Pathogen	Number of CLABSIs
Bacteroides sp	22
Clostridium sp	14
Lactobacillus sp	11
Fusobacterium nucleatum	4
Actinomyces sp	3
Prevotella sp	3
Cutibacterium acnes	1
Veillonella sp	1
Peptostreptococcus sp	1

Fig. 1.

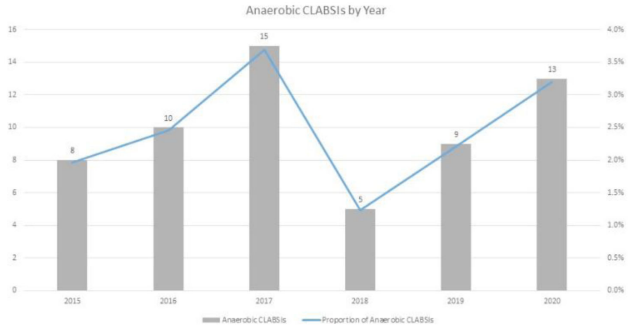

Fig. 2.

Table. Epidemiologic Criteria for Source of Healthcare Personnel (HCP) COVID-19 within Genomic Clusters

Source	Criteria
Healthcare associated: Patient source	• Clinical or patient-facing HCP • Patient diagnosed with COVID-19 before HCP diagnosed with COVID-19 • HCP exposed to COVID-19 patient 2-14 days before HCP tested positive
Healthcare associated: HCP source	• Clinical or patient-facing HCP and non-patient-facing HCP • Source HCP diagnosed with COVID-19 before recipient HCP diagnosed with COVID-19 • HCP exposed to source HCP 2-14 days before recipient HCP tested positive
Not healthcare associated	Inconclusive evidence to support a patient or HCP source within the healthcare setting

Abbreviations in table: healthcare personnel (HCP)

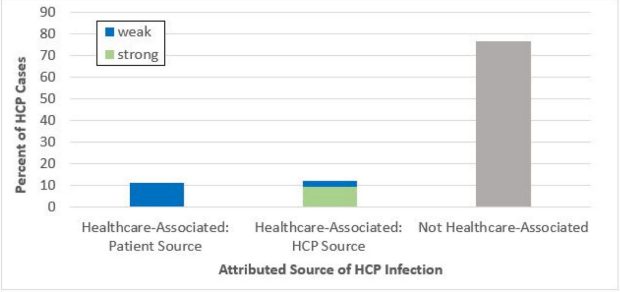

Figure. Epidemiologic links supporting transmission from symptomatic patients and/or staff to healthcare personnel (HCP) was uncommon. Genomic clusters were independently evaluated for valid epidemiologic links using metadata extracted from the electronic medical record. Most HCP infections were judged as not healthcare-associated (88/115, 76.5%). We did not identify any strong linkages for patient-to-HCP transmission. Thirteen HCP cases (11.3%) were attributed to patient source (weak linkage). Fourteen HCP cases (12.2%) were attributed to HCP source (11 strong and 3 weak linkages).

in the 53 community hospitals over the 6-year study period. Of these 29 anaerobic CLABSIs, 23 (79%) were clinically consistent with secondary bloodstream infections (BSIs) due to gastrointestinal or genitourinary source, but they lacked appropriate documentation to meet NHSN criteria for secondary BSI or MBI-LCBI based on case reviews by infection prevention physicians. The other 6 anaerobic CLABSIs did not have a clear clinical etiology and did not meet MBI-LCBI criteria. In addition, 27 (93%) of 29 anaerobic CLABSIs occurred in patients who were either solid-organ transplant recipients, were stem-cell transplant recipients, or were receiving chemotherapy. Lastly, 27 (93%) of 29 anaerobic CLABSIs were treated with antibiotics. **Conclusions:** Anaerobic CLABSIs are uncommon events, but CLABSI may disproportionately affect large, academic hospitals caring for a high proportion of medically complex patients. Additional criteria could be added to the MBI-LCBI to better classify anaerobic BSI.

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Disclosures: None

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Poster Presentation - Oral Presentation
Subject Category: COVID-19

Genomic investigation to identify the source of SARS-CoV-2 infection among healthcare personnel

Sarah Sansom; Hannah Barbian; Evan Snitkin; Christine Fukuda; Nicholas Moore; Lahari Thotapalli; Elias Baied; DO Young Kim; Mary Hayden and Michael Lin

Background: Contact tracing alone is often inadequate to determine the source of healthcare personnel (HCP) COVID-19 when SARS-CoV-2 is widespread in the community. We combined whole-genome sequencing (WGS) with traditional epidemiologic analysis to investigate the frequency with which patients or other HCP with symptomatic COVID-19 acted as the source of HCP infection at a large tertiary-care center early in the pandemic. **Methods:** Cohort samples were selected from patients and HCP with PCR-positive SARS-CoV-2 infection from a period with complete retention of samples (March 14, 2021–April 10, 2020) at Rush University Medical Center, a 664-bed hospital in Chicago, Illinois. During this period, testing was limited to symptomatic patients and HCP. Recommended respiratory equipment for HCP evolved under guidance, including a 19-day period when medical face masks were recommended for COVID-19 care except for aerosol-generating procedures. Viral RNA was extracted and sequenced (NovaSeq, Illumina) from remnant nasopharyngeal swab samples in M4RT viral transport medium. Genomes with >90% coverage underwent cluster detection using a 2 single-nucleotide variant genetic distance cutoff. Genomic clusters were independently evaluated for valid epidemiologic links by 2 infectious diseases physicians (with a third adjudicator) using metadata extracted from the electronic medical record and according to predetermined criteria (Table 1). **Results:** In total, 1,031 SARS-CoV-2 sequences were analyzed, identifying 49 genomic clusters with HCP (median, 8; range, 2–43 members per cluster; total, 268 patients and 115 HCP) (Fig. 1). Also, 20,190 flowsheet activities were documented for cohort HCP and patient interactions, including 686 instances in which a cohort HCP contributed to a cohort patient's chart. Most HCP infections were considered not healthcare associated (88 of 115, 76.5%). We did not identify any strong linkages for patient-to-HCP transmission. Moreover, 13 HCP cases (11.3%) were attributed to patient source (weak linkage). Also, 14 HCP cases (12.2%) were attributed to HCP source (11 strong and 3 weak linkages). Weak linkages were due to lack of epidemiologic data for HCP location, particularly nonclinical staff (eg, an environmental service worker who lacked location documentation to rule out patient-specific contact). Agreement for epidemiologic linkage between the 2 evaluators was high (κ, 0.91). **Conclusions:** Using genomic and epidemiologic data, we found that most HCP COVID-19 infections were not healthcare associated. We found weak evidence to support symptomatic patient-to-HCP transmission of SARS-CoV-2 and stronger evidence for HCP-to-HCP transmission.

Large genomic clusters without plausible epidemiologic links were identified, reflecting the limited utility of genomic surveillance alone to characterize chains of transmission of SARS-CoV-2 during extensive community spread.

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Poster Presentation - Oral Presentation
Subject Category: COVID-19
The SHIELD Study: A preliminary analysis of nasal and oral antisepsis to prevent COVID-19

Julie Keating; Linda McKinley; Lin Zhao; KyungMann Kim; Thomas Friedrich; David O'Connor; Daniel Shirley and Nasia Safdar

Background: Povidone-iodine and chlorhexidine gluconate are commonly used antiseptics that have broad antiviral properties, including against SARS-CoV-2. Nasal and oral antisepsis is a possible option to reduce viral transmission; however, effectiveness data are limited. The acceptability of this method for adjunct infection control is also unknown. We are conducting a clinical randomized controlled trial (NCT04478019) to evaluate the effectiveness and feasibility of nasal and oral antisepsis to prevent COVID-19. **Methods:** Healthcare and other essential workers with in-person job duties were recruited into a 10-week clinical trial. Participation did not require in-person activities: all communication was web- or telephone-based, supplies were shipped directly to the participant, and participants self-collected specimens. Participants completed a 3-week intervention and 3-week control phases and were randomized to the timing of these phases (Fig. 1). During the 3-week intervention phase, participants applied povidone-iodine nasal swabs 2 times per day and chlorhexidine gluconate oral rinse 4 times per day following the manufacturers' instructions for use. Participants continued all usual infection control measures (eg, face masks, eye protection, gowns, hand hygiene) as required by their workplace. To measure effectiveness against viral transmission, participants collected midturbinate nasal swabs 3 times per week to measure SARS-CoV-2 viral load. Participants also self-reported COVID-19 tests they received and why (eg, symptoms or exposure). To assess acceptability, participants completed pre- and post-surveys about their perceived and actual experience with the interventions. Participants also self-reported adverse effects due to the intervention. **Results:** As of December 3, 2021, 221 participants (148 healthcare workers and 73 non–healthcare essential workers) had enrolled. Moreover, 20 adverse effects have been reported, including skin irritation, epistaxis, and mouth discoloration; 9 participants withdrew due to side effects. Laboratory analyses are ongoing to measure effectiveness in reducing SARS-CoV-2 viral load. We performed an interim analysis of intervention acceptability. Survey responses were given on a Likert scale of 1 (not at all) to 5 (extremely). Although 36% of respondents (n = 74) reported on the postsurvey that the intervention was less acceptable than they had expected on the presurvey, the overall acceptability measure was still relatively high (3.76) (Fig. 2). In addition, 76% of respondents reported that they would use the intervention in the future (n = 56). **Conclusions:** Participant recruitment is ongoing, and data continue to be collected to analyze effectiveness and feasibility. Preliminary data suggest that participants find the nasal and oral antisepsis intervention to be an acceptable option to complement standard infection control methods to prevent COVID-19.

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Subject Category: COVID-19
Effect of COVID-19 vaccination on transmission among healthcare workers in South Korea

Jiyun Kim; Jiwon Jung; Songhee Namgung; Jihye Jung; Sun Kyung Kim; Young-ju Lim; Eun Ok Kim and Sung-Han Kim

Background: SARS-CoV-2 infection of healthcare workers (HCWs) occasionally occurs via acquisition from their colleagues. Data regarding the infection rates of HCWs with close contact and non–close contacts of HCWs are limited. In addition, the protective effect of COVID-19 vaccination against transmission between HCWs is unknown. We evaluated the

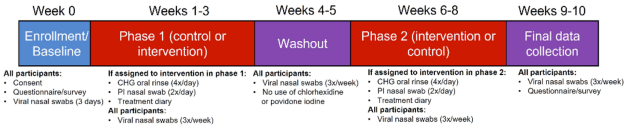

Fig. 1.

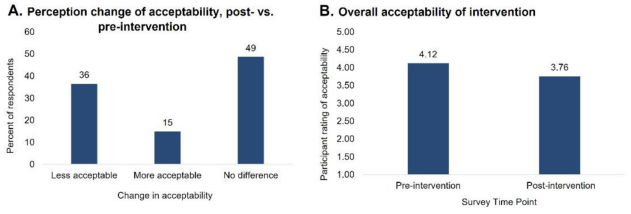

Fig. 2.

Table 1. Infection rate stratified by classification of contact, vaccination status of index and that of contacts, and vaccine type.

Value for infection rate	Close contact	Non-close contact	P value
Total	1.52% (18/1186)	0.86% (13/1507)	0.11
Stratification by vaccination status of index			
Infection rate	**Fully vaccinated index**	**Non-fully vaccinated index**	**P value**
Close contact	0.85% (7/820)	3.01% (11/366)	0.005
Non-close contact	0.83% (6/723)	0.89% (7/784)	0.90
Stratification by vaccination status of contacts			
Infection rate	**Fully vaccinated contact**	**Non-fully vaccinated contact**	**P value**
Close contact	1.15% (9/783)	2.23% (9/403)	0.15
Non-close contact	0.93% (7/752)	0.79% (6/755)	0.63
Subgroup analysis – during the delta variant being dominant			
Infection rate	**Fully vaccinated index**	**Non-fully vaccinated index**	**P value**
Close contact	0.85% (7/820)	5.88% (8/136)	<0.001
Non-close contact	0.83% (6/723)	0.75% (2/266)	>0.99
Infection rate	**Fully vaccinated contact**	**Non-fully vaccinated contact**	**P value**
Close contact	1.15% (9/783)	3.47% (6/173)	0.04
Non-close contact	0.93% (7/751)	0.42% (1/238)	0.69
Subgroup analysis – by vaccine type			
Infection rate from fully vaccinated index	**ChAdOx1 nCoV-19**	**mRNA vaccine (BNT162b2 or mRNA-1273)**	**P value**
Close contact	1.07% (7/654)	0% (0/69)	>0.99
Non-close contact	0.99% (6/608)	0% (0/64)	>0.99
Infection rate in fully vaccinated contacts	**ChAdOx1 nCoV-19**	**mRNA vaccine (BNT162b2 or mRNA-1273)**	**P value**
Close contact	1.25% (8/640)	1.12% (1/89)	>0.99
Non-close contact	0.99% (6/605)	1.11% (1/90)	>0.99