	Rural		Urban			
<b>Discharged Patients</b>	Mean (SD)	Median (IQR)	Mean (SD)	Median (IQR)	p-value	
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.

Disclosures. All Authors: No reported disclosures

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

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

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 (ÂRI) 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.

Disclosures. All Authors: No reported disclosures

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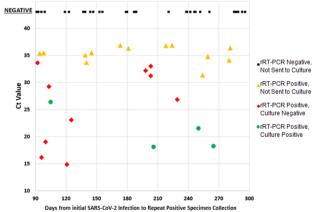
## Session: P-16. COVID-19 Epidemiology and Screening

Background. Background. Understanding the viral load and potential infectivity of individuals in nursing homes (NH) with repeat positive SARS-CoV-2 tests  $\geq$  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  $\geq$  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  $\ge$  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 (<u>https://w</u> 1, 2021. ww.cdc.gov/coronavirus/2019-ncov/c

Table 1. Characteristics of nursing home individuals with repeat positive SARS-CoV-2 specimens 90 days or more following initial infection: July 2020 – March 2021.

		Low RNA Viral	
	· · · · · ·		P-value*
N (%)	n (%)	n (%)	-
64	10	54	-
67 [51-80]	62 [47-79]	68 [53-80]	0.56
194 [124-			
251]	122 [103-229]	201 [139-254]	0.13
-	-	-	
40 (63%)	4 (40%)	36 (67%)	0.16
24 (38%)	6 (60%)	18 (33%)	
-	-	-	
30 (47%)	6 (60%)	24 (44%)	0.49
32 (50%)	7 (70%)	25 (46%)	0.30
7 [6-14]	4 [4-7]	8 [6-14]	0.05
-	-	-	-
31 (84%)	5 (50%)	26 (96%)	-0.04
6 (16%)	5 (50%)	1 (4%)	<0.01
-	-	-	
			0.18
12 (21%)	0 (0%)	12 (25%)	
48 (91%)	10 (100%)	38 (88%)	0.57
5 (9%)	0 (0%)	5 (12%)	0.57
	67 [51-80] 194 [124- 251] - 40 (63%) 24 (38%) - - 30 (47%) 32 (50%) 7 [6-14] - 31 (64%) 6 (16%) - 46 (79%) 12 (21%) - 48 (91%)	N (%)         n (%)           64         10           67 [51-80]         62 [47-79]           194 [124-         251]         122 [103-229]           -         -         -           40 (63%)         4 (40%)         -           24 (38%)         6 (60%)         -           -         -         -           30 (47%)         6 (60%)         7 (70%)           7 [6-14]         4 [4-7]         -           -         -         -           31 (84%)         5 (50%)         6 (16%)           -         -         -           -         -         -           -         -         -           31 (84%)         5 (50%)         6 (16%)           -         -         -           -         -         -           -         -         -           -         -         -           -         -         -           -         -         -           -         -         -           -         -         -           -         -         -           -         -	High RNA Viral Load (Ct 2 30 or negative at re- testing)*         Load (Ct 2 30 or negative at re- testing)*           N(%)         n (%)         n (%)           64         10         54           67 [51:60]         62 [47:79]         68 [53:80]           194 [124- 251]         122 [103:229]         201 [139:254]           -         -         -           40 (53%)         4 (40%)         36 (67%)           24 (38%)         6 (60%)         18 (33%)           -         -         -           30 (47%)         6 (60%)         24 (44%)           32 (50%)         7 (70%)         25 (46%)           7 [6-14]         4 (4-7]         8 [6-14]           -         -         -           31 (64%)         5 (50%)         1 (4%)           -         -         -           -         -         -           31 (64%)         5 (50%)         1 (4%)           -         -         -           -         -         -           -         -         -           32 (50%)         7 (70%)         26 (6%)           6 (16%)         5 (50%)         1 (4%)           -         -

 L
 No
 5 (9%)
 0 (0%)
 5 (12%)
 100

 C = Cycle threshold value; HCP = healthcare personnel; RT+PCR = real-time reverse transcriptase polymerase chain reaction
 137 specimens had undetectable viral load when re-tested
 197 specimens had undetectable viral load when re-tested
 197 specimens had undetectable viral load when re-tested

 \* Symptom status at time of repeat positive test is unknown for 37 cases (0 with C< 30, 27 with Ct 2 30)</td>
 Provide test when indicated

 \* Symptom status at time of repeat positive test is unknown for 37 cases (0 with Ct 2 40, 27 with Ct 2 30)
 Provide test is unknown for 58 cases (5 with Ct<23 and 53 with Ct 2 30)</td>

\_\_\_rected C with Ct ≥ 30) Unkn ure status for 12 individuals (12 with Ct ≥ 30)

Conclusion. In this study, nearly 1 in 6 NH residents and staff with repeat positive tests after 90 days demonstrated high viral RNA loads and viable virus, indicating possible infectivity. While individuals with high RNA viral load may be more likely to be symptomatic, distinguishing asymptomatic individuals who have high viral loads may be difficult with timing since initial infection, other test results, or exposure history alone.

Disclosures. John A. Jernigan, MD, MS, Nothing to disclose.

394. Descriptive Evaluation of Epidemiology and Microbiology of Patients with COVID-19 Pre/post Implementation of Corticosteroids as Standard of Care Goran Flajc, PharmD<sup>1</sup>; Ahmed Zaki, PharmD<sup>1</sup>; <sup>1</sup>Baylor St. Luke's Medical Center, Houston, Texas

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

Background. The coronavirus disease 2019 (COVID-19) pandemic continues to present a significant global public health concern. As of June 2021, nearly 174 million cases of SARS-CoV-2 infection worldwide have been reported to the World Health Organization. Rigorous data on the efficacy of corticosteroids have now established its role as standard of care (SOC). Less recognition has been given to corticosteroid therapy and its association with risk of infection especially in those who are critically ill and prone to nosocomial pathogens.

Methods. This is a retrospective study of mechanically ventilated patients with COVID - 19 from March 2020 to September 2020 at a single center. The primary endpoint for this study was description of microbiology and epidemiology of secondary infections and co -infections, defined as any infection following treatment for COVID - 19. Secondary endpoints included the duration of corticosteroid use, length of hospital stay, ICU length of stay, and mortality.

Results. Of the 104 patients, 73% had co-infections or secondary infections. Pre-SOC patients were more likely to receive >10 days of corticosteroids (71% vs 30%). Co-infections were present in 12% of patients (13% in pre-SOC vs 11% in post-SOC), secondary infections occurred in 61% of patients (74% in pre-SOC vs 53% in post-SOC). The most common causative organism of co-infections and secondary infections were Staphylococcus aureus in the pre-SOC group and Escherichia coli and Pseudomonas aeruginosa in the post-SOC group. The mean hospital length of stay was 43 days pre-SOC vs 33 days post-SOC with a mean ICU length of stay of 33 vs 29 days, respectively. Mortality rate was similar between the two groups (55% vs 58%).

*Conclusion.* Differences in epidemiology and microbiology was seen pre and post implementation of dexamethasone in June, 2020. Higher rates of co-infections were seen with this prolonged use of corticosteroids pre-SOC but it is unclear whether patients developed more co-infections as result of extended corticosteroid use, a longer hospital stay, or other factors. Further studies are needed to assess the optimal duration of corticosteroid use in this patient population with consideration to weigh benefit vs risk.

Disclosures. All Authors: No reported disclosures

#### 395. Early Predictors of Intensive Care Unit Admission among COVID-19 Patients in Oatar

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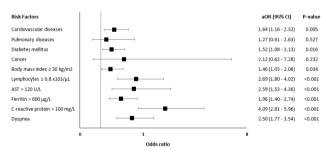
# Session: P-16. COVID-19 Epidemiology and Screening

Background. Coronavirus disease (COVID-19) is associated with significant morbidity and mortality. This study aimed to explore the early predictors of intensive care unit (ICU) admission and in-hospital mortality among patients diagnosed with COVID-19

Methods. This was a case-control study of adult patients with confirmed COVID-19. Cases were defined as patients admitted to ICU during the period February 29 - May 29, 2020. For each case enrolled, one control was matched by age and gender.

Results. A total of 1560 patients with confirmed COVID-19 were included. Each group included 780 patients with a predominant male gender (89.7%) and a median age of 49 years (interquartile range = 18). Predictors independently associated with ICU admission were cardiovascular disease (CVD) (adjusted odds ratio (aOR)=1.64, 95% confidence interval (CI): 1.16 - 2.32, p=0.005), diabetes (aOR=1.52, 95% CI: 1.08 - 2.13, p= 0.016), obesity (aOR=1.46, 95% CI: 1.03-2.08, p= 0.034), lymphopenia (aOR=2.69, 95% CI: 1.80-4.02, p< 0.001), high aspartate aminotransferase (AST) (aOR= 2.59, 95% CI: 1.53-4.36, p< 0.001), high ferritin (aOR=1.96, 95% CI: 1.40-2.74, p< 0.001), high C-reactive protein (CRP) (aOR=4.09, 95% CI: 2.81-5.96, p< 0.001), and dyspnea (aOR=2.50, 95% CI: 1.77-3.54, p< 0.001). Similarly, significant predictors of mortality included CVD (aOR=2.16, 95% CI: 1.32- 3.53, p=0.002), diabetes (aOR=1.77, 95% CI: 1.07-2.90, p=0.025), cancer (aOR=4.65, 95% CI: 1.50-14.42, p= 0.008), lymphopenia (aOR=2.34, 95% CI: 1.45-3.78, p= 0.001), and high AST (aOR= 1.89, 95% CI: 1.04-3.43, p=0.036).

Risk Factors for ICU admission among patients with COVID-19 (N=1560)



Conclusion. Having CVD, diabetes, lymphopenia, and increased AST were independent predictors for both ICU admission and in-hospital mortality in patients with COVID-19. In addition, obesity, high ferritin, and CRP levels were associated with increased risk of ICU admission, while cancer was strongly associated with in-hospital mortality. Early identification and monitoring of patients at risk is essential in planning the level of care needed to prevent delay in medical intervention.

Disclosures. Adel Abou-Ali, PharmD, PhD, Astellas Pharma Global Development, Inc. (Employee)

396. Disparities in SARS-CoV-2 Antibody Prevalence: Findings from a Citywide Serosurvey in Holyoke, Massachusetts, November 2020-January 2021 Wilfredo Matias, MD MPH<sup>1</sup>; Isabel Fulcher, PhD<sup>2</sup>; Cody Nolan, MD<sup>3</sup>; Yodeline Guillaume, MA<sup>4</sup>; Jack Zhu, MPH<sup>4</sup>; Francisco Molano, MD<sup>4</sup>; Elizabeth Uceta, BA<sup>4</sup>; Shannon Collins, BA<sup>4</sup>; Damien Slater, PhD<sup>4</sup>; Vanessa Sanchez, BS<sup>4</sup>; Serina Moheed, BS<sup>5</sup>; Jason Harris, MD MPH<sup>4</sup>; Richelle Charles, MD<sup>4</sup>; Ryan Paxton, MPH<sup>6</sup>; Sean Gonsalves, BS<sup>6</sup>; Molly Franke, ScD<sup>7</sup>; Louise Ivers, MD, MPH<sup>4</sup>; <sup>1</sup>Mass GeneralBrigham, Boston, Massachusetts; <sup>2</sup>Harvard Data Science Initiative, Boston, Massachusetts; <sup>3</sup>Brigham and Women's Hospital, Boston, Massachusetts; <sup>4</sup>Massachusetts General Hospital, Boston, Massachusetts; 5smoheed@mgh.harvard.edu, Boston, Massachusetts; 6Holyoke Board of Health, Holyoke, Massachusetts; <sup>7</sup>Harvard Medical School, Boston, Massachusetts