370. Clinical Features and Outcomes of COVID-19 Infection Among Cancer Patients in Seattle, Washington

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Background: High morbidity and mortality has been observed with COVID-19 infection; however, there are limited data on clinical characteristics including exposures, coinfections, and antimicrobial use among cancer patients. We aimed to better characterize clinical features and outcomes in this population.

Methods: We conducted a retrospective chart review of consecutive patients at the Seattle Cancer Care Alliance diagnosed with SARS-CoV-2 infection by RT-PCR between February 28, 2020 and May 3, 2020. We obtained demographic and clinical data including coinfections, antimicrobial use and outcomes at 30 days after diagnosis.

Results: Of 60 patients reviewed, the median age was 62 years (range 22–98) and 43% were male. 34 (57%) patients had solid tumors and 16 (27%) hematologic malignancies. Breast (12%), colorectal (8%) and non-Hodgkin lymphoma (8%) were the most prevalent cancers. 34 (57%) had ≥ 2 comorbidities. The majority of identified exposures were from long-term care facilities (LTCF) (27%) or household contacts (25%) (Fig 1). The most common symptoms at diagnosis were cough (72%), fevers/chills (57%), shortness of breath (38%), nasal congestion/rhinorrhea (35%), and diarrhea (30%). 18 (31%) patients were prescribed at least one course of antibiotics within 30 days of diagnosis; antibiotics were prescribed to 54% of hospitalized patients (Fig 2). 6 (10%) had a documented bacterial infection; of these, 3 were respiratory coinfections. No viral or fungal copathogens were reported. 26 (43%) patients were hospitalized, 9 (15%) admitted to intensive care, and one (2%) required mechanical ventilation. 12 (20%) died within 30 days of diagnosis (Fig 3); of these, 10 (83%) had ≥ 2 comorbidities and 8 (67%) had LTCF exposure.

Figure 1: Distribution of COVID-19 Exposures

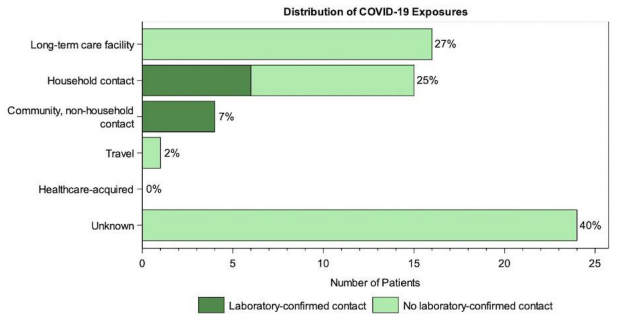
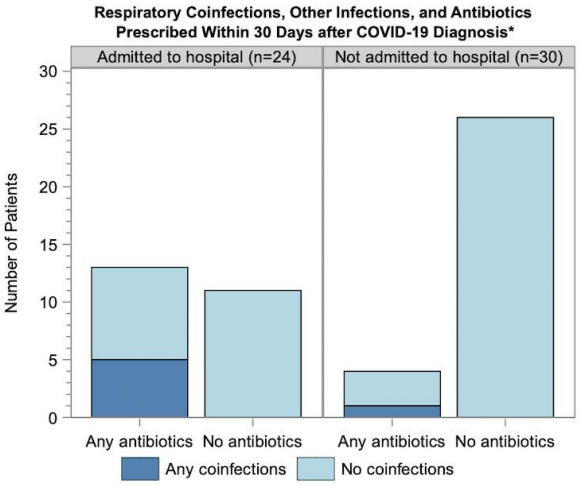


Figure 1. Distribution of COVID-19 exposures. Total length of bars represents the number of patients in each COVID-19 exposure category with percentages for patients in each exposure category shown to the right of the bars. Dark green shaded portions show the number of patients with laboratory-confirmed COVID-19 contacts and light green portions show patients without laboratory-confirmed contact.

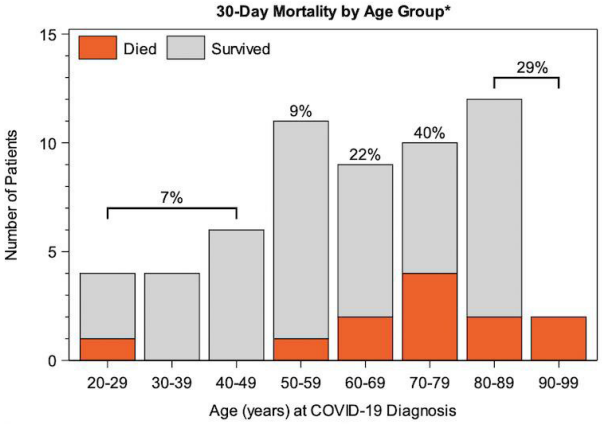
Figure 2: Respiratory Coinfections, Other Infections, and Antibiotic Use in the 30 Days after COVID-19 Diagnosis



*All infections identified in the 30 days after COVID-19 diagnosis were bacterial. Pathogens detected by specimen source: **Sputum**: *Moraxella catarrhalis* (1); *Pseudomonas aeruginosa* (1, this patient started antibiotics the day prior to COVID-19 diagnosis); *Staphylococcus aureus* (1); **Blood**: *Staphylococcus aureus* (1); coagulase-negative *Staphylococci* (1); **Urine**: *Staphylococcus aureus* (1); *Proteus vulgaris* (1); Enterobacteriaceae (1); **Stool**: *Clostridioides difficile* (1). One patient diagnosed with parainfluenza prior to COVID-19 diagnosis was not included as a coinfection; it was not possible to determine whether the parainfluenza or COVID-19 infection came first.

Figure 2. Frequency of antibiotic use and coinfections during 30 days of follow-up after COVID-19 diagnosis. Patients admitted to the hospital at least once during the 30-day follow-up period are shown in the left panel and patients not admitted to the hospital during the 30-day follow-up period are shown in the right panel. The total height of the bars represents the number of patients in each category, medium blue shaded portion represents the number of patients with a coinfection, light blue shaded portion represents patients without a coinfection in the 30 days after COVID-19 diagnosis.

Figure 3: 30 Day Mortality by Age Group



*Two deaths were not thought to be directly attributable to COVID-19: one 24-year-old and one 72-year-old.

Figure 3. 30-day all-cause mortality by age group at COVID-19 diagnosis. Total height of the bars represents the number of patients in each age category, orange shaded portion represents the number of patients who died within 30 days after COVID-19 diagnosis, grey shaded portion represents patients who survived at least 30 days after COVID-19 diagnosis. Of the 12 total deaths, 10 were directly attributable to COVID-19 and 2 (one 24-year-old, one 72-year-old) were thought to be most likely related to the patient's underlying disease but could not exclude COVID-19 as a contributing factor.

Conclusion: COVID-19 is associated with significant morbidity and mortality in cancer patients, particularly among older age groups with multiple comorbidities and those with LTCF exposure. More than half of cases appeared to acquire SARS-CoV-2 from LTCF or household exposures, indicating need for infection prevention and family/caregiver education. Despite few documented bacterial coinfections, antibiotic use within 30 days of diagnosis was common and likely empiric due to limited diagnostics in the era of COVID-19.

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

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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

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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

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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.