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371. Cluster of carbapenemase-producing Enterobacterales secondary infections during the COVID-19 crisis at a New York City hospital

Angela Gomez-Simmonds, MD[1]; Medini K. Annavajhala, PhD[2]; Thomas H. McConville, MD[1]; Donald E. Dietz, MD[1]; Sherif M. Shoucri, MD[1]; Justin C. Laracy, MD[1]; Brian Nelson, PharmD[3]; Susan Whittier, PhD[4]; Anne-Catrin Uhlemann, MD, PhD[1]; Anne-Catrin Uhlemann, MD, PhD[1]; [1]Columbia University Irving Medical Center, New York, NY; [2]Columbia University, New York, New York; [3]NewYork-Presbyterian Hospital, New York, NY; [4]Columbia University Medical Center, New York, NY

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

Background: Patients with COVID-19 may be at increased risk for secondary bacterial infections. At our quaternary care hospital in New York City, the rapid escalation of COVID-19 cases was accompanied by a massive surge in the need for hospital and critical care capacity. During this time, we noted a increase in infections caused by carbapenemase-producing Enterobacterales (CPE).

Methods: We retrospectively assessed microbiology data to identify patients with positive testing for SARS-CoV-2 who had clinical cultures with meropenem-resistant and/or carbapenemase gene-positive Enterobacterales. We obtained microbiological and clinical data by manual chart review. Available clinical isolates underwent long-range genomic sequencing using the MinION (Oxford) for rapid genotyping, resistance gene detection, and phylogenetic analysis.

Results: From March 1 to May 18, we identified 33 CPE isolates from 13 patients, including 29 *Klebsiella pneumonia* and four *Enterobacter cloacae*. Most patients (11/13) had a positive respiratory culture, and 7/13 developed bacteremia. All patients had prolonged, complex hospitalizations with extensive antibiotic exposure. We performed long-range sequencing on 19 isolates from 12 patients. 15/16 *K. pneumoniae* isolates belonged to sequence type (ST) 258 encoding KPC (14 KPC-2; 1 KPC-3); one ST70 isolate encoded KPC-2. All four *E. cloacae* isolates belonged to ST270 and encoded NDM-1. Phylogenetic analysis of ST258 isolates including historical isolates from our hospital revealed a distinct lineage of isolates from COVID-19 patients (72% bootstrap support), with expected clustering of isolates from the same patient and patients that were cohorted together.

Conclusion: While CPE have declined substantially in New York City in recent years, increased detection in patients with COVID-19 may signal a reemergence of these highly resistant pathogens in the wake of the global pandemic. System-level factors, such as the rapid scale-up of critical care capacity, while clearly needed to address the unprecedented reach of COVID-19, may have contributed to isolate clustering in these patients. Increased surveillance and antimicrobial stewardship efforts will be needed to mitigate the impact of CPE in the future.

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372. Comparing the Outcome of COVID-19 in Cancer and Non-Cancer Patients: an International Multicenter Study

Ray Y. Hachem, MD[1]; Tarcila Datoguia, MD[2]; Bilal Siddiqui, MD[3]; Ana Fernandez Cruz, MD[4]; Nobuyoshi Mori, MD[5]; Suha Fakhreddine, MD[6]; Dong-Gun Lee, MD, PhD[7]; Edward Gorak, MD[8]; Robert Somer, MD[9]; Arvinder Bhinder, MD[10]; Samuel Shelanski, MD[11]; Tomislav Dragivich, MD[12]; Arnaud Bayle, MD[13]; Roy F. Chemaly, MD, MPH, FACP, FIDSA[14]; Victor Mulonovich, MD[15]; Javier Adachi, MD[16]; Alexandre Malek, MD[15]; Monica Slavin, MBBS,MD[17]; Ying Jiang, MS[1]; Anne-Marie Chaftari, MD[14]; Issam I. Raad, MD[14]; Issam I. Raad, MD[14]; [1]MD Anderson Cancer Center, Houston, TX; [2]Hospital Israelita Albert Einstein, Sao Paulo, Sao Paulo, Brazil; [3]Community Health Network, Indiannapolis, Indiana; [4]Hospital Universitario Puerta de Hierro, Madrid, Madrid, Spain; [5]St. Luke's International Hospital, Tokyo, Tokyo, Japan; [6]Rafik Hariri University Hospital, Beirut, Beqaa, Lebanon; [7]Division of Infectious Diseases, Department of Internal Medicine, College of Medicine, The Catholic University of Korea, Seoul, Korea, Seoul, Seoul-t'ukpyolsi, Republic of Korea [8]Baptist MD Anderson Cancer Center, Jacksonville, Florida; [9]Cooper University Healthcare, Camden, New Jersey; [10]OhioHealth Physician Group, Marion, Ohio; [11]Banner MD Anderson at Mckee Medical Center, Loveland, Colorado; [12]Banner Health, Gilbert, Arizona; [13]Gustave Roussy Cancer Hospital, Villejuif, Lorraine, France; [14]The University of Texas MD Anderson Cancer Center, Houston, TX; [15]UT MD Anderson Cancer Center, Houston, Texas; [16]University of Texas MD Anderson Cancer Center, Houston, TX; [17]National Centre for Infections in Cancer, Peter MacCallum Cancer Centre, Melbourne, Victoria, Australia

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Background: Our objective was to describe the clinical course, risk factors and outcomes of patients infected with COVID-19 around the globe comparing cancer to non-cancer patients.

Methods: We conducted a retrospective cohort study of COVID-19 confirmed cases through an international multicenter collaboration including 17 centers around the world including the United States of America, Brazil, Europe, Far East, Middle East and Australia from January to date. We evaluated the patients' clinical characteristics, clinical course of the disease, hospitalization and outcome. Death was considered to be COVID-associated if it occurred within 30 days from the time of diagnosis.

Results: Preliminary data on 571 patients included 186 cancer patients and 385 non-cancer patients.

Cancer patients were more likely to have COPD and received steroids but were less likely to have COVID-related symptoms compared to non-cancer patients (84% vs 97%, p< 0.0001). The rate of pneumonia with hypoxia, non-invasive ventilation and mechanical ventilation were similar in both groups. Despite the fact that hospital admissions were significantly higher in non-cancer patients (70% vs 56%, p< 0.001), promising antiviral and immune-related therapy including remdesivir, convalescent plasma and immunomodulators were more commonly used in cancer patients compared to non-cancer patients (P=0.04). Cancer patients had a higher COVID-associated mortality rate compared to non-cancer patients (20% vs 11%, p=0.006).

Conclusion: Despite the fact that cancer patients received more frequent antiviral and immune-related therapy, the mortality rate among cancer patients was significantly higher than non-cancer patients.

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373. Comparison of the Epidemiology and Pathogens Cultured from Patients Hospitalized with SARS-CoV-2 Positive versus SARS-CoV-2 Negative in the US: A Multicenter Evaluation

Laura A. Puzniak, PhD[1]; Lyn Finelli, DrPH, MS[1]; Karri A. Bauer, PharmD[2]; Pamela Moise, PharmD[3]; Kalvin Yu, MD[4]; Carisa De Anda, PharmD[5]; Latha Vankeepuram, MS[6]; Prashant Parikh, n/a[4]; Vikas Gupta, PharmD, BCPS[4]; [1]Merck & Co., Inc., Kenilworth, NJ; [2]Merck & Co, Inc, Kenilworth, New Jersey; [3]Merck Research Labs, Merck & Co., Inc., Kenilworth, New Jersey; [4]Becton, Dickinson and Company, Franklin Lakes, New Jersey; [5]Merck & Co Inc, Kenilworth, New Jersey [6]BD, Franklin Lakes, NJ

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

Background: Past experiences with viral epidemics have indicated an increased risk for bacterial, fungal, or other viral secondary or co-infections due to patient characteristics, healthcare exposures and biological factors. It is important to understand the epidemiology of these infections to properly treat and manage these complex patients. This study evaluates the frequency, source, and pathogens identified among SARS-CoV-2 tested patients.

Methods: This was a multi-center, retrospective cohort analysis of SARS-COV-2 tested patients from 271 US acute care facilities with >1 day inpatient admission with a discharge or death between 3/1/20–5/31/20 (BD Insights Research Database [Becton, Dickinson & Company, Franklin Lakes, NJ]). We evaluated pathogens identified from blood, respiratory tract (upper/lower), urine, intra-abdominal (IA), skin/wound and other sources and classified them with respect to Gram-negative (GN), and Gram-positive (GP) bacteria, fungi, and viruses among those SARS-CoV-2 positive and negative.

Results: There were 599,709 admissions with 142,054 (23.7%) patients tested. Among those SARS-CoV-2 tested, 17,075 (12%) were positive and 124,979 (78%) were negative. The most common specimen collection sites (Table 1) and pathogens (Table 2) are shown. Higher rates of urine and respiratory cultures and higher rates of *P. aeruginosa* and fungi were seen in SARS CoV-2 positive patients. The top pathogens for urine cultures were *Escherichia coli* and *Klebsiella pneumoniae,* for blood *Staphylococcus aureus* and *Escherichia coli* and respiratory *Staphylococcus aureus* and *Pseudomonas aeruginosa.* SARS-CoV-2 positive patients had an overall longer length of stay (LOS) than negative, which almost doubled when a positive pathogen was identified.