

390. Can Testing the Environment for SARS-CoV-2 Be a Signal for Staff Infections in Nursing Homes (NHs)?

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Session: P-16. COVID-19 Epidemiology and Screening

Background. Federal mandate requires NHs to perform weekly COVID-19 testing of staff. Testing is effective due to barriers to disclosing mild illness, but it is unclear how long the mandate will last. We explored if environmental samples can be used to signal staff COVID-19 cases as an alternative screening tool in NHs.

Methods. We conducted a cross sectional study to assess the value of environmental sampling as a trigger for COVID-19 testing of NH staff using data from currently performed weekly staff sweeps. We performed 35 sampling sweeps across 21 NHs from 6/2020-2/2021. For each sweep, we sampled up to 24 high touch objects in NH breakrooms (N=226), entryways (N=216), and nursing stations (N=194) assuming that positive samples were due to contamination from infected staff. Total staff and positive staff counts were tallied for the staff testing sweeps performed the week of and week prior to environmental sampling. Object samples were processed for SARS-CoV-2 using PCR (StepOnePlus) with a 1 copy/mL limit of detection. We evaluated concordance between object and staff positivity using Cohen's kappa and calculated the positive and negative predictive value (PPV, NPV) of environmental sweeps for staff positivity, including the attributable capture of positive staff. We tested the association between the proportion of staff positivity and object contamination by room type in a linear regression model when clustering by NH.

Results. Among 35 environmental sweeps, 49% had SARS-CoV-2 positive objects and 69% had positive staff in the same or prior week. Mean positivity was 16% (range 0-83%) among objects and 4% (range 0-22%) among staff. Overall, NPV was 61% and Cohen's kappa was 0.60. PPV of object sampling as an indicator of positive staff was 100% for every room type, with an attributable capture of positive staff of 76%, with values varying by room type (Table). Breakroom samples were the strongest indicator of any staff cases. Each percent increase in object positivity was associated with an increase in staff positivity in entryways (7.2% increased staff positivity, P=0.01) and nursing stations (5.7% increased staff positivity, P=0.05).

Table. Performance of Environmental Sampling of High-Touch Objects for SARS-CoV-2 as a Mechanism to Detect COVID-19 Infections Among Nursing Home Staff

	All Areas	Breakroom	Entryway	Nursing Station
Positive Predictive Value (PPV)	100%	100%	100%	100%
Negative Predictive Value (NPV)	61%	55%	46%	44%
Attributable Capture of Staff Cases*	76%	68%	51%	53%
2x2 Contingency Table <i>Staff and Environmental (Env) SARS-CoV-2 Positivity Across 35 Nursing Home Sweeps</i>	Staff +	Staff +	Staff +	Staff +
	Env -	Env -	Env -	Env -
	17 0 7 11	15 0 9 11	11 0 13 11	10 0 14 11

We explored if environmental sampling could be used to signal staff COVID-19 cases as an alternative screening tool in nursing homes. If the environment can accurately predict staff infections, then it may offer an efficient, cost-effective way to assess when comprehensive testing of staff should be undertaken, especially when current testing mandates end.

*Attributable capture was calculated as the total number of COVID-19 cases among staff in sweeps where environmental SARS-CoV-2 contamination was detected divided by the total number of staff cases across all sweeps.

Conclusion. If mandatory weekly staff testing ends in NHs, environmental sampling may serve as an effective tool to trigger targeted COVID-19 testing sweeps of NH staff.

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391. Small Towns, Big Cities: Rural and Urban Disparities Among Hospitalized Patients with COVID-19

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Background. More than half of all hospitals in the U.S. are rural hospitals. Frequently understaffed and resource limited, community hospitals serve a population that tends to be older and have less access to care with increased poverty and medical co-morbidities. There is a lack of data surrounding the impact of COVID-19 among rural minority communities. This study seeks to determine rural and urban disparities among hospitalized individuals with COVID-19.

Methods. This is a descriptive, retrospective analysis of the first 155 adult patients admitted to a tertiary hospital with a positive COVID-19 nasopharyngeal PCR test. Augusta University Medical Center serves the surrounding rural and urban counties of the Central Savannah River Area. Rural and urban categories were determined using patient address and county census data. Demographics, comorbidities, admission data and 30-day outcomes were evaluated.

Results. Of the patients studied, 62 (40%) were from a rural county and 93 (60%) were from an urban county. No difference was found when comparing the number of comorbidities of rural vs urban individuals; however, African Americans had significantly more comorbidities compared to other races (p-value 0.02). In a three-way comparison, race was not found to be significantly different among admission levels of care. Rural patients were more likely to require an escalation in the level of care within 24 hours of admission (p-value 0.02). Of the patients that were discharged or expired at day 30, there were no differences in total hospital length of stay or ICU length of stay between the rural and urban populations.

Baseline Characteristics of Hospitalized Patients with COVID-19

	No. (%)
Total Subjects	155 (100)
Gender	
Male	74 (47.7)
Female	81 (52.3)
Age	
Mean Age (SD)	59.85 (17.9)
Median Age (IQR)	62 (22.5)
18-29	9 (5.8)
30-44	26 (16.8)
45-64	55 (35.5)
65+	65 (41.9)
Race	
African-American	90 (58.8)
White	52 (34.0)
Hispanic	10 (6.5)
Asian	1 (0.7)
County type	
Rural	62 (40.0)
Urban	93 (60.0)

Day 30 Outcomes and Characteristics

Discharged Patients	Rural		Urban		p-value
	Mean (SD)	Median (IQR)	Mean (SD)	Median (IQR)	
Total Hospital Length of Stay (n=111)	11.32 (8.2)	8.5 (10.0)	9.61 (8.2)	7 (11.5)	0.10
ICU Length of Stay (n=73)	5.36 (7.7)	0 (9.3)	3.51 (6.8)	0 (2.5)	0.12
Expired Patients (n=22)					
	Mean (SD)	Median (IQR)	Mean (SD)	Median (IQR)	p-value
Age	67.86 (8.9)	67 (7.0)	69 (18.8)	66 (24.0)	0.94
Number of Comorbidities	3.00 (1.4)	3 (1.0)	3.4 (2.1)	3 (1.5)	0.97
Total Hospital Length of Stay	9.71 (8.1)	7 (6.0)	9.47 (6.9)	8 (3.0)	0.92
ICU Length of Stay	7.71 (7.3)	5 (8.0)	6.07 (8.3)	3 (6.5)	0.41

Level of Care at Time of Admission

	Admitted to the general medical ward	Admitted to general medical ward then transferred to ICU within 24 hrs	Admitted to ICU
Total Subjects (n, %)	92 (59.4)	14 (9.0)	48 (31.0)
Age group (n, %)			
18-29	8 (89.0)	0 (0)	1 (11.1)
30-44	21 (80.8)	2 (7.7)	3 (11.5)
45-64	29 (52.7)	5 (9.1)	21 (38.2)
65+	34 (52.3)	7 (10.8)	23 (35.4)
p-value	0.01	0.97	0.04
Race (n, %)			
African-American	51 (56.7)	9 (10.0)	30 (33.3)
White	33 (63.5)	3 (5.8)	15 (28.9)
Hispanic	7 (70.0)	2 (20.0)	1 (10.0)
p-value	0.62	0.25	0.34
County type (n, %)			
Rural	29 (46.8)	10 (16.1)	23 (37.1)
Urban	63 (67.7)	4 (4.3)	25 (26.9)
p-value	0.01	0.02	0.22

Conclusion. This study suggests that patients in rural communities may be more critically ill or are at a higher risk of early decompensation at time of hospitalization compared to patients from urban communities. Nevertheless, both populations had similar lengths of stay and outcomes. Considering this data is from an academic medical center with a large referral area and standardized inpatient COVID-19 management, these findings may prompt further investigations into other disparate outcomes.

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392. 3D-DOSS – Using Digital Twins and Spatiotemporal Data Mapping for Infectious Disease Surveillance and Outbreak Investigations

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Background. The COVID-19 pandemic has brought to light the importance of contact tracing in outbreak management. Digital technologies have been leveraged to enhance contact tracing in community settings. However, within complex hospital environments, where patient and staff movement and interpersonal interactions are central to care delivery, tools for contact tracing and cluster detection remain limited. We aimed to develop a system to promptly, identify contacts in infectious disease exposures and detect infectious disease clusters.

Methods. We prototyped a 3D mapping tool 3-Dimensional Disease Outbreak Surveillance System (3D-DOSS), to have a spatial representation of patients in the hospital inpatient locations. Based on the AutoCAD drawings, the hospital physical spaces are built within a game-development software to obtain accurate digital replicas. This concept borrows from the way gamers interact with the virtual world/space, to mimic the interactions in physical space, like the SIMS franchise. Clinical, laboratory and patient movement data is then integrated into the virtual map to develop syndromic and disease surveillance systems. Risk assignment to individuals exposed is through mathematical modeling based on distance coordinates, room type and ventilation parameters and whether the disease is transmitted via contact, droplet or airborne route.

Results. We have mapped acute respiratory illness (ARI) data for the period September to December 2018. We identified an influenza cluster of 10 patients in November 2018. In a COVID-19 exposure involving a healthcare worker (HCW), we identified 44 primary and 162 secondary contacts who were then managed as per our standard exposure management protocols. MDRO outbreaks could also be mapped.

Conclusion. Through early identification of at-risk contacts and detection of infectious disease clusters, the system can potentially facilitate interventions to prevent onward transmission. The system can also support security, environmental cleaning, bed assignment and other operational processes. Simulations of novel diseases

outbreaks can enhance preparedness planning as health systems that had been better prepared have been more resilient in this current pandemic.

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393. Characteristics of SARS-CoV-2 RNA Viral Loads among Nursing Home Residents and Staff with Repeat Positive Tests ≥ 90 Days After Initial Infection: 5 US Jurisdictions, July 2020–March 2021

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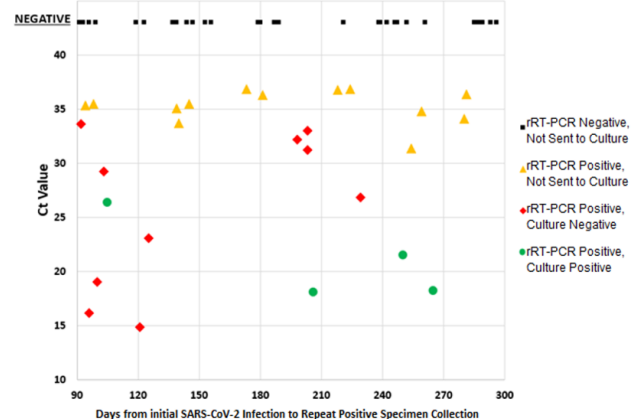
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Background. Background. Understanding the viral load and potential infectivity of individuals in nursing homes (NH) with repeat positive SARS-CoV-2 tests ≥ 90 days after initial infection has important implications for safety related to transmission in this high-risk setting.

Methods. Methods. We collected epidemiologic data by reviewing records of a convenience sample of NH residents and staff with respiratory specimens who had positive SARS-CoV-2 rRT-PCR test results from July 2020 through March 2021 and had a SARS-CoV-2 infection diagnosed ≥ 90 days prior. No fully vaccinated individuals were included. Each contributed one repeat positive specimen ≥ 90 days after initial, which was sent to CDC and retested using rRT-PCR. Specimens were assessed for replication-competent virus in cell culture if Cycle threshold (Ct) < 34 and sequenced if Ct < 30. Using Ct values as a proxy for viral RNA load, specimens were categorized as high (Ct < 30) or low (if Ct ≥ 30 or rRT-PCR negative at retesting). Continuous variables were compared using Wilcoxon signed-rank tests. Proportions were compared using Chi-squared or Fisher's exact tests.

Results. Results. Of 64 unvaccinated individuals with specimens from 61 unique NHs, 14 (22%) were sent for culture and sequencing. Ten of 64 (16%) had a high viral RNA load, of which four (6%) were culture positive and none were known variants of interest or concern (Figure 1). Median days to repeat positive test result were 122 (interquartile range (IQR): 103–229) and 201 (IQR: 139–254), respectively, for high versus low viral load specimens (p=0.13). More individuals with high viral loads (5/10, 50%) reported COVID-19 symptoms than with a low viral load (1/27, 4%, p=0.003). Most individuals (46/58, 79%) were tested following known or suspected exposures, with no significant differences between high and low viral load (p=0.18).

Figure 1. Cycle threshold (Ct) values for repeat positive SARS-CoV-2 specimens re-tested at CDC and days to specimen collection from initial infection: July 2020 – March 2021 (n=64) *



*One specimen with Ct=31 was inadvertently not sent to viral culture

*No specimens had genetic sequences matching variants of interest or concern per CDC SARS-CoV-2 Variant Classifications and Definitions (<https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html>) accessed June 1, 2021.