

**Presentation Type:**

Poster Presentation

**Subject Category:** COVID-19**Transmission of *Acinetobacter baumannii* by Surgical Masks During the COVID-19 Pandemic**

Lisa Saidel; Abraham Borer and Orli Sagi

**Background:** *Acinetobacter baumannii*, one of the major causes of nosocomial infections in modern healthcare systems, is characterized by its great persistence in the environment and by its ability to rapidly develop resistance to many antimicrobials. Most *A. baumannii* infections occur in intubated critically ill patients, causing ventilator-associated pneumonia which is a leading cause of mortality. During the coronavirus disease 19 (COVID-19) pandemic an increase in hospital-acquired carbapenem-resistant *A. baumannii* (CRAB) infection and colonization in acute-care hospitals has been described. CRAB healthcare-associated infections are often linked to breaches of infection prevention and control (IPC). Beginning in April 2020, our hospital's IPC unit ordered mandatory universal masking for all healthcare workers (HCWs). Shortages of personal protective equipment during the COVID-19 pandemic led to extended use of surgical face masks by HCWs in our hospital. We investigated whether the extended use of surgical face masks was linked to an increase of CRAB colonization in our intubated critically ill patients. **Methods:** Surgical masks were collected from doctors, nurses, and housekeeping staff working in 2 internal medicine departments, each including a 4-bed unit for intubated critically ill patients. All surgical masks were worn continuously for 4–5 hours before removal. "Cases" were defined as HCWs who treated CRAB colonized critically ill patients. "Controls" were defined as HCWs who did not enter the critically ill patient unit. Surgical masks were incubated with BHI enrichment broth (HyLabs Rehovot, Israel) for 48 hours at 35°C. BHI was seeded on multidrug-resistant (MDR)-selective CHROMagar plates (HyLabs) and incubated overnight at 35°C. Identification was performed using MALDI-ToF mass spectrophotometry (bioMérieux, France). Susceptibility was tested using Vitek 2 (bioMérieux). **Results:** In total, 55 HCWs participated in the study: 25 cases and 30 controls. Masks from 10 cases (40%) were colonized with *Acinetobacter* spp versus only 3 masks (10%) from controls (OR, 5.98; 95% CI, 1.42–25;  $P = .012$ ). Of 13 masks contaminated with *Acinetobacter* spp, 8 of 10 contaminated masks among cases were colonized with CRAB, whereas only 1 of 3 masks of controls was colonized with CRAB. **Conclusions:** During the COVID-19 pandemic, extended surgical mask use while treating patients colonized with CRAB increased mask contamination with this bacterium. Surgical masks should be changed after treating a patient colonized with CRAB the same way gown and glove removal and hand hygiene are performed.

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**Subject Category:** COVID-19**Whole-Genome Sequencing: The Key to Unlocking a Nosocomial Outbreak of Coronavirus Disease 2019 (COVID-19)**

Lindsey Gottlieb; Emilia Sordillo; Harm van Bakel; Barbara Smith; Bernard Camins; Sarah Alsamarai; Viviana Simon and Kilyoub Kim

**Background:** Accurately tracing nosocomial transmission of coronavirus disease 2019 (COVID-19) is critical to developing effective infection prevention policies. Given the high prevalence and variable incubation period of SARS-CoV-2 infection, the utility of traditional contact tracing is limited. We describe a nosocomial outbreak in which whole-genome sequencing (WGS) was pivotal to identifying the primary case. **Methods:** This study was conducted at a New York City academic hospital. The index case was identified on August 13, 2020, and the last case on September 9, 2020. Hospital policy required all inpatients to be screened for COVID-19 on

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admission by SARS-CoV-2 molecular amplification testing. All healthcare workers (HCWs) were required to wear masks and eye protection for patient care. After a patient (patient 1), who tested SARS-CoV-2 negative on admission, was positive on preprocedure screening on hospital day 9, contact tracing was initiated. Two patients (patients 2 and 3) and 13 HCWs with high-risk exposures (HREs) to patient 1 were quarantined and referred for testing. Additional surveillance testing was performed on 18 inpatients and 84 HCWs on the affected unit. Patients 2 and 3 and 3 HCWs (HCW-1, -2, and -3), only 1 of whom had a high-risk exposure to patient 1, tested positive. WGS was performed to further investigate this outbreak. **Results:** The outbreak variant (clade 20A) was found in samples from 6 patients and 2 HCWs. Patients 2 and 3 were roommates of patient 1 in the 2 days before patient 1's positive test, and they did not consistently wear masks in the room. HCW-1 placed a peripheral IV in patient 1 the day before patient 1's positive test without wearing eye protection. Four additional cases in this cluster (patients 4–6 and HCW-4) were identified by surveillance WGS of positive tests. A review indicated that patient 1 was located ~3 m (~10 feet) away from patient 4 in the emergency department (ED) for 6 hours on hospital day 1, when the admission SARS-CoV-2 test from patient 4 was not positive. No epidemiologic link was found to patient 5 or 6 or HCW-4. The specimen from HCW-2 was inadequate for WGS. The specimen from HCW-3 was not linked to this cluster. **Conclusions:** This complex nosocomial outbreak highlights the importance of WGS in understanding transmission events. Patient 4 was not identified by traditional contact tracing but was linked to patient 1 and was recognized as the primary case through WGS, having likely infected patient 1 in the ED. Based on these findings, we focused our corrective actions on more promptly isolating suspected COVID-19 cases in the ED, increasing inpatient masking, and improving HCW adherence to universal eye protection.

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**Subject Category:** COVID-19**Predicting SARS-CoV-2 Asymptomatic Infection Rate of Inpatients: A Time Series Analysis**

Frida Rivera; Kwang Woo Ahn and L. Silvia Munoz-Price

**Background:** Asymptomatic SARS-CoV-2 infections play a crucial role in viral transmission. However, they are often difficult to identify given that widespread surveillance has not been the norm. We sought to determine whether COVID-19 rates reported at the county level could predict the positivity rates for SARS-CoV-2 among asymptomatic patients tested in a large academic health system. **Methods:** This observational study was conducted from April 23, 2020, to December 10, 2020, at Froedtert Health (FH) system, the largest academic health system in Wisconsin. On April 23, 2020, FH implemented SARS-CoV-2 surveillance among all consecutive admissions not suspected of COVID-19, all patients scheduled for elective procedures and deliveries, and all asymptomatic patients with known exposures. Samples were processed by the FH laboratory using molecular methods (RT-PCR). To obtain the daily number of newly confirmed COVID-19 cases in Milwaukee County, we accessed the Wisconsin Department of Health Services publicly available COVID-19 database. For the purpose of this study, COVID-19 rates were defined as the percentage of positive tests among all daily tests performed at the county level, while SARS-CoV-2 positivity rates were the percentage of positive tests among all daily surveillance tests performed at FH among asymptomatic patients. The association between COVID-19 rates in Milwaukee County and asymptomatic rates at FH were assessed using an autoregressive moving average time series analysis. To examine the association between these rates, we fitted a seventh-order autoregression for the residuals based on autocorrelation function and partial autocorrelation function plots of the residuals from linear regression. **Results:** From April 23, 2020, to