351. Antibiotic Management Decisions and Use of a Multiplex PCR Panel for Pneumonia Diagnosis Among Critically Ill Patients with COVID-19

Neda Bionghi, MD, MPH[1]; Donald E. Dietz, MD[2]; Jason Zucker, MD, MS[2]; Jason Zucker, MD, MS[2]; Simian Huang, MPH[1]; Susan Whittier, Ph.D.[3]; Daniel A. Green, M.D.[3]; Fann Wu, M.D.[3]; Magdalena Sobieszczyk, MD, MPH[2]; Deborah Theodore, MD[2]; [1]Columbia University Irving Medical Center and New York-Presbyterian Hospital, New York, New York; [2]Columbia University Irving Medical Center, New York, New York; [3]Columbia University Medical Center, New York, NY

Session: P-14. COVID-19 Complications, Co-infections, and Clinical Outcomes

Background. Antibiotic use among patients with COVID-19 is common, exceeds the prevalence of probable bacterial co-infection, and promotes development of resistant organisms. Lack of diagnostic microbiological data may prolong empiric broad-spectrum therapy. Here we evaluate the use of the BioFire FilmArray pneumonia panel (PP), a novel rapid diagnostic test, and antibiotic decisions among intensive care unit (ICU) patients with COVID-19.

Methods. We conducted a retrospective review of adult ICU patients admitted with COVID-19 between January 2020 and May 2021 at an academic medical center. ICU patients who underwent bronchoscopy/bronchoalveolar lavage (BAL) with PP (PP group) were matched by age (< 65 or ≥65), BMI (< 30 or ≥30), and BAL date (within 60 days) to ICU patients who did not undergo BAL (no-BAL group). PP patients were matched by age and BMI to ICU patients who underwent BAL without PP (no-PP group). Antibiotic use was compared between groups. Chi squared analysis, t-test, and ANOVA were used for comparisons as appropriate.

Results. 65 patients were included; the majority were male (65%), < 65 years (86%), and had BMI ≥30 (54%) (Table 1). Only 17 no-PP matches were identified for PP patients due to infrequent BALs. Similar proportion of patients in PP and no-PP groups had organisms identified from BAL (54% vs. 47%, p=0.65). Among PP patients with a detected organism, all (n=13) had subsequent changes in antibiotic regimen ≤72 hours after BAL; 10/13 (77%) had a change targeted to detected organism and 5/13 (39%) had antibiotic narrowing. Among PP patients with no detected organism, only 4/11 (36%) had antibiotic narrowing or maintenance off antibiotics. In all groups, average antibiotic use exceeded 70% of admission duration.

Table 1. Patient characteristics and antibiotic management. Abbreviations: BAL - bronchoalveolar lavage

Characteristics	All patients N = 65 (%)	Underwent bronchoscopy with pneumonia panel ("PP") N=24 (%)	Underwent bronchoscopy without pneumonia panel ("No-PP") N=17 (%)	Did not undergo bronchoscopy ("No-BAL") N=24 (%)	P value (α=0.05)
Male	42 (64.6)	18 (75)	12 (70.6)	12 (50)	0.162
Female	23 (35.4)	6 (25)	5 (29.4)	12 (50)	
Age (years)					
Less than 65	56 (86.2)	21 (87.5)	14 (82.3)	21 (87.5)	0.870
65 or greater	9 (13.8)	3 (12.5)	3 (17.6)	3 (12.5)	
BMI					
Less than 30	35 (53.8)	12 (50)	11 (64.7)	12 (50)	0.579
30 or greater	30 (46.2)	12 (50)	6 (35.3)	12 (50)	
Race					
Declined	26 (40.0)	12 (50.0)	4 (23.5)	10 (41.7)	0.508
Other, not described	19 (29.2)	4 (16.7)	6 (35.3)	9 (37.5)	
White	12 (18.5)	5 (20.8)	4 (23.5)	3 (12.5)	
Black or African American	5 (7.7)	1 (4.2)	2 (11.8)	2 (8.3)	
Asian	3 (4.6)	2 (8.3)	1 (5.9)	0 (0)	
Ethnicity					
Hispanic/Latino	26 (40.0)	8 (33.3)	7 (41.1)	11 (45.8)	0.531
Not Hispanic/Latino	23 (35.3)	8 (33.3)	6 (35.3)	9 (37.5)	
Declined	16 (24.6)	8 (33.3)	4 (23.5)	4 (16.7)	
Organism detected from BAL					
Yes	-	13 (54.2)	8 (47.0)	-	0.654
No	-	11 (45.8)	9 (53.0)	-	
Antibiotic regimen changed after BAL					
Yes	-	13 (54.2)	11 (64.7)	-	0.500
No	-	11 (45.8)	6 (35.3)	-	
Antibiotic management among patients with antibiotic change after BAL		PP N = 13 (%)	No-PP N = 11 (%)	No-BAL	P value (α=0.05)
Antibiotic regimen broadened					
Yes	-	7 (53.8)	4 (36.4)	-	0.365
No	-	6 (46.2)	7 (63.6)	-	
Antibiotic regimen narrowed					
Yes	-	7 (53.8)	8 (72.7)	-	0.341
No	-	6 (46.2)	3 (27.3)	-	
Antibiotic changes targeted to identified organism					
Yes	-	10 (76.9)	6 (54.5)	-	0.204
No	-	3 (23.1)	5 (45.5)	-	
Characterization of antibiotic use		PP N = 24	No-PP N = 17	No-BAL N = 24	P value (α=0.05)
Number of days on antibiotics from time of inpatient admission Median (IQR)	-	46.5 (27.5-73.0)	39.0 (26.0-58.0)	17.5 (10.3-32.3)	-
Number of days on antibiotics from time of ICU admission Median (IQR)	-	43.5 (27.5-63.5)	42.0 (28.0-70.5)	13.5 (6.5-23.0)	-
Proportion of days on antibiotics during inpatient admission Mean (SD)	-	0.791 (0.196)	0.752 (0.166)	0.712 (0.374)	0.830
Proportion of days on antibiotics from time of ICU admission Mean (SD)	-	0.799 (0.215)	0.752 (0.174)	0.780 (0.347)	0.858

Abbreviations: BAL - bronchoalveolar lavage

Conclusion. Rapid, highly sensitive diagnostic tests have potential to guide clinical decisions and promote antibiotic stewardship among patients with severe viral pneumonia and suspected bacterial co-infection. In this descriptive analysis, antibiotic management did not differ significantly with use of PP. While most patients with detected organism on PP had targeted antibiotic changes, a negative PP did not appear to influence antibiotic narrowing. Larger studies and provider education are needed to evaluate potential of the PP for antibiotic stewardship.

Disclosures. **Jason Zucker, MD, MS**, Nothing to disclose **Daniel A. Green, M.D.**, **BioFire** (Grant/Research Support, Scientific Research Study Investigator, Advisor or Review Panel member) **Deborah Theodore, MD**, **BioFire Diagnostics** (Other Financial or Material Support, Donation of testing materials to support investigator-initiated research)

352. COVID-19 Not a Risk Factor of Alopecia Areata: Results of a National Cohort Study in South Korea

Jeehyun Kim, MPH, PhD Student[1]; Kwan Hong, MD MPH[2]; Sujin Yum, MPH Student[1]; Raquel Elizabeth Gomez Gomez, MPH Student[1]; Byung Chul Chun, MD[2]; [1]Korea University, Seoul, Seoul-t'ukpyolsi, Republic of Korea; [2]Korea University College of Medicine, Seoul, Seoul-t'ukpyolsi, Republic of Korea

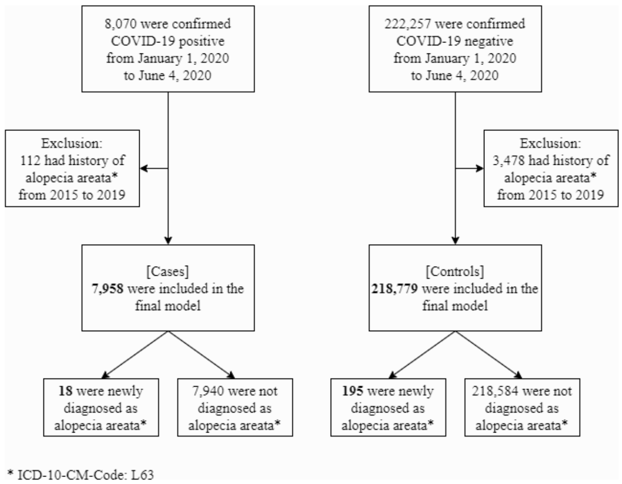
Session: P-14. COVID-19 Complications, Co-infections, and Clinical Outcomes

Background. There have been approximately 158 million coronavirus disease 2019 (COVID-19) pandemic survivors worldwide by June 9, 2021. As a result, concerns about hair loss in COVID-19 patients have emerged among dermatologists. However, most of extant literature have limited implications by relying on cross-sectional studies with restricted study subjects without control group. Therefore, our study aims to investigate the risk of developing alopecia areata (AA) among COVID-19 patients in South Korea using adequate control based on national representative data.

Methods. We used the National Health Insurance Service (NHIS) COVID-19 cohort database, comprising COVID-19 patient and control group, all of whom were diagnosed from January 1, 2020 to June 4, 2020. Patients were defined as individuals who were confirmed as COVID-19 positive, regardless of disease severity. Controls were defined as whom confirmed as COVID-19 negative. People with a history of AA during the period 2015–2019 were excluded. The primary endpoint was a new diagnosis of AA (ICD-10-CM-Code: L63). Adjusted incidence rate ratio (IRR) of developing AA was estimated using log-link Poisson regression model based on incidence density of case and control group. The model adjusted for (1) age and sex (2) demographic variables (age, sex, place of residence, and income level). Statistical significance was set at $p < 0.05$.

Results. A total of 226,737 individuals (7,958 [3.5%] cases and 218,779 [96.5%] controls) were included in the final analysis. There were more females than males, both in test positives and negatives at 59.9% and 52.3%, respectively. The largest test positive population was those in age group 20 to 29 years (25.5%),. The test negatives had the largest population in age group 30 to 39 years (17.1%). The ratio of newly diagnosed AA was 18/7,958 (0.2%) in cases and 195/218,779 (0.1%) in controls. IRRs of COVID-19 patients having newly diagnosed AA compared to controls were 0.78 (0.48–1.27) when age and sex were adjusted for, and 0.60 (0.35–1.03) when all demographic variables were adjusted for.

Flowchart of study subject selection



Conclusion. Diagnosis of COVID-19 was not significantly associated with development of AA even after appropriately adjusting for covariates.

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

353. New-Onset Diabetes as an Acute Complication of COVID-19: A National Population Cohort Analysis

Kwan Hong, MD MPH[1]; Jeehyun Kim, MPH, PhD student[2]; Sujin Yum, MPH student[2]; Raquel Elizabeth Gómez Gómez, MS[1]; Byung Chul Chun, MD[1]; [1]Korea University College of Medicine, Seoul, Seoul-t'ukpyolsi, Republic of Korea; [2]Korea University, Seoul, Seoul-t'ukpyolsi, Republic of Korea

Session: P-14. COVID-19 Complications, Co-infections, and Clinical Outcomes

Background. Diabetes is emerging as one of the complications of coronavirus disease 2019 (COVID-19), but this is hard to be revealed with cross-sectional studies since it is also known as the major predisposing factor for high-risk COVID-19. Therefore, this study aimed to estimate the risk of new-onset diabetes after COVID-19 through a population follow-up study.

Methods. All COVID-19 confirmed cases in Korea from January 20 to June 4, 2020, were matched with national health insurance data and their health screening data, both provided by the National Health Insurance Service of Korea. Controls were selected as the people who received the PCR test for COVID-19 and showed negative results in the same period and followed up until July 19, 2020. We selected the outcome as the diagnosis of diabetes according to the 10th revision of the International Statistical Classification of Diseases and Related Health Problems (ICD-10, E10 – E14). People who were diagnosed with diabetes in the past five years were excluded from both groups. After performing a log-rank test between groups, adjusted incidence rate and hazard ratio were estimated using Cox proportional hazard modeling. Demographic characteristics (age, sex, region, family histories of hypertension/diabetes, and income) and underlying health conditions such as hypertension, dyslipidemia, heart disease, alcohol consumption, cigarette smoking, and BMI were adjusted. Proportional assumptions were tested by the zph test and the sensitivity analysis by excluding each factor in turn and comparing results.

Results. A total of 6,247 COVID-19 patients and 143,594 controls without diabetes in the past were included for the analysis. The number of new-onset diabetes were 759 (12.15%) in COVID-19 patients and 3,465 (2.41%) in controls (P < 0.01). The adjusted incidence of diabetes was 15.34 (95% confidence interval, CI: 14.10 – 16.66) and 11.18 (95% CI: 10.67 – 11.72) per 100 person-year, respectively, with the mean follow-up time as 46.31 (standard deviation: 16.37) days. The adjusted hazard ratio of diabetes in COVID-19 cases was 2.97 (95% CI: 2.44 – 3.63).

Conclusion. Since COVID-19 patients showed a higher incidence of new-onset diabetes in a short-time follow-up, we should consider diabetes as one of the possible complications of COVID-19.

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

354. SARS-CoV-2 Viral Viability Culture and Sequencing from Immunocompromised Patients with Persistently Positive SARS-CoV-2 PCR Results

Abby Sung, MD[1]; Adam Bailey, MD, PhD[2]; Meghan Wallace, BS[3]; Henry B. Stewart, N/A, Undergraduate Student[1]; David McDonald, B.A.[3]; Candace R. Miller, MA[3]; Kimberly Reske, MPH[3]; Caroline O'Neil, MA, MPH[3]; Victoria J. Fraser, MD[4]; Victoria J. Fraser, MD[4]; Michael S. Diamond, MD, PhD[3]; Carey-Ann Burnham, PhD[3]; Carey-Ann Burnham, PhD[3]; Hilary Babcock, MD, MPH, FIDSA, FSHEA[5]; Hilary Babcock, MD, MPH, FIDSA, FSHEA[5]; Jennie H. Kwon, DO, MSCI[5]; [1]Washington University School of Medicine in St. Louis, Saint Louis, Missouri; [2]UW-Madison, Madison, Wisconsin; [3]Washington University, St. Louis, Missouri; [4]Washington University in St. Louis, St. Louis, MO; [5]Washington University School of Medicine, St. Louis, MO

Session: P-15. COVID-19 Diagnostics

Background. Immunocompromised (IC) patients (pts) can have prolonged SARS-CoV-2 PCR positivity, even after resolution of COVID-19 symptoms. This study aimed to determine if viable virus could be detected in samples collected > 21 days after an initial positive (pos) SARS-CoV-2 PCR in IC pts.

Methods. We obtained 20 remnant SARS-CoV-2 PCR pos nasopharyngeal swabs from IC pts (bone marrow or solid organ transplant, high dose steroids, immunosuppressive medications) with a pos repeat PCR within the previous 30 days. The repeat specimens were cultured on Vero-hACE2-TMPRSS2 cells and incubated for 96 hours to assess viral viability. Viable RNA and infectious virus in the cultured cells were measured by qPCR and infectious plaque assays. RNA sequencing was performed on a HiSeq platform (Illumina). Samples also underwent SARS-CoV-2 antigen (Ag) testing (BD Veritor). Clinical data were extracted from the electronic health record by chart review.

Results. Pt characteristics are in Table 1. Viral cultures from the repeat specimen were negative (neg) for 18 pts and pos for 2 (Table 2). Pt 1 is a 60M treated with obinatuzumab 19 days prior to his first pos PCR test, with repeat specimen collected 21 days later (cycle threshold (Ct) not available). Pt 1 had a low viral titer (27 PFU/mL) & a D614G mutation on sequencing. Pt 2 is a 75M treated with rituximab 10 days prior to his first pos PCR test, with repeat specimen collected 23 days later (Ct 27.56/27.74). Pt 2 had a high viral titer (2e6 PFU/mL) and D614G, S98F, and S813I mutations.

Demographics of Study Population (N=20)

Variable	Viral culture (-) (n=18) N (%) or Median (range)	Viral culture (+) Patient 1	Viral culture (+) Patient 2
Sex			
Male	9 (50)	Yes	Yes
Race[a]			
White	14 (78)		
African American	4 (22)	Yes	Yes
BMI	26.7 (20.1 – 52.0)	37.0	27.2
Age at date of first positive PCR	64 (20 – 79)	60	75
Time between positive PCRs (days)	22.5 (12 – 62)	23	21
Positive PCR after the initial positive test	6 (33)	7 PCR+ repeated tests total	8 PCR+ tests repeated total
Immunosuppressive condition			
Autologous BMT/HCT in 6 months before positive PCR date	1 (6)		
Hematologic malignancy	3 (17)	Yes	Yes
Solid organ transplant, on immunosuppressive medication	10 (56)		
Receiving high dose steroids	3 (17)		Yes
Prednisone >20mg/day for >14 days at time of positive PCR test	1 (6)[a]		
Immunosuppressive meds in previous 30 days	12 (67)		
Other comorbidities			
COPD	4 (22)		
Chronic lung disease	6 (33)		
Hypertension	12 (67)		Yes
Heart condition	10 (56)	Pulmonary embolism	Congestive heart failure
Diabetes, Type 2	7 (39)		
Chronic kidney disease	8 (44)	Yes	
Dialysis	3 (17)	Yes	
Autoimmune or rheumatologic disease[b]	3 (17)		
Cancer, active	4 (22)	Chronic lymphocytic leukemia	Marginal zone lymphoma
Other immunosuppressing condition	15 (83)		
Chronic liver disease	1 (6)		
Alcohol abuse	1 (6)		
Current smoker	2 (11)		
Obesity	5 (28)	Yes	

[a]All patients were non-Hispanic

[b]Prednisone status unknown for 1 patient; autoimmune diseases status unknown for one patient

Characteristics of patients with a positive SARS-CoV-2 viral culture

Variable	Patient #1	Patient #2
History at time of first + PCR	60 year old male with chronic lymphocytic leukemia on obinutuzumab and venetoclax presented with a cough for several weeks, and acute on chronic diarrhea.	75 year old male with marginal zone lymphoma with treatment with bendamustine and rituxan presented with 2 weeks of cough.
Other medical conditions	Fibromyalgia Acute encephalopathy Hyperlipidemia Anemia	Hyperlipidemia Deep vein thrombosis Methemoglobinemia Acute hemolytic anemia
Dates and results of SARS-CoV-2 PCR tests (study specimens in **bold**)	3/23/20 + **4/15/20 +** 5/07/20 + 5/28/20 + 6/12/20 + 7/13/20 + 7/22/20 +	4/05/20 + 4/27/20 + 5/04/20 + 5/11/20 + **5/18/20 +** 6/01/20 + 6/11/20 + 6/23/20 + 7/07/20 -
Any other respiratory viruses?	No	No
Cause of death	COVID-19	Alive as of June 2021
Viral culture results from the repeat test	27 PFU/mL	2e6 PFU/mL
Spike protein mutations from the repeat test	D614G	D614G, S98F, S813I

Conclusion. 90% of specimens collected > 21 days after an initial pos SARS-CoV-2 PCR did not have viable virus detected on their repeat specimen. The 2 pts with pos viral cultures had active hematologic malignancies treated with an anti-CD20 mAb at the time of COVID-19 diagnosis. One pt had a high concentration of active, viable virus. No known variants of concern were noted in this cohort, collected in Q2 2020, though prolonged replication is a risk for variant development. Further data are needed about risk factors for persistent viable viral shedding & methods to prevent transmission of viable virus from IC hosts.

Disclosures. **Victoria J. Fraser, MD**, **CDC Epicenters** (Grant/Research Support)**Cigna/Express Scripts** (Other Financial or Material Support, Spouse is Chief Clinical Officer)**Doris Duke Fund to Retain Clinical Scientists** (Grant/Research Support, Research Grant or Support)**Foundation for Barnes-Jewish Hospital** (Grant/Research Support, Research Grant or Support)**NIH** (Grant/Research Support, Research Grant or Support) **Victoria J. Fraser, MD**, Centers for Disease Control and Prevention (Individual(s) Involved: Self): Grant/Research Support, Research Grant or Support; Cigna/Express Scripts (Individual(s) Involved: Spouse/Partner): Employee; Doris Duke Charitable Foundation (Individual(s) Involved: Self): Grant/Research Support, Research Grant or Support; National Institutes of Health (Individual(s) Involved: Self): Grant/Research Support, Research Grant or Support; The Foundation for Barnes-Jewish Hospital (Individual(s) Involved: Self): Grant/Research Support, Research Grant or Support **Michael S. Diamond, MD, PhD**, **Carnival Corporation** (Consultant)**Emergent BioSolutions** (Grant/Research Support)**Fortress Biotech** (Consultant)**Immunome** (Advisor or Review Panel member)**Inbios** (Consultant)**Moderna** (Grant/Research Support, Advisor or Review Panel member)**Vir Biotechnology** (Consultant, Grant/Research Support) **Carey-Ann Burnham, PhD**, **BioFire** (Grant/Research Support, Other Financial or Material Support)**bioMerieux** (Grant/Research Support)**Cepheid** (Consultant, Grant/Research Support)**Luminex** (Grant/Research Support)**Roche** (Other Financial or Material Support) **Carey-Ann Burnham, PhD**, BioFire (Individual(s) Involved: Self): Grant/Research Support; bioMerieux (Individual(s) Involved: Self): Grant/Research Support, Scientific Research Study Investigator, Speakers' bureau; Cepheid (Individual(s) Involved: Self): Consultant, Grant/Research Support, Scientific Research Study Investigator; Luminex (Individual(s) Involved: Self): Scientific Research Study Investigator **Hilary Babcock, MD, MPH, FIDSA, FSHEA**, Nothing to disclose

355. A Novel Likelihood-Based Model to Estimate SARS-CoV-2 Viral Titer from Next-Generation Sequencing Data

Heather L. Wells, MPH[1]; Joseph Barrows, MS[1]; Mara Couto-Rodriguez, MS[1]; Xavier O. Jirau Serrano, B.S.[1]; Marilyne Debieu, PhD[1]; Karen Wessel, PhD[2]; Colleen B. Jonsson, PhD[3]; Bradley A. Connor, M.D.[4]; Christopher Mason, PhD[1]; Dorottya Nagy-Szakal, MD PhD[1]; Niamh B. O'Hara, PhD[1]; [1]Biotia, New York, New York; [2]Labor Zotz/Klimas, Duesseldorf, Nordrhein-Westfalen, Germany; [3]UTHSC, Memphis, Tennessee; [4]Weill Cornell Medicine, New York, New York

Session: P-15. COVID-19 Diagnostics

Background. The quantitative level of pathogens present in a host is a major driver of infectious disease (ID) state and outcome. However, the majority of ID diagnostics are qualitative. Next-generation sequencing (NGS) is an emerging ID diagnostics and research tool to provide insights, including tracking transmission, evolution, and identifying novel strains.

Methods. We built a novel likelihood-based computational method to leverage pathogen-specific genome-wide NGS data to detect SARS-CoV-2, profile genetic variants, and furthermore quantify levels of these pathogens. We used de-identified clinical specimens tested for SARS-CoV-2 using RT-PCR, SARS-CoV-2 NGS Assay (hybrid capture, Twist Bioscience), or ARTIC (amplicon-based) platform, and COVID-DX software. A training (n=87) and validation (n=22) set was selected to establish the strength of our quantification model. We fit non-uniform probabilistic error profiles