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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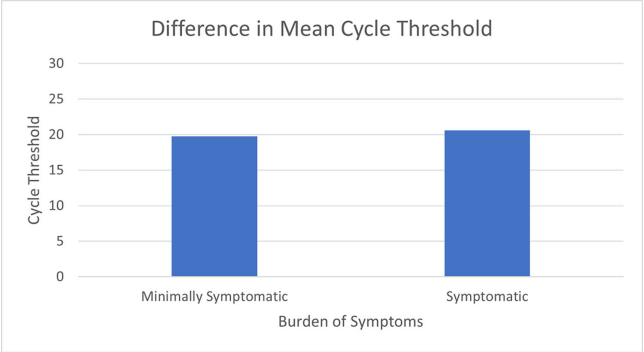

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Other
Detecting fecal microbiota transplantation–associated infection transmission using shotgun metagenomic sequencing and clonality analysis
Emma Briars; Mohamad Sater; Nicole Billings; Ian Herriott; Emily MacLeod and Miriam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