393. Prevalence of HIV in Patients Hospitalized for COVID-19 and Associated Mortality Outcomes: A Systematic Review and Meta-analysis

Paddy Ssentongo, MD, MPH[1]; Anna E. Ssentongo, Mph[2]; Emily S. Heilbrunn, BS[2]; Ping Du, MD, PhD[3]; [1]Penn State University, Harrisburg, Pennsylvania; [2]Penn State College of Medicine, Hershey, Pennsylvania; [3]Penn State Hershey College of Medicine, Hershey, PA

Session: P-12. COVID-19 Complications, Co-infections, and Clinical Outcomes

Background: As of June 3rd, 2020, the number of confirmed cases of novel SARS-CoV-2, the causative agent of COVID-19, was approximately 6,538,456, with 386,503 deaths globally. Individuals with pre-existing conditions are particularly susceptible to and more likely to die from Covid-19. However, individuals with human immunodeficiency virus (HIV) are unique due to their use of antiretroviral therapy, including protease inhibitors, which have been used to treat COVID-19. We aimed to conduct a systematic review and meta-analysis exploring the prevalence and prevalence of HIV in patients hospitalized for COVID-19 and delineating the mortality rates.

Methods: MEDLINE, SCOPUS, and Cochrane Library databases and medrxiv.org were searched from January 1st, 2020, to June 15th, 2020. Studies reporting on the prevalence of HIV among hospitalized COVID-19 patients among and outcome of mortality were extracted. Two reviewers independently extracted appropriate data of interest and assessed the risk of bias. All analyses were performed using random-effects models on log-transformed proportions and risk ratio estimates, and heterogeneity was quantified.

Results: A total of 144,795 hospitalized COVID-19 patients were identified from 14 studies (United States 8, Spain 3, China 1, Italy1, and Germany 1). The pooled prevalence of HIV in COVID-19 patients was 1.22 % [95% confidence interval (CI): 0.61%-2.43%)] translating to a 2-fold increase compared to the respective local-level pooled HIV prevalence in the general population of 0.65% (95% CI: 0.48%-0.89%. When we stratified the analysis by country, pooled HIV prevalence among COVID-19 patients in United States (1.43%, 95% CI: 0.98% -2.07%) was significantly higher compared to Spain (0.26%, 95% CI: 0.23%-0.29%) but not different from China (0.99 %, 95% CI: 0.25 %-3.85%). The pooled mortality rates in HIV-positive patients hospitalized for COVID-19 was 14.1 % 95% CI: 5.78%-30.50% and was substantially higher in the United States compared to other countries.

Conclusion: The prevalence of HIV among COVID-19 patients may be higher compared to the general population, suggesting higher susceptibility to COVID-19. The mortality rates are high but vary significantly across countries.

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

394. Pseudo-outbreak of Coagulase-negative Staphylococcus Species from Blood Cultures Highlights Unique Challenges in Care of Critically Ill Patients With COVID-19

Stacy Park, MD[1]; April E. Attai, BS, MA, MLS (ASCP)[2]; Kyle Enfield, MD[1]; Taison Bell, MD[3]; Brandon Hill, PharmD, BCIDP, BCPS[4]; Rick Carpenter, DNP, MSN, RN, CCRN[1]; Heather L. Cox, PharmD, BCPS-AQID, BCIDP[5]; Amy Mathers, MD[1]; [1]University of Virginia, Charlottesville, Virginia; [2]University of Virgnia Health System, Charlottesville, VA; [3]UVa Health System, Charlottesville, VA; [4]UVA Health, Charlottesville, Virginia; [5]University of Virginia Health System, Charlottesville, VA

Session: P-12. COVID-19 Complications, Co-infections, and Clinical Outcomes

Background: In response to the COVID-19 pandemic, a dedicated intensive care unit for patients infected with SARS-CoV-2 was created at our institution. We noticed a marked increase in the number of blood cultures positive for coagulase-negative *Staphylococcus* species (CoNS) that highlights unique challenges that arise with the creation of new units and workflows.

Methods: We reviewed all blood culture results from the COVID-19 intensive care unit (CoVICU) from April 15 to May 29. We reviewed all blood cultures taken from the oncology ward, medical intensive care unit (MICU), and emergency department (ED) for the same time frame as a comparison. We calculated contamination rates, using the clinical microbiology laboratory criteria for possible contaminants based on species and number of positive blood cultures.

Results: There were 324 total blood cultures collected from the CoVICU with 27/324 (8.3%) positive for organisms deemed contaminant, 10/324 (3.1%) were positive considered bloodstream infections (BSI); the ratio of BSI:contaminant was 1:2.7. For the MICU, ED, and oncology units contamination rates were 2/197 (1%), 33/747 (4.4%), and 2/334 (0.6%), respectively; and the ratio of BSI:contaminant was 5:1, 2.2:1, and 17.5:1, respectively. There was a significant relationship between contamination rates and unit, $X^2(3, N = 1602) = 30.85$, $p < 0.001$.

Conclusion: Upon investigation, peripheral blood draw kits were not stocked in the CoVICU. Additionally, certain components of standard work for blood culture collection (e.g. glove exchange) could not be performed per usual practice due to isolation precautions. Peripheral blood draws were routinely performed by nurses in CoVICU and MICU while phlebotomy performed these in other comparison units. We suspect that lack of availability of blood draw kits and disruption of typical workflow in isolation rooms contributed to an unusually high number of contaminated blood cultures among patients admitted to the CoVICU. Notably, the CoVICU and MICU providers were the same pool of caregivers, further supporting a process issue related to isolation precautions. Institutions should be aware of the need for extra attention to supply chain management and examination of disruption to standard work that arise in the management of COVID-19 patients.

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

395. Rapid, Non-invasive Detection of Infection Using Plasma-based Next-Generation Sequencing for Microbial Cell-free DNA in Individuals Testing Negative for SARS-CoV-2 in a Pandemic Setting

William V. La Via, MD[1]; Sudeb Dalai, MD[2]; Christiaan R. de Vries, MD, PhD[1]; Ann Macintyre, DO[1]; Asim A. Ahmed, MD[2]; [1]Karius, Pacific Palisades, California; [2]Karius, Inc, Redwood City, CA

Session: P-12. COVID-19 Complications, Co-infections, and Clinical Outcomes

Background: The clinical presentation of patients with severe COVID-19 infection can be protracted and deteriorate to ARDS and multi-organ dysfunction with prolonged fever. As such, there is clinical overlap with many infectious diseases especially those that cause pneumonia. Due to of the prevalence of COVID-19 illness amidst the pandemic, concerns about testing sensitivity and the attendant risk to health care personnel (HCP) delivering care, patients are frequently tested multiple times to ascertain that they are SARS-CoV-2 free. Often, alternative diagnoses are not considered because some diagnostic modalities—such as bronchoalveolar lavage (BAL)—pose an unacceptable risk to the patient and/or HCP.

Methods: We interrogated plasma for microbial cell-free DNA from 58 patients who were known to be SARS-CoV-2 negative. Clinical information is taken from information submitted with the test requisition or obtained at the time of result reporting from clinical consultations with the ordering provider. In each case, a plasma sample was analyzed with the Karius Test (KT) which is a CLIA certified/CAP-accredited next-generation sequencing (NGS) plasma test designed to detect and quantify circulating microbial cell-free DNA (mcfDNA), which can assist with the diagnosis of deep-seated infections. After mcfDNA is extracted and NGS performed, human reads are removed and remaining sequences are aligned to a curated database of >1400 organisms. Organisms present above a statistical threshold are reported. The time to result is on average 24 hours from sample receipt.

Results: In a subset of 20 samples, we found a broad range of pathogens. *Pneumocystis jirovecii* was the most common. These detections were unexpected in the majority of these patients. (see Table)

Broad range of Karius detected pathogens (including fastidious bacteria, mycobacteria, fungi and viruses)

Case	Detected Organism(s)	Type of infection	Underlying condition
1	*Legionella micdadei*	Multifocal pneumonia	Chronic corticosteroids
2	*Legionella jordanis*	Pneumonia	Solid organ transplantation
3	*Nocardia veterana*	Pneumonia	Interstitial lung disease (ILD)
4	*Coxiella burnetii*	FUO	None
5	*Leptospira kirschneri*	FUO	None
6	*Mycobacterium avium complex*	FUO/necrotic pulmonary lesions	Unknown
7	*Mycobacterium kansasii*	Cavitary pulmonary lesions	None
8	*Histoplasma capsulatum*	Nodular pneumonia	HIV (new Dx)
9	*Pneumocystis jirovecii*	Pneumonia	HIV
10	*Pneumocystis jirovecii*	Pneumonia	HIV (new Dx)
11	*Pneumocystis jirovecii*	Pneumonia	Multiple myeloma
12	*Pneumocystis jirovecii*	Pneumonia	HIV
13	*Pneumocystis jirovecii*	Pneumonia	HIV (new Dx)
14	*Pneumocystis jirovecii*	Pneumonia	Chronic corticosteroids
15	*Pneumocystis jirovecii*	Pneumonia	Immunocompromised NOS
16	*Aspergillus fumigatus*	Nodular pneumonia	Solid organ transplantation
17	*Aspergillus calidoustus*	Nodular pneumonia	Fever/neutropenia
18	*Mucor indicus*	FUO/sinusitis	Stem cell transplantation
19	*Cunninghamella*	Pneumonia	Aplastic anemia
20	Human papillomavirus	Pulmonary/endocardial mass—due to viral driven tumor	Myelodysplastic syndrome

Conclusion: Open-ended, plasma-based NGS for mcfDNA with the KT provides a rapid, non-invasive method to diagnose deep-seated infection like pneumonia. This broad-based test detected a wide range of pathogens – many unsuspected – in patients with severe pneumonia and other invasive infections during the COVID-19 pandemic. These detections highlight the utility of the tool; which allowed better management including de-escalation of SARS-CoV-2 testing and selection of appropriate antibiotic therapy for the unexpected diagnoses.

Disclosures: William V. La Via, MD, Karius (Employee) Sudeb Dalai, MD, Karius (Employee) Christiaan R. de Vries, MD, PhD, Karius (Consultant, Independent Contractor)Stanford University (Employee) Ann Macintyre, DO, Karius (Employee) Asim A. Ahmed, MD, Karius (Employee)

396. Relationship Between Patient Characteristics and Critical Illness in Patients Admitted for CoVID-19

Samuel L. Windham, MD, MS[1]; Melissa P. Wilson, MS[1]; Connor Fling, BS[1]; David W. Sheneman, BA, MPH[1]; Taylor Wand, BS[1]; Lyndsey Babcock, BS[1]; Samantha Delson, ScD[1]; Kristine M. Erlandson, MD MS[2]; [1]University of Colorado, Denver, Colorado; [2]University of Colorado Denver, School of Medicine, Aurora, Colorado

Session: P-12. COVID-19 Complications, Co-infections, and Clinical Outcomes

Background: While several studies have explored hospitalization risk factors with the novel coronavirus (COVID-19) infection, the risk of poor outcomes during hospitalization has primarily relied upon laboratory or hospital-acquired data. Our goal was to identify clinical characteristics associated with intubation or death within 7 days of admission.

Methods: The first 436 patients admitted to the University of Colorado Hospital (Denver metropolitan area) with confirmed CoVID-19 were included. Demographics, comorbidities, and select medications were collected by chart abstraction. Missing height for calculating body mass index (BMI) was imputed using the median height