42. Outbreak of SARS-CoV-2 in Hospitalized Hemodialysis Patients: an Epidemiologic and Genomic Investigation

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Session: O-09. COVID-19 in Healthcare Settings

Background. Healthcare-associated transmission of SARS-CoV-2 is relatively rare and may be difficult to quantify. We performed an epidemiological investigation and SARS-CoV-2 genome sequencing to define the source and scope of a SARS-CoV-2 outbreak in a cluster of hospitalized patients

Methods. We conducted an outbreak investigation after identifying hospital-onset COVID-19 in patients receiving hemodialysis in January 2021. Electronic medical record review, staff interviews, review of employee schedule logs, and contact tracing were used to determine the outbreak timeline and identify exposed healthcare workers (HCW).

SARS-CoV-2 genomes were sequenced from residual nasopharyngeal swab samples from 6 individuals in the outbreak investigation and compared to sequences from 14 patients in the same facility, 54 patients in nearby facilities, and 375 publicly available sequences from individuals in the state of Georgia.

Results. Eight patients with hospital-onset COVID-19 were identified (Cases 1-8); all were receiving hemodialysis and 5 were bedded in a single inpatient nursing unit. Among 53 potentially exposed HCW, 29 underwent testing and 5 were positive (Cases 9-13). The suspected index patient (Case 1) was found to have been coughing inconsistently during a hemodialysis session on the same day that 6 of the 7 other patients and 1 HCW (Case 10) were in close proximity in the hemodialysis unit (Figure 1A). Further investigation revealed lack of use of curtain barriers in the hemodialysis bays, inconsistent use of personal protective equipment by HCW, and overcrowding of staff breakrooms. Among the 6 samples available for phylogenetic analysis, SARS-CoV-2 sequences from 5 (4 patients and 1 HCW, Case 9) were identical and at least 4 SNPs removed from the next closest sequence in this study, supporting a transmission cluster (Figure 1B). The sequence from the sixth sample (HCW Case 10) was phylogenetically distinct, indicating an independent source of infection.

Figure 1

Exposure and onset of symptoms for the 6 cases in the outbreak with samples available for SARS-CoV-2 sequencing. Four patients with hospital-onset COVID-19 (Cases 1-4) were receiving hemodialysis and bedded in a single inpatient nursing unit, with two exposed healthcare workers (Cases 9-10). A phylogenetic tree of SARS-CoV-2 genomes from individuals in this outbreak investigation (red), as well as 14 patients in the same facility and 54 patients in nearby facilities between 12/12/2020 and 1/13/2021 (blue). These were aligned with 375 publicly available sequences from individuals in the state of Georgia from the same time period using Mafft. A maximum-likelihood phylogenetic tree was generated under a generalized time-reversible model with 1,000 bootstrap replicates using IQtree v2.0.3 and visualized and annotated using Interactive Tree of Life (iTOL) v4 (B).

Conclusion. Lack of appropriate respiratory hygiene led to SARS-CoV-2 transmission during a single hemodialysis session, based on clinical and genomic epidemiology. Use of appropriate PPE for both patients and HCW and other infection prevention measures are critical to prevent SARS-CoV-2 transmission.

Disclosures. All Authors: No reported disclosures

43. SARS-CoV-2 Cycle threshold (Ct) values predict future COVID-19 cases

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Session: O-09. COVID-19 in Healthcare Settings

Background. The threat of surging COVID-19 cases prompted many hospitals in the United States to preemptively suspend elective procedures throughout the pandemic. Utilizing samples from a large hospital in Los Angeles, we sought to determine if temporal trends in SARS-CoV-2 Cycle threshold (Ct) values (proxy for viral RNA loads) were predictive for the number of future COVID-19 cases.

Methods. Nasopharyngeal specimens on symptomatic patients and asymptomatic admissions were tested using the Xpert Xpress SARS-CoV-2 and SARS-CoV-2/Flu/RSV assays (Cepheid). Ct values for all SARS-CoV-2 detections between October 2020 to March 2021 were compiled for analysis.

Results. A total of 2,114 SARS-CoV-2-positive samples were included. The number of tests performed per week increased dramatically in December peaking the first week of January before returning to pre-surge numbers by Mid-February. Ct values fell during this same period with values in December and January (25.6±7.8 and 27.7±7.9, respectively) significantly lower than those of the other months (30±9.3 to 37.7±6.3). Average weekly Ct values for all patients were significantly, negatively correlated with the number of tests run the following week (R=-0.71, P< 0.001) and two weeks later (R=-0.75, P< 0.0001). Ct values for patients who were asymptomatic at the time of testing most strongly correlated with total number of tests performed one month later (R=-0.86, P< 0.0001).

Average weekly Ct values and number of test run

As cases (light grey) increased during December and January, there was a significant decrease in Ct values (dark grey) during that same time period. Average Ct values are a leading indicator of cases.
Average weekly Ct values for all patients (light grey) were significantly, negatively correlated with the number of tests run the following week (R = -0.71, P<0.001) and two weeks later (R = -0.75, P<0.0001). Ct values for patients who were asymptomatic at the time of testing (dark grey) most strongly correlated with total number of tests performed one month later (R = -0.86, P<0.0001).

**Conclusion.** Lower Ct values, representing higher levels of viral RNA, have been associated with risk of intubation and infectivity. During the winter surge, we observed significantly lower Ct values suggesting that the increased transmission and morbidity of COVID-19 was temporarily associated with higher viral loads. Interestingly, Ct values for asymptomatic patients were most strongly associated with number of cases observed 1 months in the future, suggesting that asymptomatic viral load may be a leading indicator for forthcoming outbreaks. Given this association, Ct values may be a useful tool for predicting regional outbreaks of COVID-19 and more judicious cessation of elective procedures.

**Disclosures.** All Authors: No reported disclosures

### 44. Impact of Nursing Home (NH) Universal Decolonization and COVID Prevention Training on COVID-19 Burden During the 2020-2021 Winter Surge in Orange County (OC), California (CA)

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**Session:** O-09. COVID-19 in Healthcare Settings

**Background.** OC is the 6th largest U.S. county with 70 NHs. Universal decolonization (chlorhexidine for routine bathing, and twice daily nasal iodophor Mon-Fri every other week) was adopted in 24 NHs prior to the COVID-19 pandemic, and 12 NHs (11 of those adopting decolonization) participated in a COVID prevention training program with a rolling launch from July–Sept 2020. We evaluated the impact of these initiatives on staff and resident COVID cases.

**Methods.** We conducted a quasi-experimental study of the impact of decolonization and COVID prevention training on COVID cases in OC. Decolonization NHs received weekly visits for encouraging adherence during the pandemic, and NHs in the COVID training program received 3 in-person training sessions for all work shifts plus weekly feedback about adherence to hand hygiene, masking, and breakroom safety using video monitoring. We calculated incident 1) staff COVID cases, 2) resident COVID cases, and 3) resident COVID deaths adjusting for NH average daily census. We assessed impact of initiatives on these outcomes using linear mixed effects models testing the interaction between any training participation and calendar date when clustering by NH. Because of the overlap of the two initiatives, we evaluated 'any training' vs 'no training.'

**Results.** 63 NHs had available data. 24 adopted universal decolonization, 12 received COVID training (11 of which participated in decolonization), and 38 were not enrolled in either. During the winter surge, the 63 NHs experienced 1867 staff COVID cases, 2186 resident COVID cases, and 251 resident deaths due to COVID, corresponding to 29.6, 3.47, and 4.0 events per NH, respectively. In NHs participating in either initiative, staff COVID cases were reduced by 31% (OR=0.69 (0.52, 0.92), P=0.01), resident COVID cases were reduced by 43% (OR=0.57 (0.39, 0.82), P=0.003), and resident deaths were reduced (non-significantly) by 26% (OR=0.74 (0.46, 1.21), P=0.23).

**Conclusion.** NHs are vulnerable to COVID-19 outbreaks. A universal decolonization and COVID prevention training initiative in OC, CA significantly reduced staff and resident COVID cases in this high COVID burden period.

**Disclosures.** Gabrielle Gussin, MS, Medline (Other Financial or Material Support, Conducted studies in which participating hospitals and nursing homes received contributed antiseptic and cleaning products) Stryker (Sage) (Other Financial or Material Support, Conducted studies in which participating hospitals and nursing homes received contributed antiseptic products) Xtrium (Other Financial or Material Support, Conducted studies in which participating hospitals and nursing homes received contributed antiseptic and cleaning products) Stryker (Sage) (Other Financial or Material Support, Conducted studies in which participating hospitals and nursing homes received contributed antiseptic and cleaning products) Xtrium (Other Financial or Material Support, Conducted studies in which participating hospitals and nursing homes received contributed antiseptic and cleaning products) Shrutii K. Gohil, MD, MPH, Medline (Other Financial or Material Support, Co-Investigator in studies in which participating hospitals and nursing homes received contributed antiseptic and cleaning products) Molnycke (Other Financial or Material Support, Co-Investigator in studies in which participating hospitals and nursing homes received contributed antiseptic and cleaning products) Raheeb Saavedra, AS, Medline (Other Financial or Material Support, Conducted studies in which participating hospitals and nursing homes received contributed antiseptic and cleaning products) Stryker (Sage) (Other Financial or Material Support, Conducted studies in which participating hospitals and nursing homes received contributed antiseptic and cleaning products) Xtrium (Other Financial or Material Support, Conducted studies in which participating hospitals and nursing homes received contributed antiseptic and cleaning products) Robert Pedroza, BS, Medline (Other Financial or Material Support, Conducted studies in which participating hospitals and nursing homes received contributed antiseptic and cleaning products) Molnycke (Other Financial or Material Support, Conducted studies in which participating hospitals and nursing homes received contributed antiseptic and cleaning products) Raveena Singh, MA, Medline (Other Financial or Material Support, Conducted studies in which participating hospitals and nursing homes received contributed antiseptic and cleaning products) Molnycke (Other Financial or Material Support, Conducted studies in which participating hospitals and nursing homes received contributed antiseptic and cleaning products)

### 45. COVID-19 Vulnerability and Data Reporting in Africa: Reflections from Cameroon

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**Session:** O-10. Disparities in COVID Access to Care and Diagnostic Testing

**Background.** At the beginning of the COVID-19 pandemic there were many questions about vulnerability and data reporting among African countries. We previously found that policymakers in Cameroon value region-specific risk maps for emerging diseases. Therefore, we created regional vulnerability indices for COVID-19 in Cameroon. As the pandemic grew, we aimed to compare how these predictions related to reported COVID-19 cases in Cameroon and whether additional African countries had available data to assess vulnerability for COVID-19.