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asymptomatic positive COVID19 patients allowed timely implementation of mitigation plans that included patient placement and isolation, rapid contact tracing, strict adherence to social distancing and at times enhanced masking requirements among other strategies.

Results: Serial testing of patients in communal settings led to a reduced number of days a treatment area was closed by having the early identification of potential transmission and real time interventions. The addition of an electronic alert proved valuable to ensure timely testing. While unable to calculate the true benefit beyond offering needed services to patients, the use of serial testing limited transmission to patients and staff. Ultimately, this helped alleviate the impact to the stretched workforce.

Conclusions: Serial testing in defined populations was beneficial in the early waves of COVID19. Modifications continue based on the rapidly changing backdrop of the pandemic and evaluation of current data.

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Successful Implementation of an Electronic Application in Reinvigorating a Healthcare Organization's Hand Hygiene Program

Maria Vacca MSN, RN, CIC, APIC Philadelphia; **Lisa Gillen MS, BS, CIC**, Jefferson Health New Jersey; **Cindy M. Hou DO, MA, MBA, FACOI, FACP, FIDSA**, Jefferson Health New Jersey; **Ashlee Hlester BSN, RN, CIC**, APIC South Jersey; **Joseph DeRose DO**, Jefferson Health New Jersey; **Raquel Fedele**, Jefferson Health; **Mary E. Miller RN, BSN, CIC**, Jefferson New Jersey

Background: Our organization prioritizes the importance of a comprehensive hand hygiene program in promoting patient safety but found it challenging to meet regulatory requirements and to operationalize an efficient program. Recognizing that manual observations were labor intensive and automated hand hygiene was cost prohibitive, we looked to an innovative, inexpensive electronic application (app) to reinvigorate our hand hygiene program.

Methods: In 2021, our facility's hand hygiene committee, with support from senior leadership, developed and led a strategic plan to develop and implement a meaningful hand hygiene campaign with timeline for completion. This plan included a beta pilot to implement an innovative, affordable electronic app in all licensed inpatient and outpatient departments including nursing units, and surgical services over a five-month time period. Each area is required to submit a minimal number of observations per month which was calculated using regulatory guidelines. Manual tallies are no longer required. Data is submitted and analyzed electronically and available to act upon in real time. The strategic plan included comprehensive training, education, and continued feedback at all levels from bedside staff to administration.

Results: Upon complete implementation of our electronic application our monthly hand hygiene observations went from averaging a few hundred per month to 9000 observations per month. Transitioning from a manual to an electronic program has also resulted in a staggering cost savings of four full time employees for an approximated cost savings of 250,000 dollars annually. Additionally, a survey of all staff observers revealed that ninety

three percent found the app to improve their workflow and save them time.

Conclusions: Through development, and implementation of this comprehensive electronic hand hygiene initiative our organization was able to meet all regulatory requirements, engage staff, increase patient safety, and recognize a significant cost savings for our organization. Senior leadership's support was key in the success of this program.

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Whole Genome Sequencing (WGS) for COVID-19 Outbreak Evaluations – How Much Does It Add to Bootstrap Epidemiology & Contact Tracing?

Keith Olenslager MPH, UCI Health; **Jennifer Yim BSN, RN, CIC, CPHQ**, UCI Health; **Linda Dickey RN, MPH**, UCI Health; **Emily Bueno MSN, RN**, UCI Health; **Delia F. Tifrea PhD**, UC Irvine Pathology Department; **Megan Crumpler PhD**, Orange County Public Health Laboratory; **Susan Huang MD, MPH**, UCIMC; **Shruti K. Gohil MD, MPH**, UC Irvine Health

Background: Epidemiologic investigations are foundational in outbreak evaluations but are unable to fully capture the innumerable interactions that lead to exposure. Whole Genome Sequencing (WGS) offers clonality information that can suggest potential transmission links but is costly and resource intensive. We compared COVID-19 exposure source as determined by contact tracing investigations with linkages inferred by WGS data for a COVID-19 outbreak among healthcare workers (HCWs) and patients.

Methods: Contact tracing investigations were conducted for HCWs identified in three COVID-19 hospital clusters and included interviews to assess exposure history and infection prevention breaches and categorized as either: Community, HCW-to-HCW, Patient-to-HCW, HCW-to-Patient, or Unknown. WGS evaluations were completed for 45 (34 HCWs, 11 patients) COVID-19 positive samples (Quiagen EZ1 RNA extraction, Illumina Nextera FLEX library/Illumina NextSeq 500). Exposure source determinations were reevaluated using WGS data. Agreement between the two strategies were described as percentage and compared using Cohen's Kappa.

Results: Among 45 samples submitted, 37 were successfully sequenced, and 19 (51%, 17 HCWs and 2 patients) were identified as potentially linked clonal Epsilon (B.1.429) COVID-19 variant strains. WGS identified 13 identical and 6 closely related strains that suggested linkages between 15 HCW-HCW, 2 HCW-Patient, 1 community, and 1 unknown transmission. Contact tracing categorized the 19 cases as: 8 HCW-HCW, 1 Patient-HCW, 3 Community, and 7 Unknown. After incorporating WGS data, these were reclassified as 9 HCW-HCW, 5 Community, and 5 Unknown. Combining contact tracing with WGS information resulted in 6 (32%) reclassifications; agreement between the two strategies was 58% (Cohen's kappa=0.19), identifying 1 previously unrecognized 1 HCW-HCW and 2 community cases. While contact tracing had suggested 1 patient-HCW transmission, WGS results did not show matching strains.

Conclusions: WGS can improve the precision of COVID-19 outbreak investigation of transmission links in almost one third of cases.