COVID-19. Median age for patients was 62 (range, 38-79), and all were male. In total, 17 samples (6 patients, 1 visitor, and 10 HCWs) were available for WGS. Cluster 2: A hospital-onset case was identified via serial testing in a non-COVID-19 intensive care unit in September



© The Author(s), 2021. Published by Cambridge University Press on behalf of The Society for Healthcare Epidemiology of America. This is an Open Access article, distributed under the terms of the Creative Commons Attribution licence (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted re-use, distribution, and reproduction in any medium, provided the original work is properly cited.