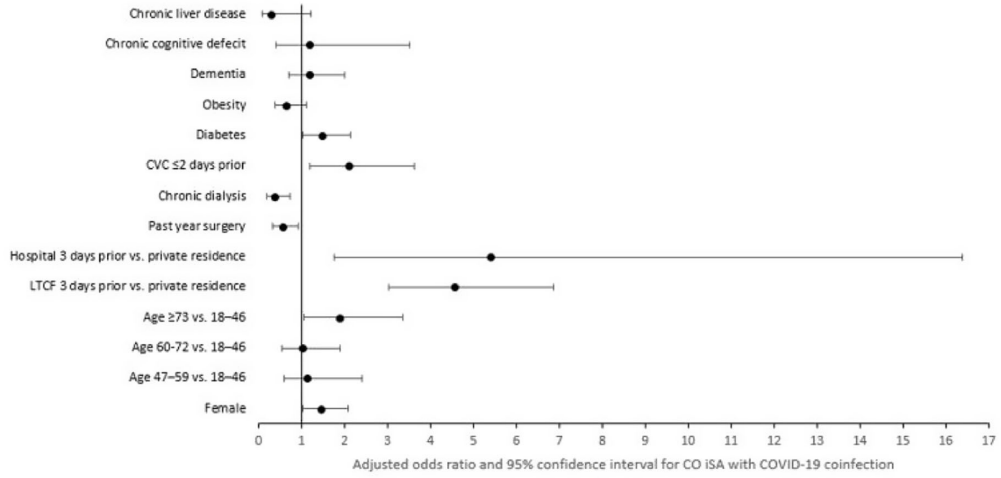
Figure 2. Multivariable analysis of demographic and epidemiologic characteristics associated with SARS-CoV-2 coinfection among community-onset invasive *Staphylococcus aureus* cases, 11 US counties, March 1–December 31, 2020.



Ghinwa Dumyati; Marissa Tracy; William Schaffner; Holly Biggs and Isaac See

Background: Previous analyses describing the relationship between SARS-CoV-2 infection and *Staphylococcus aureus* have focused on hospital-onset *S. aureus* infections occurring during COVID-19 hospitalizations. Because most invasive *S. aureus* (iSA) infections are community-onset (CO), we characterized CO iSA cases with a recent positive SARS-CoV-2 test (coinfection). **Methods:** We analyzed CDC Emerging Infections Program active, population- and laboratory-based iSA surveillance data among adults during March 1–December 31, 2020, from 11 counties in 7 states. The iSA cases (*S. aureus* isolation from a normally sterile site in a surveillance area resident) were considered CO if culture was obtained <3 days after hospital admission. Coinfection was defined as first positive SARS-CoV-2 test ≤14 days before the initial iSA culture. We explored factors independently associated with SARS-CoV-2 coinfection versus no prior positive SARS-CoV-2 test among CO iSA cases through a multivariable logistic regression model (using demographic, healthcare exposure, and underlying condition variables with P<0.25 in univariate analysis) and examined differences in outcomes through descriptive analysis. **Results:** Overall, 3,908 CO iSA cases were reported, including 138 SARS-CoV-2 coinfections (3.5%); 58.0% of coinfections had iSA culture and the first positive SARS-CoV-2 test on the same day (Fig. 1). In univariate analysis, neither methicillin resistance (44.2% with coinfection vs 36.5% without; $P = .06$) nor race and ethnicity differed significantly between iSA cases with and without SARS-CoV-2 coinfection ($P = .93$ for any association between race and ethnicity and coinfection), although iSA cases with coinfection were older (median age, 72 vs 60 years , P<0.01) and more often female (46.7% vs 36.3%, P=0.01). In multivariable analysis, significant associations with SARS-CoV-2 coinfection included older age, female sex, previous location in a long-term care facility (LTCF) or hospital, presence of a central venous catheter (CVC), and diabetes (Figure 2). Two-thirds of co-infection cases had ≥1 of the following characteristics: age > 73 years, LTCF residence 3 days before iSA culture, and/or CVC present any time during the 2 days before iSA culture. More often, iSA cases with SARS-CoV-2 coinfection were admitted to the intensive care unit ≤2 days after iSA culture (37.7% vs 23.3%, P<0.01) and died (33.3% vs 11.3%, P<0.01). **Conclusions:** CO iSA patients with SARS-CoV-2 coinfection represent a small proportion of CO iSA cases and mostly involve a limited number of factors related to likelihood of acquiring SARS-CoV-2 and iSA. Although CO iSA patients with SARS-CoV-2 coinfection had more severe outcomes, additional research is needed to understand how much of this difference is related to differences in patient characteristics.
Disclosures: None

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Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: MRSA/VRE
Methicillin-resistant *Staphylococcus aureus* mupirocin resistance rates in a large healthcare system
Mindy Sampson; Robert Fairman; Elizabeth Palavecino; Werner Bischoff; Julie Williamson; Shelley Keste and Catherine Passaretti

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a common etiology of hospital-acquired infections (HAIs). One strategy to reduce HAIs due to MRSA involves a multistep decolonization process. This often involves nasal application of mupirocin 2% ointment. In our institution, when individuals meet criteria for decolonization, we recommend 5 days of treatment given twice daily. High levels of mupirocin resistance have been reported in some hospital systems, with >80% of tested isolates being resistant. To better understand our resistance levels, we selected 238 MRSA isolates from blood cultures to be tested for mupirocin resistance to correlate the presence of resistance and use of mupirocin for decolonization. We choose to assess MRSA blood isolates rather than nasal swabs given that we aim to prevent invasive MRSA infections, including blood stream infections, with decolonization. The blood cultures were collected from 11 acute-care facilities within our system from March 2021 through June 2022. High-level resistance was defined as an MIC >1,024 µg/mL according to Clinical and Laboratory Standards Institute guidelines. Of those, 7.14% showed high level resistance, and 76.47% occurred in those who were exposed to mupirocin and 23.53% occurred in those without mupirocin exposure ($P = .0094$). On average, those with high-level resistance had had more recent exposure to mupirocin compared to those without resistance, which was statistically significant. Also, those with high resistance, on average, received more doses of mupirocin, although this was not statistically significant. **Conclusions:** More recent and higher number of doses of mupirocin were associated with the development of resistance, which is consistent with what we know from pharmacodynamics of antibiotic resistance with other agents. These findings may be

Table 1: Comparison of Mupirocin dosing and hospitalizations in those with mupirocin resistance

	High Level Resistance	Absence of High Level Resistance	t-value	p-value
Mean doses of mupirocin in the year prior	18	13.4105	-1.32	0.1898
Mean number of mupirocin courses in the year prior	2	1.6632	-0.57	0.5717
Mean days from last exposure to mupirocin to collection of blood culture isolate	30	76	3.28	0.0016
Mean number of hospitalizations in the year prior	2.5	2.2	-0.35	0.7257

particularly important for those patients who have frequent hospitalizations and often require decolonization. Understanding baseline mupirocin resistance levels in an institution can assist with determining decolonization strategies.

Disclosures: None

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Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Occupational Health
Correlating symptoms to infectivity among vaccinated healthcare workers with COVID-19
Abdulaziz Almulhim; Francine Touzard Romo; Leonard Mermel; Amy Mathers and Joshua Eby

Background: Directing COVID-19 diagnostic testing to healthcare workers (HCWs) who are likely to be infected has potential to reduce staffing shortages and decrease opportunity for in-hospital transmission; however, HCWs with COVID-19 may exhibit a range of symptoms. We assessed the burden of symptoms in relation to cycle threshold (Ct) values as a surrogate for viral shedding in vaccinated healthcare workers. **Methods:** We retrospectively reviewed employee health records of COVID-19–vaccinated employees who tested positive for SARS-CoV-2 between December 2020 and January 2022 at 2 academic hospital systems. We reviewed demographic data, reasons for testing including symptoms, exposure history, medical history, vaccination dates, Ct values, and genotypes when available. We compared mean Ct values between symptomatic and minimally symptomatic cases using independent sample *t* tests. Patients were defined as minimally symptomatic if they had no symptoms or a single symptom that is not cough, fever, or anosmia at the time of testing. Patients were defined as more symptomatic if they reported >1 symptom or cough, fever, or anosmia. **Results:** In total, 298 HCWs tested positive for COVID-19. Most positive cases were female (73%), white (78%), and had patient-facing roles (77%). Genotypic testing (n = 109) revealed that most genotypes belonged to the SARS-CoV-2 delta variant (AY lineages, B1.617.2). More cases were minimally symptomatic (62%) than were more symptomatic (38%). None required hospitalization during the study period. Mean Ct values (n = 141) showed no significant difference between more symptomatic and minimally symptomatic cases (19.8 vs 20.6; $P = .40$) (Fig. 1). Also, there was no significant difference in mean Ct value, comparing those with vaccination 90 days prior to positive (20.52 vs 19.88; $P = .537$). **Conclusions:** Our study shows no significant difference in cycle threshold values between minimally symptomatic and more symptomatic infections in vaccinated HCWs. In addition, HCWs exhibit high viral load even when infected within 90 days after vaccination. When considering whether to attend work, HCWs should be aware that mild symptoms and recent vaccination do not necessarily reflect low transmissibility and that they should follow CDC guidance regarding when to return to work.

Disclosures: None

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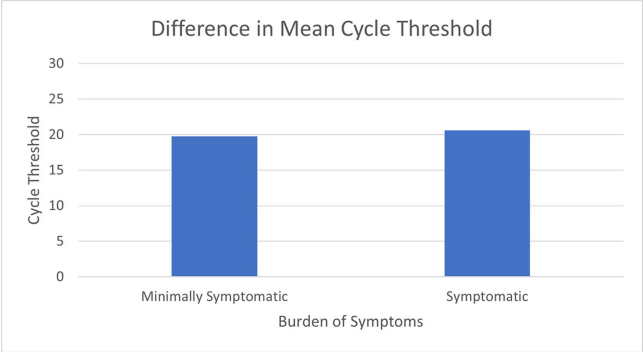

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Other
Detecting fecal microbiota transplantation–associated infection transmission using shotgun metagenomic sequencing and clonality analysis
Emma Briars; Mohamad Sater; Nicole Billings; Ian Herriott; Emily MacLeod and Miriam Huntley

Background: Fecal microbiota transplantation (FMT) is a widely used modality for safe and effective treatment of recurrent *Clostridium difficile* infections, and FMT is being explored for the treatment of additional indications including gastrointestinal diseases and neurological disorders. Although microbiota-based therapies like FMT utilize rigorous donor screening procedures, these procedures are limited in resolution and scope, and there remains a risk of transmission of FMT-associated infectious agents from donor stool to a FMT recipient. Critically, these health concerns led the FDA to issue a 2019 safety alert for the transmission risks associated with FMT and to update its guidelines for screening and reporting. In a suspected transmission event, there is uncertainty around the source of infection; thus, methods are needed to rapidly determine whether a patient's infection is linked to the donor stool product. **Methods:** Here, we developed a laboratory service sequencing and bioinformatics pipeline within our CLIA-certified laboratory for investigating suspected FMT infection transmission by measuring genomic relatedness. Our pipeline performs deep sequencing of a metagenomic sample, whole-genome sequencing (WGS) of an isolate derived from the implicated patient infection and determines the genomic relatedness between the 2 using a SNP-based analysis. The workflow was validated in silico with synthetic metagenomic samples spiked-in with WGS of clinically relevant isolate strains at varying abundance. **Results:** The sample and sequencing library preparation workflow was optimized across a panel of metagenomic and mock fecal microbiome samples demonstrating reproducible and reduced-bias sequencing of metagenomic samples. Our pipeline demonstrates high sensitivity and specificity for clonality calls when a spiked in isolate genome achieves 5× depth for >50% of the genome. We also demonstrated an interplay between abundance rate and sequencing depth for determining a clonality limit of detection. **Conclusions:** Taken together, our pipeline represents a new method that can support the clinical efforts of FMT and other microbiota-based therapies. **References:** US Food and Drug Administration. Important safety alert regarding use of fecal microbiota for transplantation and risk of serious adverse reactions due to transmission of multidrug-resistant organisms. Rockville, MD: Food and Drug Administration, 2019. DeFilipp Z, Bloom PP, Torres Soto M, et al. Drug-resistant *E. coli* bacteremia transmitted by fecal microbiota transplant. *N Engl J Med* 2019;381:2043–2050.

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Disclosures: None

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