393. Prevalence of HIV in Patients Hospitalized for COVID-19 and Associated Mortality Outcomes: A Systematic Review and Meta-analysis
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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 modeling and 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, Italy, 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 the United States (1.43%, 95% CI: 0.98%-1.95%) 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 hospitalised for COVID-19 was 14.1% (95% CI: 7.8%-30.0%) 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.
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394. Pseudo-outbreak of Coagulase-negative Staphylococcus Species from Blood Cultures Highlights Unique Challenges in Care of Critically Ill Patients With COVID-19
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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 first 436 patients admitted to the University of Colorado Hospital as admitted for COVID-19 (CoVID-19) and emergent 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 BSL-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 BSL:contaminant was 51:2, 2:21:1, and 17:51, 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 the continuing issue of disruption of standard work that arise in the management of COVID-19 patients.
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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
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Session: P-12. COVID-19 Complications, Co-infections, and Clinical Outcomes
Background: The clinical presentation of patients with severe COVID-19 infection appears to be exacerbated in those with pre-existing conditions, including diabetes, hypertension, and/or obesity. 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 (mcdNA), which can assist with the diagnosis of deep-seated infections. After mcdNA 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 jiroveci was the most common. These detections were unexpected in the majority of these patients. (see Table)

| Case | Organism(s) | Type of infection | Underlying condition |
|------|-------------|-------------------|----------------------|
| 1    | Legioella maitanii | Pulmonary pneumonia | Solid organ transplantation |
| 2    | Legionella pneumophila | Pneumonia | Pulmonary hypertension |
| 3    | Mucorales verrucarum | Pneumonia | Interstitial lung disease (ILD) |
| 4    | Coagulase-negative Staphylococcus | BSI | None |
| 5    | Leptospira interrogans | FIO | None |
| 6    | Mycobacterium avium complex | Pulmonary tuberculosis | Pulmonary tuberculosis |
| 7    | Mycobacterium kansaii | Pulmonary lesions | None |
| 8    | Haemophilus influenzae | Bloodstream infection | HIV (Acquired) |
| 9    | Pneumocystis jiroveci | Pneumonia | HIV |
| 10   | Pneumocystis jiroveci | Pneumonia | HIV (AIDS) |
| 11   | Pneumocystis jiroveci | Pneumonia | Multisystem myeloma |
| 12   | Pneumocystis jiroveci | Pneumonia | HIV |
| 13   | Pneumocystis jiroveci | Pneumonia | Pneumonia (AIDS) |
| 14   | Pneumocystis jiroveci | Pneumonia | Chronic connective tissue disease |
| 15   | Pneumocystis jiroveci | Pneumonia | Immunocompromised NODS |
| 16   | Aspergillus fumigatus | Sepsis | Sepsis due to Amphotericin B |
| 17   | Aspergillus fumigatus | Pulmonary infection | Aspergillosis |
| 18   | Mycobacterium | Pulmonary infection | Pneumonia |
| 19   | Congophilamia | Pneumonia | Aseptic abscess |
| 20   | Human papillomavirus | Pulmonary/endothelial | Myocarditis/endothelial |

Conclusion: Open-ended, plasma-based NGS for mcdNA 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; Karuis (Employee) Sudeb Dalai, MD, Karuis (Employee) Christiana R. de Vries, MD, PhD; Karuis (Consultant, Independent Contractor)Stanford University (Employee) Ann Macintyre, DO; Karuis (Employee) Amin A. Ahmed, MD, Karuis (Employee)

396. Relationship Between Patient Characteristics and Critical Illness in Patients Admitted for CoVID-19
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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 high rely 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 confirmed COVID-19) and who were positive for 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