

environmental services workers who had passed the temperature and symptom screening evaluation on entry to the campus. Samples were obtained from both nares of consenting individuals and ran daily on a validated polymerase chain reaction (PCR) platform.

Results: A total of 1394 employees consented to participate by June 15, 2020 and none of them had a positive result for COVID-19. Thus, the prevalence rate among asymptomatic employees was zero during this period (95%CI 0%-0.26%). Thirteen employees developed symptoms after initial enrollment and testing of which 1 tested positive for COVID-19. Based on these data, we estimate a monthly incidence rate of 0.8 new COVID-19 cases per 1000 asymptomatic employees (95%CI 0.2 - 4.4 per 1000). Of note, at the time of submission the R_0 for our region was 1.4, and the prevalence of COVID-19 infection among symptomatic employees was 9.9% (68/686 tested in our system, 95%CI: 7.8%-12.3%).

Conclusion: We did not identify any COVID-19-positive asymptomatic hospital employees who passed screening measures. This suggests very low risk of nosocomial transmission to other employees, patients, and families. Along with low community prevalence and capture of COVID-19-positive symptomatic employees, we could confidently advise staff that universal surgical masking and eye protection were likely adequate to prevent significant exposure.

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464. Rapid whole genome sequence typing reveals multiple waves of SARS-CoV-2 spread

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Session: P-14. COVID-19 Epidemiology and Screening

Background: As the pandemic SARS-CoV-2 virus has spread globally its genome has diversified and distinct clones can now be recognized, tracked, and traced. Identifying clonal groups allows for assessment of geographic spread, transmission events, and identification of more virulent or transmissible emerging strains.

Methods: All SARS-CoV-2 genomes (n=17,504) that are complete and high coverage were downloaded from GISAID on May 17th 2020. We developed a GNU-based Virus Identification (GNUVID) tool that implements a whole genome multiloocus sequence typing (wgMLST) scheme composed of all ten ORFs in the SARS-CoV-2 genome. The 10,422 genomes that passed our quality check were fed to the GNUVID tool, which assigned a ST profile to each genome. Global optimum eBURST was then used to cluster the STs in clonal complexes (CCs).

Results: Our ST/CC analysis uncovered strong associations of ST/CCs with certain geographical regions but also dynamic local changes in ST/CC prevalence. We also identified several unexpected putative global transmission events (e.g., from the US to the Middle East and reintroduction to China later in the pandemic). We have made our tool (GNUVID) available so that new WG sequences can be rapidly assigned to an ST/CC (<https://github.com/ahmedmagds/GNUVID>).

Conclusion: Our sequence typing system uncovered previously unappreciated transmission events and waves of expansion and replacement of SARS-CoV-2 STs and CCs in different geographical locations, suggesting complex dynamics in viral populations that previously seemed monomorphic. Because, our tool can be rapidly updated with new sequencing data it can track emerging clones and identifying new hotspots.

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465. Risk Factors Associated with Critical COVID-19 Requiring Mechanical Ventilation

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Session: P-14. COVID-19 Epidemiology and Screening

Background: Mechanical ventilation of patients with COVID-19 is associated with high mortality. Understanding risk factors for developing mechanical ventilation may allow for more targeted monitoring and therapeutics that may improve outcomes.

Methods: We performed a retrospective case series of all patients admitted within thirty days of a positive Sars CoV-2 test to an integrated health system near Chicago, Illinois between March 12 and May 31, 2020. Covariates evaluated included demographics, symptoms on admission, vital signs, medications, comorbidities, census tract data and social history. Univariable analysis was performed and variables with an alpha of 0.05 or less were included in multivariable regression modeling to identify factors associated with mechanical ventilation. The area under the curve (AUC) was used to assess performance of the model.

Results: Of 990 patients admitted with COVID-19 12.6% (125) were mechanically ventilated. The median age was 68 (interquartile range 55-82), 48.4% (479) were female and 49.6% (491) were Caucasian. Independent factors associated with mechanical ventilation included female sex (Adjusted OR [AOR] 0.621, Confidence Interval [CI] 0.427-0.903; p=0.0363), body mass index (BMI) (AOR 1.035, CI 1.011-1.060; p=0.0175), percent of english speaking population within patient's census tract (AOR 0.989, CI 0.979-0.998; p=0.0454), respiratory rate (AOR 1.054, CI 1.027-1.083; p=0.0011), oxygen saturation (AOR 0.922, CI 0.901-0.943; p< 0.0001),

cerebrovascular accident (CVA) (AOR 0.176, CI 0.051-0.605; p=0.0207) and hematologic malignancy (AOR 3.668, CI 1.403-9.590; p=0.0261). AUC of the model was 0.8 (0.75-0.84).

Characteristics of patients admitted with COVID-19

	Population N=990		Population N=990
Age (yr)	68.0 [55.0 - 82.0]	Past medical History	
Age <18	1 (0.1%)	Acute Myocardial Infarction	31 (3.1%)
Female	479 (48.4%)	Asthma	78 (7.9%)
Body Mass Index (Kg/m2)	28.3 [24.6 - 32.8]	Coronary Artery Disease	133 (13.4%)
Body Mass Index >=30	352 (35.6%)	Congestive Heart Failure	120 (12.1%)
Past or Current Smoker	255 (25.8%)	Chronic Kidney Disease	126 (12.7%)
Pregnant During Encounter	13 (1.3%)	Conduction Abnormalities	217 (21.9%)
Race		Chronic Obstructive Pulmonary Disease	119 (12.0%)
Caucasian	491 (49.6%)	Cerebrovascular Accident	93 (9.4%)
African American	92 (9.3%)	Diabetes	279 (28.2%)
Asian	75 (7.6%)	End Stage Renal Disease	32 (3.2%)
Other	332 (33.5%)	Hematologic Malignancy	22 (2.2%)
Ethnicity		Human Immunodeficiency Virus	2 (0.4%)
Hispanic/Latino	181 (18.3%)	Hypertension	482 (48.7%)
Non-Hispanic	809 (81.7%)	Inflammatory Bowel Disease	13 (1.3%)
Insurance		Liver Disease	56 (5.7%)
Private	277 (28.0%)	Metastatic Solid Tumor	14 (1.4%)
Medicare	503 (50.8%)	Systemic Lupus Erythematosus	4 (0.4%)
Medicaid	188 (19.0%)	Peripheral Vascular Disease	64 (6.5%)
Self-Pay/Unknown	22 (2.2%)	Solid Tumor	181 (18.3%)
Census Tract		Transplant	4 (0.4%)
Distance To Closest NorthShore Hospital (miles)	3.5 [2.0 - 5.8]	Medications Taken in the Past 6 Months	
Median Family Income in Thousands (\$)	76765.0 [57558.0 - 110666.0]	ACE/ARB	184 (18.6%)
Percent Of English Speaking Population	59.9 [43.5 - 74.5]	Chemotherapy	15 (1.5%)
Symptoms on Admission		Insulin	88 (8.9%)
Cough	133 (13.4%)	Statin	174 (17.6%)
Decreased Sense Of Taste Or Smell	0 (0.0%)	Steroid In Last Month	55 (5.6%)
Shortness Of Breath	411 (41.5%)	Relationship with NorthShore	
Fever	225 (22.7%)	Medical Group PCP	257 (26.0%)
Gastrointestinal Symptoms	60 (6.1%)	Affiliate PCP	20 (2.0%)
Fatigue	28 (2.8%)	NorthShore Encounter in Last 24 Months	457 (46.2%)
Myalgia	76 (7.7%)		
Upper Respiratory Symptoms	6 (0.6%)		
First Vital After Admission			
Temperature (F)	99.4 [98.5 - 100.9]		
Systolic Blood Pressure (mmHg)	129.0 [116.0 - 144.0]		
Diastolic Blood Pressure (mmHg)	76.0 [66.0 - 85.0]		
Respiration (per minute)	22.0 [19.0 - 26.0]		
Pulse (per minute)	94.0 [81.2 - 108.0]		
Oxygen Saturation (percent)	94.0 [91.0 - 97.0]		

Multivariable logistic regression to identify risk factors associated with mechanical ventilation

	Adjusted Odds Ratio	P-Value
Age (yr)	0.997 [0.985-1.009]	0.7023
Female	0.621 [0.427-0.903]	0.0363
Body Mass Index (Kg/m2)	1.035 [1.011-1.060]	0.0175
Percent Of English Speaking Population	0.989 [0.979-0.998]	0.0454
Shortness Of Breath	1.244 [0.844-1.835]	0.3549
Respiration (per minute)	1.054 [1.027-1.083]	0.0011
Pulse (per minute)	1.005 [0.995-1.014]	0.4005
Oxygen Saturation (percent)	0.922 [0.901-0.943]	0.0000
Conduction Abnormalities	0.634 [0.374-1.077]	0.1569
Cerebrovascular Accident	0.176 [0.051-0.605]	0.0207
Hematologic Malignancy	3.668 [1.403-9.590]	0.0261
Non-Hispanic	1.125 [0.706-1.795]	0.6771

Conclusion: Risk factors associated with mechanical ventilation included male gender, elevated BMI, census tract with lower percentage of english speakers, increased respiratory rate, low oxygen saturation, hematologic malignancy and not having a CVA. We suspect that history of CVA may have been associated with overall patient debility in which aggressive measures such as intubation were not deemed appropriate. Identifying patients with risk factors associated with mechanical ventilation may allow for early and targeted interventions to improve outcomes.

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466. SARS-CoV-2 Diagnosis And Point Prevalence in a Non-Cohorted Tertiary Care Center

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Session: P-14. COVID-19 Epidemiology and Screening

Background: The CDC recommends testing for SARS-CoV-2 in patients who present with symptoms consistent with COVID-19 and to cohort hospitalized patients diagnosed with COVID-19. Up to 35% of persons infected with SARS-CoV-2 are asymptomatic; however, no recommendations exist for universal testing in hospitalized patients. We assessed the point prevalence of SARS-CoV-2 infection amongst hospitalized patients at a tertiary care center during a time when there was a regional surge of cases.

Methods: Nasopharyngeal SARS-CoV-2 PCR testing was performed on inpatients at Georgetown University Hospital on 4/27/20, excluding those who were SARS-CoV-2 positive, tested within 72 hours or admitted to pediatric, psychiatric, labor & delivery or ICUs. Patients within the hospital were not cohorted based on COVID-19

status. Patient demographics and comorbidities were obtained from the EMR and analyzed for significance based on SARS-CoV-2 status.

Results: Hospital census on the testing date was 297; 204/297(68.7%) met inclusion criteria; 78/297(26.3%) were known COVID-19 patients. Within the study group 78/204 (38.2%) had known COVID-19, 21/204 (10.3%) were PUIs (4 of whom tested positive), 31/204 (15.1%) tested negative for COVID-19 within 72 hours and 74/204 (36.3%) met criteria for testing. The median age was 62 years (IQR, 53 to 70), 59%(n=122) were male, 56%(n=115) were Black, and 90%(n=185) had at least one co-morbidity. 0/74 of those tested on 4/27/20 were positive for SARS-CoV-2, and none were diagnosed with COVID-19 within 28 days. In adjusted analyses, patients who were hospitalized for COVID-19 were more likely to be Black(OR=10.53 95% CI 3.02, 36.68, p=0.0002); male(OR=3.27 95% CI 1.26, 8.47, p=0.0143); reside in group/nursing homes(OR= 11.78 95%CI 3.03, 45.76, p=0.0004); have a history of prior stroke(OR= 6.25 95%CI 1.49, 26.12, p=0.012); but less likely to smoke(OR=0.10 95%CI 0.02, 0.48, p=0.0039), or have active malignancy (OR= 0.11 95%CI 0.01, 0.73, p=0.0223).

Table 1: Risk Factors for SARS-CoV-2 Among Hospitalized Patients at a Tertiary Care Center

	Unadjusted Odds Ratio	Unadjusted p-value	Adjusted Odds Ratio*	Adjusted p-value
	OR (95% CI)		OR (95% CI)	
Age (per 1-year increase)	0.995 (0.976, 1.014)	0.5877	0.999 (0.970, 1.028)	0.9281
Sex (Male vs. Female)	0.997 (0.563, 1.764)	0.9909	3.278 (1.268, 8.476)	0.0143
Race (Black vs. White)	3.761 (1.679, 8.424)	0.0013	10.534 (3.025, 36.685)	0.0002
Ethnicity (Non-Hispanic vs. Hispanic)	0.025 (0.003, 0.191)	0.0004	---	---
Insurance (Private Insurance vs. Government Insurance)	0.713 (0.370, 1.374)	0.3126	---	---
Employment (Employed vs. Unemployed)	0.972 (0.492, 1.922)	0.9350	---	---
Residence (Group & nursing home vs. private residence)	11.300 (3.713, 34.392)	<0.0001	11.788 (3.036, 45.767)	0.0004
Hospital Location (ICU vs. Med-Surg)	6.937 (3.434, 14.013)	<0.0001	10.911 (3.692, 32.243)	<0.0001
Hospital Length of Stay	1.006 (0.979, 1.033)	0.6826	---	---
Healthcare Exposure (Yes vs. No)	0.580 (0.329, 1.024)	0.0604	---	---
Tobacco Use (Current vs. No)	0.143 (0.047, 0.434)	0.0006	0.103 (0.022, 0.482)	0.0039
Marijuana Use (Current vs. No)	0.743 (0.180, 3.069)	0.6813	---	---
Illicit Substance Use (Current vs. No)	1.187 (0.257, 5.468)	0.8263	---	---
Comorbidities				
Active Malignancy	0.183 (0.053, 0.634)	0.0074	0.116 (0.018, 0.736)	0.0223
Cardiac Arrhythmia	0.625 (0.297, 1.312)	0.2971	---	---
CKD on Dialysis	0.488 (0.184, 1.295)	0.1494	---	---
COPD	0.815 (0.316, 2.106)	0.7234	---	---
Congestive Heart Failure	0.817 (0.394, 1.694)	0.6482	---	---
Coronary Artery Disease	0.817 (0.394, 1.694)	0.6482	---	---
Diabetes Mellitus	0.922 (0.570, 1.489)	0.7796	---	---
Hyperlipidemia	0.870 (0.530, 1.428)	0.6446	---	---
Hypertension	0.906 (0.550, 1.492)	0.7453	---	---
HIV	1.120 (0.312, 4.024)	0.8839	---	---
Immunosuppressed	0.328 (0.136, 0.795)	0.0136	---	---
Liver Disease	0.991 (0.386, 2.542)	0.9850	---	---
Obesity (BMI >30)	1.566 (0.874, 2.805)	0.1317	---	---
Other Lung Disease	0.545 (0.222, 1.339)	0.2665	---	---
Prior Stroke	2.306 (0.970, 5.480)	0.0585	6.250 (1.496, 26.123)	0.0120
Solid Organ Transplant Recipient	0.383 (0.128, 1.149)	0.1509	---	---

*Adjusted for age, sex, location within hospital, residence, tobacco use, and active malignancy

Conclusion: The use of CDC testing criteria for PUIs were successful in identifying COVID-19 patients and limiting the need for routine testing in all hospitalized patients during a time when access to testing was limited. Nosocomial transmission did not occur in our institution despite a lack of cohorting.

Disclosures: Princy Kumar, MD, Gilead Sciences Inc. (Scientific Research Study Investigator)

467. Spatial-Temporal Prediction Model of COVID-19 Mortality across 62 Counties in New York State

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Session: P-14. COVID-19 Epidemiology and Screening

Background: COVID-19 pandemic has resulted in considerable morbidity and mortality. New York State (NY) is the hotspot with most coronavirus cases, while there are spatial/temporal variations. Yet, few examined county-level factors of mortality in COVID-19 patients in NY. Based on the sociological framework in health, this study links large and representative public data to understand COVID-19 mortality in NY over different stages of pandemic.

Methods: Mortality cases were from Mar 17 (state of emergency; 0.1 per 100,000), Apr 18 (coronavirus peak; 87.4), Apr 25 (expand testing; 108.7), and May 11 (daily reduced to original; 137.6). Three domains (compositional, contextual, and collective) and 28 county-level predictors of mortality were extracted from American Community Survey, Area Health Resources, US Crime Data, and Religious Data systems for each county. Compositional domain covered socio-demographic characteristics in local areas (e.g., age, sex, race/ethnicity, housing). Contextual domain covered include social and physical opportunities (e.g., health insurance coverage, transportation, mental health providers). Collective domain covered neighborhood safety and religious adherents. Mixed effect regression with the least absolute shrinkage selection operator (LASSO) was used to select the predictors and estimate the parameters after adjusting the time effect and cumulative prevalence of COVID-19.

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; 0.1 per 100,000 people

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Results: NYC and the nearby boroughs (i.e., Bronx, Kings, Manhattan, Queens) had the highest cumulative mortality (231.69 per 100,000 people). Counties far from New York Cities (e.g., Allegany, Cortland, Delaware) had the lowest cumulative mortality. Spatial variation showed counties with larger population density ($\beta=0.01$, $p=0.022$) and/or higher proportion of people with at least high school education ($\beta=227.24$, $p=0.03$) were at risk of higher cumulative mortality in COVID-19.

Conclusion: Unique spatial clustering mortality risk of COVID-19s was detected, highlighting important but understudied roles of contextual and collective factors. Tailored policy efforts shall be designed to support counties with large population density and high levels of education to prevent the mortality related to COVID-19 infection in NY.

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468. Specimen pooling conserves additional testing resources when patients' infection status is correlated: A simulation study

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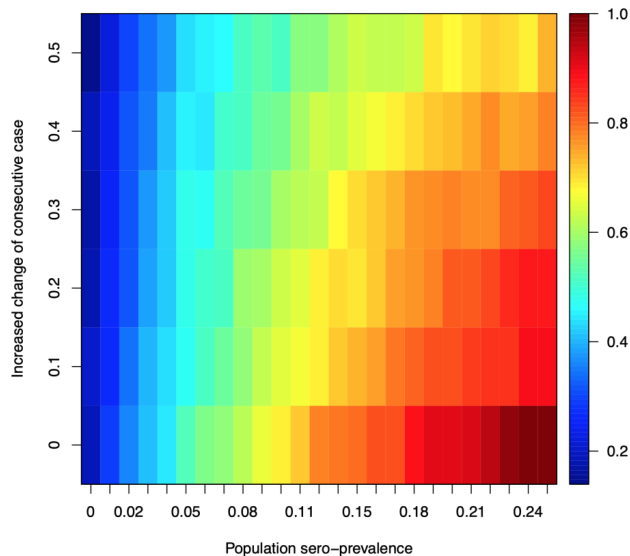
Session: P-14. COVID-19 Epidemiology and Screening

Background: In the early stages of a novel pandemic, testing is simultaneously in high need but low supply, making efficient use of tests of paramount importance. One approach to improve the efficiency of tests is to mix samples from multiple individuals, only testing individuals when the pooled sample returns a positive.

Methods: I build on current models which assume patients' sero-status is independent by allowing for correlation between consecutive tests (e.g. if a family were all infected and were all tested together). In this model, I simulate 10,000 patients being tested in sequence, with population sero-prevalence ranging from 1% to 25%, using batch sizes from 3 to 10, and assuming the increased probability of consecutive infections ranged from 0% to 50%.

Results: I find that as the likelihood of consecutive infected patients increases, the efficiency of specimen pooling increases. As well, the optimal size of the batch increases in the presence of clustered sequences of infected patients.

Heat map indicating the manner in which the number of tests needed is reduced as population prevalence and correlation between cases changes. Red indicates that there is no reduction in the number of tests, and blue indicates a near 100% reduction in the number of tests, with intermediate colors indicating intermediate fractions.



Conclusion: This analysis indicates further improvements in specimen pooling efficiency can be gained by taking advantage of the pattern of patient testing.

Disclosures: Jeffrey Rewley, PhD, MS, American Board of Internal Medicine (Employee)

469. Temporal, Spatial, and Demographic Relationships of SARS-COV-2 Gene Target Cycle Thresholds

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Session: P-14. COVID-19 Epidemiology and Screening

Background: The optimum duration of isolation precautions (IP) for SARS-COV-2-infected individuals is uncertain. Most healthcare facilities must rely on