Bacterial respiratory infections in patients with COVID-19: a retrospective study from a tertiary care center in Lebanon

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Research Article

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Abstract

Background:

Despite multiple reports of increased incidence of bacterial respiratory tract infections following COVID-19 globally, the microbiology is not fully elucidated. In this study, we describe the incidence and microbiology of bacterial infections and the burden of multidrug resistant organisms (MDROs) in hospitalized COVID-19 patients with community-acquired pneumonia (CAP), non-ventilated hospital acquired pneumonia (NVHAP) or ventilator-associated pneumonia (VAP). To our knowledge, this is the first study that compares the microbiology of VAP and NVHAP in COVID-19 patients.

Methods:

This is a longitudinal retrospective cohort study conducted at the American University of Beirut Medical Center (AUBMC), a tertiary-care center in Lebanon. Adult patients with confirmed COVID-19 who were hospitalized between March 2020 and September 2021 were included. Only pathogens isolated within 42 days of positive SARS-CoV-2 tests were included. Bacterial isolates identified in hospital-acquired pneumonia (HAP) were divided into 3 groups based on the time of acquiring pneumonia after admission: hospital day 3-14, 15-28 and 29-42.

Results:

Out of 1674 patients admitted with COVID-19, 159 (9.5%) developed one or more respiratory infections. Overall, Gram-negative bacteria were predominant (83.5%) and *S. maltophilia* was the most common pathogen (14.3%). *S. aureus* and *Haemophilus* spp. were implicated in most CAPs, while *K. pneumonia*, *S. maltophilia* and *E. coli* were the top culprits in HAP during hospital days 3-14, 15-28 and 29-42 respectively. Among 231 isolates obtained, 59 (25.5%) were MDROs, seen in higher proportion in HAP, especially among patients with prolonged hospital stay (> 4 weeks). Non-fermenter Gram-negative bacilli (NFGNB) (OR = 3.521, p-value = 0.000), particularly *S. maltophilia* (OR = 3.236, p-value = 0.022), were significantly more implicated in VAP compared to NVHAP.

Conclusions:

COVID-19 patients hospitalized at AUBMC are at a slightly lower risk for bacterial respiratory infections compared to other studies. The pathogens varied according to the time since hospitalization. The burden of NFGNB and *S. maltophilia* is particularly high in COVID-19 VAP, indicating the need for further studies targeting these pathogens. A high rate of bacterial resistance was found which has important implications in guiding therapeutic decisions in COVID-19 patients who acquire bacterial infections.

1. Background

Viral lower respiratory tract infections are associated with increased incidence of bacterial infections (1). In fact, some viruses can damage the respiratory epithelium, decrease mucociliary clearance, and impair
local immune responses, rendering the respiratory tract susceptible to bacterial invasion (2). As such, bacterial infections have been reported in around 20 to 25% of hospitalized patients with influenza and are recognized as a major cause of morbidity and mortality in those patients (3, 4).

Despite multiple reports of increased bacterial respiratory tract infections following COVID-19 globally, the microbiology is not fully elucidated, particularly in the Middle East and North Africa (MENA) region where bacterial resistance is problematic (5, 6). Furthermore, recent evidence confirms an increased incidence of ventilator associated events during the pandemic and indicates that mechanical ventilation contributes to the increased incidence of hospital acquired infections among COVID-19 patients (7, 8).

2. Methods

Aim

This retrospective study aims at describing the microbiology of bacterial respiratory infections and the burden of multi-drug resistant organisms (MDROs) in hospitalized COVID-19 patients. We describe the pathogens implicated in community-acquired pneumonia (CAP), non-ventilated hospital acquired pneumonia (NVHAP) and ventilator-associated pneumonia (VAP). This data is essential to guide empiric antimicrobial therapy in this population. To our knowledge, this is the first study that compares the microbiology of VAP and NVHAP in hospitalized COVID-19 patients.

Study Design and Setting

This is a longitudinal retrospective cohort study of bacterial respiratory infections in adult patients with confirmed COVID-19 who were hospitalized between March 2020 and September 2021 at the American University of Beirut Medical Center (AUBMC), a tertiary-care center in Lebanon.

Microbiological Data and Definitions

Hospitalized patients with COVID-19 and bacterial respiratory infections were identified using the infection control and prevention program (ICPP) records. COVID-19 infection was confirmed by reverse transcriptase-polymerase chain reaction (RT-PCR) or rapid antigen testing for SARS-CoV-2 from nasopharyngeal swab samples. Bacterial respiratory infections were confirmed with sputum or deep tracheal cultures, ordered exclusively when the clinical suspicion for bacterial pneumonia was high. Clinical diagnosis of pneumonia was based on the treating team’s assessment in the setting of new lung infiltrate with clinical evidence of new onset or worsening fever or sputum production, leukocytosis, or worsening oxygenation according to the Infectious Diseases Society of America/ American Thoracic Society guidelines (9). Diagnosis of pneumonia was confirmed by reviewing the patients’ charts from the electronic medical records (EMR). Only pathogens isolated within 42 days of positive SARS-CoV-2 tests were included. Surveillance cultures from nares and oropharyngeal swabs were excluded.

CAP was defined as pneumonia occurring before or within 48 hours of hospital admission. Hospital-acquired pneumonia (HAP) was defined as pneumonia occurring 48 hours or more after admission,
including NVHAP and VAP. VAP was defined as pneumonia that develops at least two calendar days after introduction of invasive mechanical ventilation in a patient with supportive clinical and radiographic findings (9, 10). Bacterial isolates identified in HAP were further divided into 3 groups based on the time of acquiring pneumonia after admission: hospital day 3–14, 15–28 and 29–42.

Extended Spectrum Beta-Lactamase producing Enterobacterales (ESBL-PE) were defined as isolates non-susceptible to at least one of the following: cefotaxime, ceftriaxone, ceftazidime or cefepime. Carbapenem-resistant Enterobacterales (CRE) were defined as isolates resistant to at least one carbapenem (imipenem, meropenem, or ertapenem). Carbapenem-resistant *Pseudomonas aeruginosa* (CRPA) was defined as non-susceptible to imipenem or meropenem. Methicillin-resistant *Staphylococcus aureus* (MRSA) was defined by resistance to oxacillin, cefoxitin, or methicillin. Multi-drug resistant (MDR) *Acinetobacter baumannii* was defined as non-susceptible to at least one agent in at least 3 antimicrobial classes (11, 12).

Microbiological data, including positive RT-PCR tests or rapid antigen testing, bacterial cultures and susceptibility results were extracted from the ICPP records. Data were tabulated using the Microsoft Excel database.

Data analysis

Data were analyzed using Microsoft Excel 2016 and IBM SPSS Statistics 26. The count and percentage of isolates corresponding to each organism were computed in each of the 4 infection subcategories (CAP, HAP Day 3–14, HAP Day 15–28, HAP Day 29–42) and in the whole study sample. The count and percentage of MDR organisms were determined, and the trends of antimicrobial resistance were outlined. Microbiology of infections was compared across the 4 infection subcategories and according to the type of HAP (VAP vs NVHAP) using Chi-squared test or Fischer’s exact test as appropriate. The microbiology of COVID-19 VAP was also compared with pre-COVID-19 VAP data from our center.

### 3. Results

**Patient characteristics**

Out of 1674 patients admitted with COVID-19, 159 (9.5%) developed one or more bacterial respiratory infections within 42 days of hospitalization. Most (68.6%) were males and median age was 68 years (interquartile range [IQR]: 16 years). Diabetes mellitus was the most common underlying disease (40.3%), followed by coronary artery disease (29.6%) and hypertension (28.9%). Twenty-one patients (13.2%) had a history of solid tumor, a third of whom (7 patients) had lung cancer, while 13 patients (8.2%) had a history of hematologic malignancy. As for underlying respiratory co-morbidities, 26 patients (16.4%) had chronic obstructive pulmonary disease while 5% had asthma.

**Microbiological profile**
Fifty out of 188 episodes of pneumonia (26.6%) were CAP, while 138 (73.4%) were hospital acquired (HAP), among which 89 were VAP and 49 were not (NVHAP). Most HAP episodes (74/138, 53.6%) occurred during hospital days 3–14, while 50 and 14 episodes (36.2% and 10.1%) respectively occurred during days 15–28 and 29–42.

Among 231 isolates collected from 159 subjects, 59 (25.5%) were considered MDROs according to the predefined criteria (Fig. 1). Gram-negative bacteria were predominant (83.5%) compared to Gram-positive bacteria (16.5%). *Stenotrophomonas maltophilia* was the most encountered pathogen, accounting for 14.3% of all infections, followed by *Klebsiella pneumoniae* (13.9%), *Escherichia coli* (12.6%), *Staphylococcus aureus* (12.6%) and *Pseudomonas aeruginosa* (11.3%). The frequency and percentage distribution of each organism are presented in Table 1 and Fig. 2a.

Fifty-six pathogens (56/231) were isolated from patients with CAP, most (60.7%) being Gram-negative bacteria (Fig. 2b). *S. aureus* accounted for 26.8% of CAP followed by *Haemophilus* spp. (25%) and *Streptococcus* spp. (10.7%). 175 isolates were obtained in subjects with HAP (175/231), with an overt preponderance of Gram-negative bacteria (90.9%). *S. maltophilia* (18.9%) was the most common pathogen, followed by *K. pneumoniae* (16.0%), *E. coli* (13.7%), *P. aeruginosa* (13.1%), with 8% caused by each of *E. cloacae* and *S. aureus*.

The incidence of bacterial infections was highest during hospital days 3–14, during which *K. pneumoniae* (19.1%) was the most common organism, followed by *E. coli* (15.7%), *S. maltophilia* (15.7%), and *P. aeruginosa* (13.5%). During hospital days 15–28, *S. maltophilia* was the predominant pathogen (28.4%), followed by *K. pneumoniae* (13.4%), *P. aeruginosa* (11.9%), *E. cloacae* (10.4%). Finally, for days 29–42, *E. coli* was the most common pathogen (26.3%), followed by *P. aeruginosa* (15.8%) and *S. aureus* (15.8%). Interestingly, no new cases of *S. maltophilia* infection were identified after 29 days of admission, despite it being the most common pathogen overall (Fig. 3).

Burden of Multidrug-resistant organisms

As expected, MDRO burden was substantially higher in hospital-acquired infections (30.9%) compared to community-acquired infections (8.9%). A considerably higher proportion of MDROs was seen with prolonged hospitalization, particularly after 4 weeks of hospitalization (63.2%), compared to infections occurring during hospital days 3–28 (27%). The evolution of antimicrobial resistance rates is shown in Fig. 4.

Among MDROs, ESBL-PE were predominant (45.7%) and included *E. coli* (23.7%), *K. Pneumoniae* (16.9%) and *E. cloacae* (5.1%). CRE, which represented 13.6% of MDROs, included mainly *E. coli* (6.8%) and *E. cloacae* (5.1%). Other encountered MDROs were MRSA (18.6%), MDR *A. baumannii* (11.9%) and CRPA (10.2%). The distribution of MDROs is shown in Fig. 5.

Notably, 77.8% of *A. baumannii* isolates and 62.1% of *E. coli* isolates were MDR. MRSA made up 37.9% of isolated *S. aureus*. MDR rates for other bacteria were: 34.4% for *K. pneumoniae*, 33.3% for *E. cloacae*, and
23.1% for *P. aeruginosa* (23.1%). Among Enterobacterales, 34.2% were ESBL producers and 10.1% were carbapenem-resistant.

Ventilator-associated pneumonia vs Nonventilated hospital-acquired pneumonia

Two-thirds of HAP episodes (64.5%) were ventilator-associated. NFGNB accounted for most VAP isolates (51.7%), *S. maltophilia* being the most common, representing 23.7% of isolates, followed by *P. aeruginosa* (11.9%) and *A. baumannii* (7.6%). *Burkholderia cenocepacia* and *Achromobacter xylosoxidans* were isolated less frequently but exclusively in VAP. Among lactose fermenting pathogens isolated in VAP, *E. coli* was the most common (13.6%), followed by *K. pneumoniae* (12.7%) and *Enterobacter spp.* (7.6%).

As for NVHAP, NFGNB were less common (24.6%) and involved only *P. aeruginosa* (15.8%) and *S. maltophilia* (8.8%). Enterobacterales were the most frequent cause of infection with *K. pneumoniae* being the leading pathogen (21.1%), followed by *E. coli* (15.8%), *Enterobacter spp.* (14.0%). *S. aureus* and *Haemophilus spp.* represented 10.5% and 7.0% respectively of NVHAP isolates.

Compared to other organisms, NFGNB (OR = 3.521, p-value = 0.000), particularly *S. maltophilia* (OR = 3.236, p-value = 0.022) were significantly more isolated in VAP compared to NVHAP. There was no association between invasive mechanical ventilation and MDRO pneumonia (p-value = 0.494). The distribution of pathogens implicated in each of NVHAP and VAP is shown in Figs. 2c and 2d respectively.

Compared to pre-COVID-19 data on VAP microbiology from our center, the incidence of *A. baumannii* in COVID-19 VAP was lower (7.6% versus 32.6%), while the incidence of *S. maltophilia* was higher (23.7% versus 6%) (13) (Fig. 6).
Table 1
Evolution of the microbiological profile of bacterial respiratory infections in hospitalized COVID-19 patients

<table>
<thead>
<tr>
<th>Organism</th>
<th>Community-acquired</th>
<th>Hospital Day 3–14</th>
<th>Hospital Day 15–28</th>
<th>Hospital Day 29–42</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total</td>
<td>56 %</td>
<td>89 %</td>
<td>67 %</td>
<td>19 %</td>
<td>231 %</td>
</tr>
<tr>
<td>Gram negative bacteria</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>Stenotrophomonas maltophilia</em></td>
<td>0</td>
<td>0</td>
<td>14</td>
<td>15.7%</td>
<td>33</td>
</tr>
<tr>
<td><em>Klebsiella pneumoniae</em></td>
<td>4</td>
<td>7.1%</td>
<td>17</td>
<td>19.1%</td>
<td>32</td>
</tr>
<tr>
<td>ESBL-producing</td>
<td>0</td>
<td>0</td>
<td>5</td>
<td>5.6%</td>
<td>10</td>
</tr>
<tr>
<td>Carbapenem-resistant</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1.1%</td>
<td>1</td>
</tr>
<tr>
<td><em>Escherichia coli</em></td>
<td>5</td>
<td>8.9%</td>
<td>14</td>
<td>15.7%</td>
<td>29</td>
</tr>
<tr>
<td>ESBL-producing</td>
<td>2</td>
<td>3.6%</td>
<td>7</td>
<td>7.9%</td>
<td>14</td>
</tr>
<tr>
<td>Carbapenem-resistant</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1.1%</td>
<td>4</td>
</tr>
<tr>
<td><em>Pseudomonas aeruginosa</em></td>
<td>3</td>
<td>5.4%</td>
<td>12</td>
<td>13.5%</td>
<td>26</td>
</tr>
<tr>
<td>Carbapenem-resistant</td>
<td>0</td>
<td>0</td>
<td>3</td>
<td>3.4%</td>
<td>6</td>
</tr>
<tr>
<td><em>Enterobacter cloacae</em></td>
<td>4</td>
<td>7.1%</td>
<td>6</td>
<td>6.7%</td>
<td>18</td>
</tr>
<tr>
<td>ESBL-producing</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1.1%</td>
<td>3</td>
</tr>
<tr>
<td>Carbapenem-resistant</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1.1%</td>
<td>3</td>
</tr>
<tr>
<td><em>Haemophilus spp.</em></td>
<td>14</td>
<td>25%</td>
<td>3</td>
<td>3.4%</td>
<td>18</td>
</tr>
<tr>
<td><em>Acinetobacter baumannii</em></td>
<td>0</td>
<td>0</td>
<td>3</td>
<td>3.4%</td>
<td>9</td>
</tr>
<tr>
<td>Multidrug-resistant</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>2.2%</td>
<td>7</td>
</tr>
<tr>
<td><em>Burkholderia cenocepacia</em></td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0%</td>
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</tr>
<tr>
<td><em>Enterobacter aerogenes</em></td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>2.2%</td>
<td>3</td>
</tr>
<tr>
<td>Other gram-negative bacteria</td>
<td>4</td>
<td>7.1%</td>
<td>11</td>
<td>12.4%</td>
<td>22</td>
</tr>
<tr>
<td>Organism</td>
<td>Community-acquired</td>
<td>Hospital Day 3–14</td>
<td>Hospital Day 15–28</td>
<td>Hospital Day 29–42</td>
<td>Total</td>
</tr>
<tr>
<td>--------------------------------</td>
<td>--------------------</td>
<td>------------------</td>
<td>-------------------</td>
<td>--------------------</td>
<td>-------</td>
</tr>
<tr>
<td>Staphylococcus aureus</td>
<td>15</td>
<td>26.8</td>
<td>6</td>
<td>6.7</td>
<td>29</td>
</tr>
<tr>
<td>Methicillin-resistant</td>
<td>3</td>
<td>5.4</td>
<td>3</td>
<td>3.4</td>
<td>11</td>
</tr>
<tr>
<td>Streptococcus spp.</td>
<td>6</td>
<td>10.7</td>
<td>0</td>
<td>0</td>
<td>6</td>
</tr>
<tr>
<td>Other gram-positive bacteria</td>
<td>1</td>
<td>1.8</td>
<td>1</td>
<td>1.1</td>
<td>3</td>
</tr>
</tbody>
</table>

### 4. Discussion

In the present study, 9.5% of COVID-19 patients developed bacterial respiratory tract infections. This is lower than the rates reported in most studies, despite the high variability in incidence, especially in the MENA region (10.7–67.6%) (5, 14, 15). In accordance with previous reports, Gram-negative bacteria are predominant, and HAP mostly involves *P. aeruginosa*, *K. pneumoniae*, *E. coli* and *S. aureus*, while CAP mostly involves *S. aureus*, *Streptococcus spp.* and *Hemophilus spp.* (5, 16).

Interestingly, we have found that *S. maltophilia* was the most common cause of HAP, despite not being reported in studies from the MENA region and being reported in only 3.1–5.4% of cases in other studies (5, 16). However, *S. maltophilia* was more associated with COVID-19 VAP compared to NVHAP (OR = 3.298, p-value = 0.023). Additionally, the incidence of *S. maltophilia* in VAP in this study (23.7%) was higher than the one reported prior to the pandemic in a ten-year surveillance study of VAP at our center (6%) (13) (Fig. 6) and could not be linked to a *S. maltophilia* outbreak during the pandemic, despite thorough investigation by the ICPP at our center. Pre-COVID-19 evidence indicates that *S. maltophilia* is usually identified in late onset VAP (17). In fact, a recent meta-analysis that identified mechanical ventilation as the major risk factor for *S. maltophilia* pneumonia among non-COVID-19 patients reported an increased risk with longer duration of ventilation (18). This may explain the high prevalence of *S. maltophilia* in COVID-19 VAP, considering that COVID-19 patients often require a longer duration of mechanical ventilation (19). Another interesting finding was the low incidence of *A. baumanii* in COVID-19 VAP compared with the previously reported rate in pre-COVID-19 VAP at our institution (7.6% versus 32.6%) (13) (Fig. 6). In fact, several ICU clusters and outbreaks of *A. baumanii* were reported at our institution in the pre-COVID era and were successfully contained by the ICPP (20, 21). The consistent implementation of strict infection control measures throughout the pandemic, as evidenced by the absence of outbreaks or clusters during this period, likely explains the drop in *A. baumanii* burden observed in COVID-19 VAP relative to pre-COVID cases.

We reported that 25% of the isolated pathogens were MDROs, matching previous reports. However, higher resistance rates were encountered among *A. baumanii* (77.8%) and *E. coli* (62.1%) compared to earlier reports (68% and 36% respectively) (22). The CDC reports a significant increase in the threat estimate of
MDROs during the COVID-19 pandemic, likely driven by the inappropriate and excessive use of antibiotics due to the difficulties in discerning COVID-19 pneumonia from bacterial pneumonia and differentiating between colonization and infection in COVID-19 patients (23). Besides, seeing that risk factors for CRE acquisition such as antibiotic exposure, ICU stay and mechanical ventilation are common among this patient population, we could expect some increase in the incidence of CRE infections (24). However, a 35% increase in CRE infections in hospitals during 2020 is quite alarming (23), especially that CRE HAP/VAP constitutes an independent risk factor for mortality in COVID-19 hospitalized patients (25). These findings call for strict implementation of infection control and prevention measures and antimicrobial stewardship efforts to reduce inpatient transmission of MDRO pathogens and mortality in this population.

NFGNB are emerging as a major infection control challenge. We have demonstrated that NFGNB were implicated in 51.7% of VAPs among COVID-19 patients and were more likely to occur in VAP compared to NVHAP (OR = 3.521, p-value = 0.000) (Fig. 2d), These pathogens represent a major threat owing to their intrinsic multidrug resistance and ability to acquire resistance to novel antimicrobials (26). In the CDC report, Carbapenem-resistant *Acinetobacter* showed the greatest increase in hospital-onset threat estimate among MDR organisms from 2019 to 2020 (78% increase), while MDR *P. aeruginosa*’s hospital-onset threat estimate increased by 32% (23). This high antimicrobial resistance among NFGNB can be traced back to the pre-COVID-19 era (27). VAP due to NFGNB has been reported to recur at a higher rate than VAP involving other organisms (28). Moreover, evidence suggests that a prolonged course of antibiotic therapy is particularly needed in VAP due to NFGNB, likely reflecting the difficulty in eradicating these highly resistant organisms (28). Understanding the epidemiological characteristics of this group of pathogens would allow early and targeted interventions to optimize treatment as well as infection control and prevention measures.

Our study is the first to compare the microbiology of NVHAP and VAP in hospitalized COVID-19 patients. Despite being a single centered study with limited generalizability of findings, our results can be relevant as our hospital serves as a referral tertiary care center and such results can guide empirical therapy of COVID-19 patients with pneumonia. We also acknowledge that the retrospective design of our study reduced our control over confounding factors, especially with the lack of data on previous bacterial colonization, antibiotic use prior to the onset of pneumonia and the duration of mechanical ventilation in patients who developed VAP. Furthermore, we did not include a control group of hospitalized COVID-19 patients who did not develop bacterial infections. Finally, some infections with negative cultures might have been missed since only microbiologically confirmed infections were included.

**5. Conclusion**

In this study, COVID-19 patients were at a slightly lower risk for bacterial respiratory infections compared to other studies. Overall, Gram-negative bacteria were predominant, but the pathogens differed according to the time since hospitalization. *S. aureus* and *Haemophilus spp.* were implicated in most CAPs, while *K. pneumonia*, *S. maltophilia* and *E. coli* were the top culprits in HAP during hospital days 3–14, 15–28 and
29–42 respectively. MDROs represented a major burden, especially with HAP and prolonged hospitalization. Interestingly, Non-fermenting gram-negative bacilli, particularly *S. maltophilia*, were strongly associated with VAP, indicating the need for further studies targeting this group of pathogens. Understanding the microbiology of bacterial infections, resistance patterns and predisposing factors is vital for guiding therapeutic decisions in COVID-19 patients who acquire bacterial infections.

**Abbreviations**

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
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<tbody>
<tr>
<td>AUBMC</td>
<td>American University of Beirut Medical Center</td>
</tr>
<tr>
<td>CAP</td>
<td>community-acquired pneumonia</td>
</tr>
<tr>
<td>CRE</td>
<td>Carbapenem-resistant Enterobacterales</td>
</tr>
<tr>
<td>CRPA</td>
<td>Carbapenem-resistant <em>Pseudomonas aeruginosa</em></td>
</tr>
<tr>
<td>EMR</td>
<td>electronic medical records</td>
</tr>
<tr>
<td>ESBL-PE</td>
<td>Extended Spectrum Beta-Lactamase producing Enterobacterales</td>
</tr>
<tr>
<td>HAP</td>
<td>hospital-acquired pneumonia</td>
</tr>
<tr>
<td>ICPP</td>
<td>infection control and prevention program</td>
</tr>
<tr>
<td>MDR</td>
<td>Multi-drug resistant</td>
</tr>
<tr>
<td>MDROs</td>
<td>multidrug resistant organisms</td>
</tr>
<tr>
<td>MENA</td>
<td>Middle East and North Africa</td>
</tr>
<tr>
<td>MRSA</td>
<td>Methicillin-resistant <em>Staphylococcus aureus</em></td>
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<td>NFGNB</td>
<td>Non-fermenter Gram-negative bacilli</td>
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<td>NVHAP</td>
<td>non-ventilated hospital acquired pneumonia</td>
</tr>
<tr>
<td>RT-PCR</td>
<td>reverse transcriptase-polymerase chain reaction</td>
</tr>
<tr>
<td>VAP</td>
<td>ventilator-associated pneumonia</td>
</tr>
</tbody>
</table>

**Declarations**

*Ethics for approval and consent to participate:*

This study was approved by the Institutional Review board BIO-2020-0483 at AUBMC. Since this was an observational study, informed consent was waived.
Consent for publication:

Consent for publication was waived by the Institutional Review board as this study does not contain sensitive or personal information pertaining to any individual.

Availability of Data and Material:

The data that support the findings of this study are available from the AUBMC datasets but restrictions apply to the availability of these data, which were used under license for the current study, and so are not publicly available. Data are however available from the authors upon reasonable request and with permission of AUBMC.

Competing interest:

The authors declare that they have no competing interests

Funding:

The authors declare that they have no funding for this study

Authors’ contributions:

AS and TS reviewed the patients’ charts from the electronic medical records (EMR), confirmed microbiological data and clinical diagnoses, and extracted clinical data. AS tabulated and analyzed the data and outlined the results. AS and TS wrote the manuscript with support from SH. SH and JZ reviewed the manuscript. NZ and JT provided infection control and prevention program (ICPP) data and reviewed the manuscript. SSK and NR supervised the work and reviewed the manuscript. AS and TS prepared the manuscript and supporting documents for submission. SSK and AS completed the paper’s submission.

Acknowledgements:

Not applicable

References


Figures
Figure 1

Flow chart of the study. 1674 COVID-19 patients were admitted to our center between March 2020 and September 2021. 159 patients developed one or more bacterial respiratory infections within 42 days of hospitalization. A total of 231 bacterial isolates were collected, among which 59 represented MDROs. Isolates collected from patients with community-acquired pneumonia (CAP), ventilator-associated pneumonia (VAP) and nonventilated hospital-acquired pneumonia (NVHAP) were 56, 118 and 57 respectively.
Figure 2

Distribution of respiratory pathogens identified in hospitalized COVID-19 patients according to the type of pneumonia. CAP = community-acquired pneumonia; NVHAP = nonventilator hospital-acquired pneumonia; VAP = ventilator-associated pneumonia
Figure 3

Distribution of respiratory pathogens identified in hospitalized COVID-19 patients during 4 periods of hospitalization
Figure 4

Trends of antibiotic resistance in bacterial respiratory infections identified among hospitalized COVID-19 patients. C-A = Community-acquired; D3-14, D15-28, D29-42 = Acquired during hospital day 3-14, 15-28 and 29-42 respectively.

ESBL-PE = Extended Spectrum Beta-Lactamase producing Enterobacterales; CRE = Carbapenem-resistant Enterobacterales; CRPA = Carbapenem-resistant *P. aeruginosa*; MRSA = Methicillin-resistant *Staphylococcus aureus*; MDR-A = Multidrug-resistant *A. baumannii*
Distribution of bacterial pathogens and MDROs causing respiratory infections in hospitalized COVID-19 patients. MDROs = multi-drug resistant organisms; ESBL-PE = Extended Spectrum Beta-Lactamase producing Enterobacterales; CRE = Carbapenem-resistant Enterobacterales; CRPA = Carbapenem-resistant P. aeruginosa; MRSA = Methicillin-resistant Staphylococcus aureus; MDR-A = Multidrug-resistant A. baumannii
Figure 6

Distribution of bacterial pathogens implicated in COVID-19 VAP vs. pre-COVID-19 VAP data from our center