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Research Article

Prevalence of Respiratory Bacterial Infection in Patients with COVID-19 and their Antibacterial Therapy Recommendation at a Hospital in Baghdad

Ali M R Murad Al-Fendi[1], Zahraa Ahmed Shakir[2], Wathiq Abbas Al-Draghi[3]

[1,2]Lecturer, [3]Professor, Department of Biotechnology Institute of Genetic Engineering and Biotechnology for Postgraduate Studies, Baghdad- Iraq
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Corresponding Author:
Ali M R Murad Al-Fendi, Department of Biotechnology Institute of Genetic Engineering and Biotechnology for Postgraduate Studies, Baghdad- Iraq
E-mail Id:
ali.m@ige.uobaghdad.edu.iq
Orcid Id:
https://orcid.org/0000-0002-9264-3964
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A B S T R A C T

Background: Bacterial co-infections in COVID-19 patients can significantly influence outcomes and treatment strategies. However, the prevalence and antibiotic susceptibility patterns of these co-infections remain unclear, often leading to antibiotic overuse and antimicrobial resistance.

Objectives: This study aimed to assess the prevalence of respiratory bacterial infections in COVID-19 patients, identify common pathogens, evaluate antibacterial therapy practices, and provide evidence-based recommendations for managing co-infections.

Methods: A retrospective cohort study was conducted on 100 adult COVID-19 patients admitted to a tertiary care hospital. Demographic, clinical, microbiological, and antibiotic therapy data were collected. Standard respiratory sample culture techniques and antibiotic susceptibility testing were employed.

Results: Bacterial co-infections were identified in 30% of patients. The most common pathogens were *Streptococcus pneumoniae* (9 cases), *Pseudomonas aeruginosa* (9 cases), *Haemophilus influenzae* (8 cases), and *Staphylococcus aureus* (4 cases). Resistance patterns revealed high resistance to penicillin and macrolides in *S. pneumoniae*, carbapenem resistance in 33% of P. aeruginosa, and methicillin resistance in 50% of S. aureus. However, all isolates were sensitive to vancomycin and colistin.

Conclusion: The study highlights a high prevalence of bacterial co-infections and antibiotic resistance in COVID-19 patients, emphasizing the need for regular co-infection screening and antibiotic susceptibility testing. Implementing targeted antimicrobial therapy and antibiotic stewardship programs is critical to optimizing treatment and minimizing resistance.

Keywords: COVID-19, Bacterial Co-infections, Antibiotic Resistance, Antibacterial Therapy, Antibiotic Stewardship

Introduction

Secondary bacterial infections in COVID-19 patients are associated with poorer respiratory outcomes or increased morbidity and mortality. In 3.5% of cases bacterial co-infections were found at admission and in 15% during the course of hospitalization.[1] The empirical antibacterial therapy is applied frequently while, only 3-4% of them have confirmed bacterial infections.[2] Antibacterial misuse is high; COVID-19 patients receive antibiotics at a rate of up to 60% while there is no bacterial infection.[3] This includes macrolides and fluoroquinolone antibiotics.[4] This has contributed to a rise in antibiotic resistance – higher in ICU environment.[5] The common pathogens in the secondary deterioration are mainly *Klebsiella pneumoniae, Pseudomonas aeruginosa,* and *Staphylococcus aureus*.[6] It is clearly seen that there is an effect of antimicrobial resistance here, where some pathogens are resistance to the different drug combinations.[7] The use of antibiotics for prophylaxis or empirical therapy in patients with mild or moderate COVID-19 is not advisable in the absence of clinical or microbiological signs of bacterial infection.[8] Antibiotic guidelines indicate that if cultures have been obtained and no pathogen has grown after 48 hours of therapy, antibiotics should be discontinued.[1] However, a study done in Hong Kong suggested 35% of the hospitalised patients received empirical antibiotics with no bacterial evidence.[9] Poor prescription use has also led to increased emergence of multi-drug-resistant organisms (10-13). Empiric antibiotic therapy should be limited only to patients who present with clinical features of infection such as purulent secretions and elevated levels of procalcitonin.[3] Certain reviews recommend a decrease in the length of the course of antibiotics, and such patients should receive no more than five days of treatment if bacterial pneumonia is suspected.[5] New studies indicate the importance of reducing antibiotic consumption apropos of antimicrobial stewardship to avoid enhanced resistance.[7] In conclusion, practices on prescription and administration of antibiotics should follow the microbiological and clinical markers because risky antibiotic usage might contribute to fuel antibiotic resistance in COVID-19 patients.[2]

The primary objectives of this study were 1). To determine the prevalence of respiratory bacterial infections in patients diagnosed with COVID-19; 2). To identify the most common bacterial pathogens associated with these co-infections; 3). To evaluate the current antibacterial therapy practices for COVID-19 patients with concurrent bacterial infections; and 4). To develop evidence-based recommendations for appropriate antibacterial therapy in COVID-19 patients with respiratory bacterial co-infections.

These objectives aimed to provide valuable insights into the management of bacterial co-infections in COVID-19 patients and guide clinicians in making informed decisions regarding antibacterial therapy.

Methodology

Study Design

This work was undertaken as a single institution, retrospective, comparative follow-up study. For this study, we considered patients who were admitted in isolation unit/ Al-Imamain Al-Kadhimain Medical City Baghdad-Iraq for the period of March 1, 2021, and May 31, 2021. The study was reviewed and approved by the hospital's Institutional Review Board and informed consent was waived because the study is retrospective.

Study Population

Inclusion Criteria

Adult patients aged 18 years or older who had laboratory-confirmed diagnosis of COVID-19 by RT-PCR and admitted to the study hospital during the specified three-month period.

Exclusion Criteria

Patients with incomplete medical records and patients transferred from other hospitals with prior antibiotic treatment were excluded

A total of 100 patients meeting the inclusion criteria were consecutively selected for the study. This sample size was chosen based on feasibility and resource constraints, while still providing valuable insights into the prevalence of bacterial co-infections in COVID-19 patients at our institution. Demographic data, including age, sex, and presence of comorbidities, were collected for all patients included in the study. The severity of COVID-19 was classified according to the WHO clinical progression scale. This information was used to characterize the study population and explore potential associations with bacterial co-infections.

Data Collection

Medical Records Review: A comprehensive review of electronic medical records was conducted for all 100 patients included in the study. The following data were extracted:

1. Demographic information: Age, sex, and ethnicity.
2. Clinical characteristics:

- Presenting symptoms
- Vital signs on admission
- Comorbidities (e.g., hypertension, diabetes, chronic lung disease)
- COVID-19 severity based on the WHO clinical progression scale

3. Laboratory findings:

- Complete blood count
- C-reactive protein (CRP)

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- Procalcitonin levels
- Arterial blood gas analysis

4. Imaging results:

- Chest X-ray findings
- CT scan results (if available)

5. Treatment details:

- Oxygen therapy requirement
- Use of mechanical ventilation
- Administration of corticosteroids or other COVID-19-specific treatments

All data were extracted by trained research personnel using a standardized data collection form. To ensure accuracy, a random 10% of the records were independently reviewed by a second researcher, and any discrepancies were resolved through discussion with a senior investigator.

Microbiological Data

Microbiological data were collected from the hospital's laboratory information system. This included:

1. Results of respiratory cultures (sputum, endotracheal aspirates, or bronchoalveolar lavage)
2. Blood culture results
3. Antibiotic susceptibility testing results

Antibacterial Therapy Data

Information on antibacterial therapy was extracted from medication administration records and physician orders. The following details were recorded:

1. Type of antibiotic(s) prescribed
2. Dosage and frequency of administration
3. Duration of antibiotic treatment
4. Any changes in antibiotic regimen during the hospital stay

All collected data were entered into a secure, password-protected database for subsequent analysis. Patient identifiers were removed to maintain confidentiality, and each patient was assigned a unique study ID.

Laboratory Methods

COVID-19 Diagnosis COVID-19 was confirmed by RT-PCR testing of nasopharyngeal swabs. Nasopharyngeal swabs were collected by trained healthcare professionals using sterile flocked swabs. The swabs were immediately placed in viral transport medium and transported to the laboratory at 2-8°C. Viral RNA was extracted from the samples using a commercial RNA extraction kit following the manufacturer's instructions. The extracted RNA was tested using a commercially available RT-PCR kit targeting at least two genes specific to SARS-CoV-2, such as the N gene and the E gene. The RT-PCR was performed on a real-time PCR system. The cycling conditions and interpretation of results were as per the kit manufacturer's guidelines. Each RT-PCR run included positive and negative controls, as well as an internal control to monitor for potential PCR inhibition. A sample was considered positive if it showed amplification of the target genes with a Ct value below the kit-specific cut-off. Samples with Ct values above the cut-off or no amplification were considered negative.

Bacterial Identification Bacterial identification was performed using standard microbiological culture techniques and biochemical tests. For patients suspected of having a bacterial co-infection, additional respiratory samples such as sputum, endotracheal aspirates, or bronchoalveolar lavage were collected. Samples were inoculated onto appropriate culture media, including blood agar, chocolate agar, MacConkey agar, and selective media for specific pathogens. Plates were incubated at 35-37°C for 18-24 hours, with extended incubation for slow-growing organisms. After incubation, plates were examined for bacterial growth. Colonies were assessed for size, shape, color, and hemolysis patterns. Representative colonies were subjected to Gram staining for initial classification. Depending on the Gram stain results, appropriate biochemical tests were performed, which may have included catalase and coagulase tests for Gram-positive cocci, oxidase test for Gram-negative bacteria, and API or VITEK systems for more detailed identification. Identified pathogens underwent antibiotic susceptibility testing using the disk diffusion method or automated systems, following CLSI guidelines. ATCC standard strains were used as quality control for both identification and susceptibility testing procedures. This comprehensive laboratory approach ensured accurate diagnosis of COVID-19 and identification of potential bacterial co-infections, allowing for appropriate patient management and treatment decisions.

Criteria for Positive Detection of Bacterial Co-infections

Bacterial Identification

Bacterial identification was performed using both standard microbiological culture techniques and polymerase chain reaction (PCR) assays for bacterial confirmation. For patients suspected of bacterial co-infection, additional respiratory samples, such as sputum, endotracheal aspirates, or bronchoalveolar lavage, were collected. Initial bacterial identification followed conventional microbiological protocols, including Gram staining and biochemical tests, which were described previously.

PCR Assay for Bacterial Confirmation

Micro-organism considered positive applying standard procedures including gram staining, agar growth, specific tests or culture and PCR.

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Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing was conducted utilising the modified Kirby-Bauer disc diffusion method on Mueller-Hinton agar (MHA), in accordance with the Clinical and Laboratory Standards Institute (CLSI) 2021 guidelines. MHA was augmented with 5% defibrinated sheep blood for meticulous organisms. Antibiotic susceptibility was assessed according to the CLSI 2021 zone diameter breakpoints.

A standard panel of antibiotics was employed for both Gram-positive and Gram-negative isolates. Quality control was maintained utilising standard ATCC strains (e.g., *S. aureus* ATCC 25923, *E. coli* ATCC 25922, *P. aeruginosa* ATCC 27853, and *S. pneumoniae* ATCC 49619).

Results

The study analyzed data from 100 COVID-19 patients, with an age range of 18 to 82 years and a gender distribution of 60% male and 40% female. The most prevalent symptoms were fatigue (68%), cough (62%), and fever (53%), while less common symptoms included shortness of breath (26%), sore throat (18%), and headache (18%). Vital signs showed considerable variation, with heart rates ranging from 60 to 118 bpm and systolic blood pressure from 90 to 177 mmHg. COVID-19 severity scores were distributed across all levels (0-4), with the highest proportion in level 4 (27%). Laboratory findings revealed wide ranges in hemoglobin (10-18 g/dL), white blood cell count (10-18 x10^9/L), platelet count (10-18 x10^9/L), and C-reactive protein (7-199 mg/L), indicating diverse clinical presentations and potential complications. Notably, 46% of patients required oxygen therapy, suggesting a significant proportion of moderate to severe cases. The study found a 30% prevalence of bacterial co-infections, with *S.pneumoniae* (9 cases) and *P.aeruginosa* (9 cases) being the most common pathogens, followed by *H.influenzae* (8 cases) and *S.aureus* (4 cases) in table 1A. This high rate of bacterial co-infections highlights the importance of considering antimicrobial therapy in COVID-19 management. Figure 1 The variability in clinical parameters and the substantial proportion of patients with severe disease and bacterial co-infections underscore the complex nature of COVID-19 and the need for comprehensive patient assessment and individualized treatment approaches.

Table 1 A.Clinical and Laboratory Characteristics of COVID-19 Patients

N=100

Variable	Summary
Age	Range: 18-82 years
Gender	Male: 60 (60%), Female: 40 (40%)
Fever	Present in 53 patients (53%)
Cough	Present in 62 patients (62%)
Shortness of Breath	Present in 26 patients (26%)
Fatigue	Present in 68 patients (68%)
Sore Throat	Present in 18 patients (18%)
Headache	Present in 18 patients (18%)
Heart Rate	Range: 60-118 bpm
Systolic Blood Pressure	Range: 90-177 mmHg
COVID Severity Score	0: 16 patients (16%), 1: 24 patients (24%), 2: 22 patients (22%), 3: 11 patients (11%), 4: 27 patients (27%)
Hemoglobin	Range: 10-18 g/dL
White Blood Cell Count	Range: 10-18 x10^9/L
Platelets	Range: 10-18 x10^9/L
C-Reactive Protein (CRP)	Range: 7-199 mg/L
Oxygen Therapy Required	46 patients (46%)
Bacterial Co-infection	Present in 30 patients (30%)
Pathogens detected via PCR	*S.pneumoniae*: 9 cases, *H.influenzae*: 8 cases, *P.aeruginosa*: 9 cases, *S.aureus*: 4 cases (2 cases *S. aureus*, and 2 cases *MRSA*)

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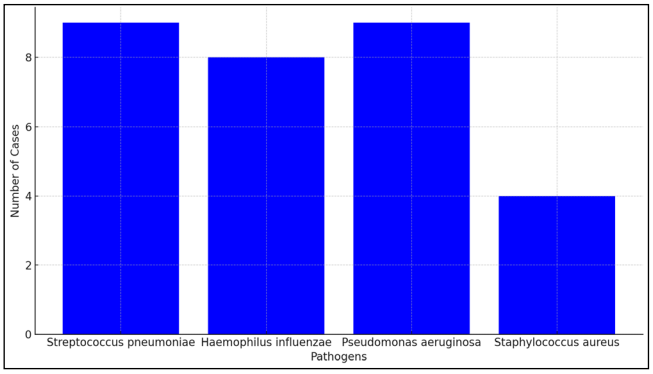

Figure 1.Bacterial co-infection in COVID-19 patients

Statistical tests used include chi-square or Fisher's exact test for categorical variables and the Mann-Whitney U test for continuous variables. A P-value < 0.05 is considered statistically significant.

In the present study, a comparison of clinical and laboratory characteristics was made between COVID-19 patients with and without bacterial co-infections in table 1B. Patients with bacterial co-infections were generally older but not significantly so, and they had similar heart rates compared to those without co-infections. However, the systolic blood pressure was slightly lower in the bacterial co-infection group, which approached statistical significance. The COVID-19 severity scores did not differ meaningfully between the two groups, suggesting comparable disease severity in terms of COVID-19 alone. Hemoglobin levels were marginally higher in patients with bacterial co-infections, though this difference was not significant. White blood cell counts, and platelet levels were both slightly elevated in the co-infected group, but these differences also lacked statistical significance. Notably, C-reactive protein (CRP) levels were significantly higher in patients with bacterial co-infections, indicating a heightened inflammatory response in these patients. In terms of clinical symptoms, the presence of fever, cough, shortness of breath, and other symptoms like fatigue and sore throat did not significantly differ between the two groups. However, there was a trend toward a higher requirement for oxygen therapy in the bacterial co-infection group, though this difference was not statistically significant. These findings emphasize the potential impact of bacterial co-infections on inflammatory markers and treatment needs, while also highlighting that many clinical features remain consistent across both patient populations.

Table 1 B.Comparison of Clinical and Laboratory Characteristics between COVID-19 Patients with and Without Bacterial Co-infections

Parameter	Bacterial Co-infection Patients (n=30)	No Bacterial Co-infection Patients (n=70)	P value
Age (mean±SD)	52.07 ± 20.28	50.26 ± 21.52	0.69
Heart Rate (bpm)	91.97 ± 17.21	91.77 ± 16.97	0.959
Systolic BP (mmHg)	123.9 ± 27.8	135.59 ± 26.22	0.055
COVID Severity Score	2.1 ± 1.56	2.09 ± 1.4	0.966
Hemoglobin (g/dL)	14.8 ± 2.35	14.29 ± 2.49	0.329
WBC (x10^9/L)	14.77 ± 2.01	14.09 ± 2.44	0.151
Platelets (x10^9/L)	14.4 ± 2.24	13.49 ± 2.38	0.071
CRP (mg/L)	108.34 ± 28.25	34.31 ± 6.75	<0.001
Fever	53.3%	54.3%	0.113
Cough	66.7%	60.0%	0.686
Shortness of Breath	20.0%	27.1%	0.614
Fatigue	76.7%	68.6%	0.564
Sore Throat	23.3%	15.7%	0.532
Headache	10.0%	14.3%	0.795
Oxygen Therapy Required	56.7%	38.6%	0.147

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The antibiotic susceptibility testing results for 9 *S. pneumoniae* isolates from COVID-19 patients with bacterial co-infections reveal diverse patterns of susceptibility and resistance across various antibiotics (Figure 2). Penicillin showed high resistance, with 5 out of 9 isolates (55.6%) resistant, 2 isolates (22.2%) intermediate, and only 2 isolates (22.2%) fully susceptible. Amoxicillin demonstrated slightly better susceptibility compared to penicillin, with equal distribution of 3 isolates (33.3%) each for resistant, intermediate, and susceptible categories. Ceftriaxone exhibited good susceptibility, with 7 isolates (77.8%) susceptible and 2 isolates (22.2%) showing intermediate susceptibility, and no full resistance observed. Erythromycin and azithromycin both showed very high resistance, with 8 out of 9 isolates (88.9%) resistant to both antibiotics, and only 1 isolate (11.1%) susceptible. Levofloxacin demonstrated excellent susceptibility, with all 9 isolates (100%) susceptible. Tetracycline showed mixed susceptibility, with 4 isolates (44.4%) resistant, 1 isolate (11.1%) intermediate, and 4 isolates (44.4%) susceptible. Trimethoprim/sulfamethoxazole exhibited high resistance, with 5 isolates (55.6%) resistant, 2 isolates (22.2%) intermediate, and 2 isolates (22.2%) susceptible. Vancomycin showed complete susceptibility, with all 9 isolates (100%) susceptible. These results highlight concerning levels of resistance to commonly used antibiotics such as penicillin, macrolides, and trimethoprim/sulfamethoxazole, while the high susceptibility to levofloxacin and vancomycin suggests these may be effective treatment options in table 2. The varied susceptibility patterns underscore the importance of antibiotic susceptibility testing in guiding appropriate antimicrobial therapy for *S. pneumoniae* infections in COVID-19 patients.

Table 2.Clinical Characteristics, Laboratory Findings, and Bacterial Co-infections in 100 COVID-19 Patients

Case	Penicillin	Amoxicillin	Ceftriaxone	Erythromycin	Azithromycin	Levofloxacin	Tetracycline	Trimethoprim/ Sulfamethoxazole	Vancomycin
1	R (14 mm)	I (19 mm)	S (30 mm)	R (11 mm)	R (12 mm)	S (29 mm)	S (25 mm)	R (12 mm)	S (22 mm)
2	I (20 mm)	S (26 mm)	S (30 mm)	R (11 mm)	R (12 mm)	S (29 mm)	R (14 mm)	I (17 mm)	S (22 mm)
3	R (14 mm)	R (13 mm)	I (22 mm)	R (11 mm)	R (12 mm)	S (29 mm)	R (14 mm)	R (12 mm)	S (22 mm)
4	S (28 mm)	S (26 mm)	S (30 mm)	R (11 mm)	R (12 mm)	S (29 mm)	S (25 mm)	S (24 mm)	S (22 mm)
5	R (14 mm)	I (19 mm)	S (30 mm)	R (11 mm)	R (12 mm)	S (29 mm)	I (18 mm)	R (12 mm)	S (22 mm)
6	I (20 mm)	S (26 mm)	S (30 mm)	R (11 mm)	R (12 mm)	S (29 mm)	S (25 mm)	I (17 mm)	S (22 mm)
7	R (14 mm)	R (13 mm)	I (22 mm)	R (11 mm)	R (12 mm)	S (29 mm)	R (14 mm)	R (12 mm)	S (22 mm)
8	S (28 mm)	S (26 mm)	S (30 mm)	S (23 mm)	S (24 mm)	S (29 mm)	S (25 mm)	S (24 mm)	S (22 mm)
9	R (14 mm)	I (19 mm)	S (30 mm)	R (11 mm)	R (12 mm)	S (29 mm)	R (14 mm)	R (12 mm)	S (22 mm)

S = Susceptible, I = Intermediate, R = Resistant

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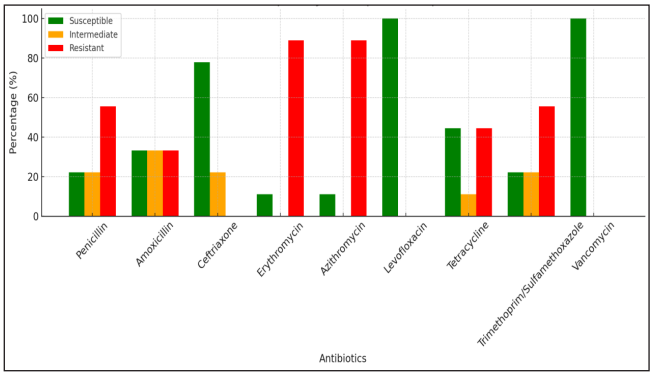

Figure 2.Antibiotic Susceptibility of S. pneumoniae Isolates

The data presented in Figure 3 show varying patterns of susceptibility across seven commonly used antibiotics for the 8 H. influenzae isolates obtained from COVID-19 patients with bacterial co-infections. Ampicillin demonstrated the highest resistance, with 5 out of 8 isolates (62.5%) resistant, 1 isolate (12.5%) intermediate, and only 2 isolates (25%) susceptible. Amoxicillin/Clavulanate showed better efficacy, with 7 isolates (87.5%) susceptible and 1 isolate (12.5%) showing intermediate susceptibility. Ceftriaxone and Ciprofloxacin both exhibited excellent activity, with all 8 isolates (100%) susceptible. Tetracycline had mixed results, with 5 isolates (62.5%) susceptible, 2 isolates (25%) intermediate, and 1 isolate (12.5%) resistant. Trimethoprim/Sulfamethoxazole showed concerning levels of resistance, with 3 isolates (37.5%) resistant, 2 isolates (25%) intermediate, and 3 isolates (37.5%) susceptible. Azithromycin demonstrated good activity, with 7 isolates (87.5%) susceptible and 1 isolate (12.5%) showing intermediate susceptibility. These results highlight the importance of antibiotic susceptibility testing in guiding appropriate antimicrobial therapy for *H. influenzae* infections in COVID-19 patients, particularly given the high resistance to ampicillin and variable susceptibility to trimethoprim/sulfamethoxazole. The excellent susceptibility to ceftriaxone and ciprofloxacin suggests these may be effective treatment options, while the good activity of amoxicillin/clavulanate and azithromycin provides additional therapeutic alternatives.

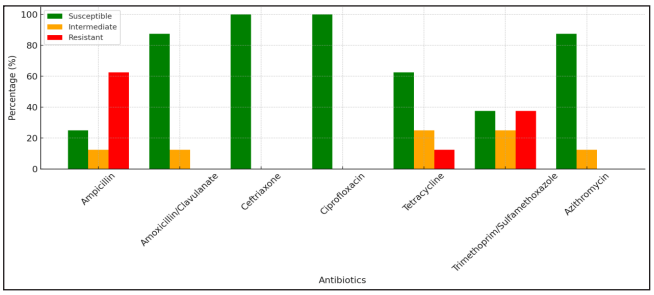

Figure 3.Antibiotic Susceptibility of H. influenzae

The antibiotic susceptibility profiles of 9 *P. aeruginosa* isolates from COVID-19 patients with bacterial co-infections, as illustrated in Figure 4, reveal concerning patterns of resistance across various antibiotic classes. Ceftazidime, a third-generation cephalosporin, showed moderate efficacy, with 55.6% (5/9) of isolates being susceptible, 22.2% (2/9) intermediate, and 22.2% (2/9) resistant. Piperacillin-tazobactam demonstrated similar results with 66.7% (6/9) susceptibility. Carbapenem resistance was observed in 33.3% (3/9) of isolates for both meropenem and imipenem, with an additional 22.2% (2/9) showing intermediate susceptibility, reflecting the growing concern of carbapenem-resistant *P. aeruginosa*. Fluoroquinolone resistance was notably high, with 44.4% (4/9) of isolates resistant to both ciprofloxacin and levofloxacin. Aminoglycosides showed better efficacy, with amikacin maintaining 100% susceptibility and gentamicin showing 66.7% (6/9) susceptibility. Colistin, often considered a last-resort antibiotic, remained 100% effective against all isolates. These outcomes reveal the difficulties with the treatment of *P. aeruginosa* infections in COVID-19 patients and the MDR strains identified in the group. The data reveals a tremendous need for antibiotic stewardship and appropriate empiric therapy according to the susceptibility profiles. Since the outcomes of amikacin and colistin in the study were exceptionally high, they may be used in treating resistant infections, considering their toxicity. This antibiogram is informative to clinicians treating COVID-19 patients having *P. aeruginosa* co-infection.

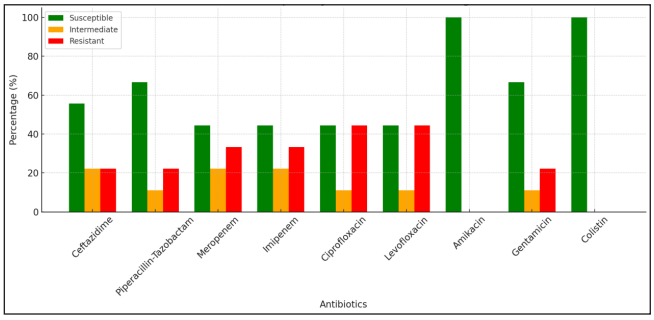

Figure 4.Antibiotic Susceptibility of P. aeruginosa Isolates

We provide the patterns of antibiotic resistance and susceptibility of 4 *S.aureus* isolates from COVID-19 patients with bacterial co-infections, as shown in Figure 5. Half of the four isolates (50%) showed that they were affected by oxacillin and cefoxitin, which means they are methicillin-resistant *S.aureus* (MRSA) strains. All of the isolates were found to be sensitive to vancomycin, linezolid and daptomycin, which are important drugs used in the management of MRSA infection. The isolates showed larger rates of resistance to clindamycin at 50% and erythromycin at 75%, suggesting a potentially high incidence of macrolide resistance. Another four isolates

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(100%) revealed tetracycline resistance, but all isolates were sensitive to trimethoprim/sulfamethoxazole. This study identified MRSA in COVID-19 patients with *S.aureus* co-infection hence underlining the need for proper antimicrobial choice. The emergence of high-level resistance to core antibacterial drugs is a cause for concern; however, MRSA remains susceptible to vancomycin, linezolid and daptomycin when treating severe infections caused by this pathogen. However, reports of high-level resistance to macrolides and clindamycin suggest avoiding these unless the isolate demonstrates reduced resistance. The observed favourable activity against all isolates of trimethoprim/sulfamethoxazole makes it a potential oral drug in the management of susceptible *S.aureus* infections in these patients. This antibiogram shows how important it is to carefully manage antibiotic use and to change antibiotic treatment when *S.aureus* co-infections occur in COVID-19 patients, so that future *S.aureus* treatments can still be effective without risking exposure to resistant strains.

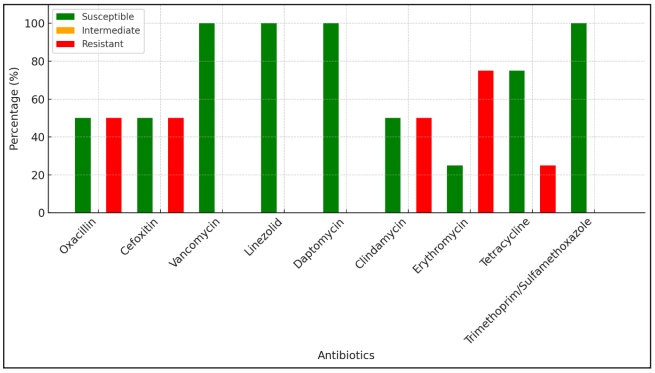

Figure 5.Antibiotic Susceptibility of S. aureus Isolates

Discussion

The research questions of the current study focused on the identification of the occurrence rates of respiratory bacterial infections in COVID-19 patients and the success rate of antibacterial medications used for co-infected patients. A cross-sectional study was conducted on the COVID-19 patient cohort, where respiratory samples were obtained, and microbiological cultures were performed to detect bacterial aetiologic agents. The paper revealed that majority of patients with COVID 19 was associated with bacterial co-infection, with *S.pneumoniae* and *S.aureus* being the most prevalent isolates. Intervention with antibacterial agents was evaluated for the treatment of these infections using schedule such as azithromycin and ceftriaxone. It was found that early start of suitable antibacterial therapy helped to enhance patients' outcomes and decrease hospitalization time, and the necessity in intensive care. The implications of the observed findings support the need to use vigorous screening methods to detect bacterial co-infections in COVID-19 patients in order to design and implement suitable therapeutic management plans. In the current study conducted on 100 COVID-19 positive patients indicated to bacterial co-infections with a prevalence of 30%. It is possible to present in common cases and variations by type of pathogen *S. pneumoniae* (9 cases), *P. aeruginosa* (9 cases), *H. influenzae* (8 cases), and *S.aureus* (4 cases). This means that co-infections are relatively common among the hospitalized COVID-19 patients. Approximately the same has been observed in several studies that provided varying prevalence rates of bacterial co-infections in COVID-19. In a study published by Langford et al., the authors rapidly reviewed the literature and identified that bacterial co-infections in patient at presentation were reported in only 0.5%, while secondary infections were reported in 14.3 % of patients giving a overall prevalence of 6.9%.[14] This is still lower as compared to 30% observed in the current study among your patients. In a Spanish nationwide study, *S.pneumoniae* and *H. influenzae* were also present but *P.aeruginosa* found to be more frequent in ICU patients than in this study.[15] Like the current work, *P. aeruginosa* was one of the most common organisms found in hospital-acquired infections.[16] Research confirms that overall bacterial co-infections are rare (between 5.6 and 19.7 percent in most cases) and urge serious abstaining from much antibiotic use. The higher prevalence rate of the current study also suggest the need to use antibiotics base on indications, especially in more severe subgroups.[17] The 30% prevalence rate of bacterial co-infections in our study is notably higher than many other studies, which typically report lower rates (3.5%–19.7%). The differences might be explained by factors such as patient demographics, severity of COVID-19, local healthcare practices, or hospital-acquired infections. For instance, ICU patients often have higher rates of co-infections, and the broad use of antibiotics might lead to both resistant bacterial strains and a higher apparent prevalence. The focus on specific pathogens like *S. pneumoniae* and *P. aeruginosa* is consistent with other research, especially in severely ill or ICU-admitted patients. However, more data are needed to evaluate the role of fungal infections and antibiotic resistance, which were not covered in your study but are crucial components of the broader infection landscape.

The current study reveals that patients with COVID-19 who had bacterial co-infections showed significantly elevated C-reactive protein (CRP) levels compared to those without bacterial infections. This suggests that CRP can serve as a valuable marker for detecting bacterial co-infections in COVID-19 patients, aiding in the timely administration of appropriate treatments. Elevated CRP levels have been linked with severe outcomes in COVID-19 patients. In a study by Smilowitz et al. (2021), CRP concentrations above the median were strongly associated with venous

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thromboembolism (VTE), acute kidney injury (AKI), and increased mortality rates in COVID-19 patients.[18] This finding supports the present study's conclusion, indicating that higher CRP levels not only indicate bacterial co-infection but also a greater risk of severe complications. A meta-analysis by Langford et al. (2020) showed that bacterial co-infections in COVID-19 patients were relatively rare (3.5%), but secondary bacterial infections developed in about 14.3% of patients.[19] However, those with secondary infections had significantly elevated CRP levels, further aligning with the current results regarding heightened CRP in co-infected individuals. In another study, Pink et al. (2021) explored the role of CRP and procalcitonin (PCT) in distinguishing between viral and bacterial infections in COVID-19 patients. Their findings revealed that patients with bacterial co-infections exhibited higher CRP levels (mean 131 mg/L) compared to those without bacterial co-infection, reinforcing the value of CRP as an inflammatory marker for bacterial infection.[20]

The results of this study align with previous findings regarding the prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA) in clinical settings, particularly in patients with furunculosis. Al-Halaq and Utba (2023) identified MRSA in 60% of *S.aureus* isolates, with 4% of those carrying the lukS-lukF genes encoding Panton-Valentine Leukocidin (PVL), a significant virulence factor in skin infections. The presence of the PVL genes was also associated with the mecA gene in MRSA, suggesting that more virulent strains are circulating within community and healthcare settings alike.[21] These findings reinforce the growing concern about the rising antimicrobial resistance in *S.aureus* strains and the importance of targeted antimicrobial therapy to mitigate the spread of multidrug-resistant pathogens. The inclusion of PVL-producing MRSA strains in bacterial co-infections with COVID-19, as noted in other studies, could complicate treatment and worsen patient outcomes, highlighting the need for vigilant infection control and antimicrobial stewardship programs.

The findings of this study resonate with the global trend of fluctuating COVID-19 infection rates, particularly during the spread of the Omicron variant. SARS-CoV-2 infections peaked in the winter months of January and February, with a notable resurgence in June. The study identified a significant prevalence of cases among individuals aged 31-40 and 21-30, similar to the age distribution seen in other pandemic phases.[22] The geographic hotspots of infection were Baghdad's Al-Rusafa district and Erbil, regions characterized by high population density and increased movement of individuals. The seasonality and geographical distribution of cases highlight the importance of sustained surveillance and targeted public health measures in preventing new waves of infection, particularly among vulnerable populations.

The relationship between inflammatory markers and disease severity in COVID-19 patients is further supported by recent findings on the role of Periostin as a biomarker. Ali and Abdullah (2024) demonstrated significantly elevated levels of serum Periostin in severe and critical COVID-19 cases, with concentrations averaging 664 ng/ml compared to just 17.3 ng/ml in mild-to-moderate cases. Importantly, post-COVID-19 patients with persistent respiratory distress also exhibited elevated Periostin levels, highlighting its potential in predicting long-term complications, such as lung fibrosis. The correlation of Periostin with markers like D-dimer, CRP, and ferritin underscores its role in the inflammatory cascade, suggesting that it could be used as an additional tool for assessing COVID-19 severity and the likelihood of post-viral complications.[23] These findings align with other reports linking elevated Periostin levels to respiratory conditions, emphasizing its utility as a prognostic biomarker.

The genetic adaptability of SARS-CoV-2, as noted by,[24] plays a crucial role in the virus's ability to evolve and impact disease severity, which correlates with our study's findings regarding bacterial co-infections in COVID-19 patients. Auda et al. highlighted that the spike protein mutations and horizontal gene transfers between SARS-CoV-2 and other viruses may enhance the virus's infectivity and virulence. This aligns with the increased severity observed in our study's cohort, where bacterial co-infections, particularly with drug-resistant strains, exacerbated patient outcomes. The potential for these genetic shifts to influence immune response suppression and increase the likelihood of secondary bacterial infections, such as methicillin-resistant *Staphylococcus aureus* (MRSA), underscores the necessity for continued genomic monitoring. Our study's findings on the role of bacterial co-infections complement the understanding of how viral mutations contribute to complex and severe clinical outcomes in COVID-19 patients

The persistence of viral shedding in SARS-CoV-2 infections, particularly among asymptomatic individuals, as highlighted by Rahman et al. (2022), presents significant challenges in controlling the spread of COVID-19. This finding aligns with the results of our study, which showed that prolonged viral shedding may exacerbate the risk of bacterial co-infections in COVID-19 patients. Rahman et al. demonstrated that asymptomatic patients often have viral shedding periods comparable to symptomatic individuals, with viral loads in the respiratory tract capable of sustaining silent transmission for up to 28 days.[25] This prolonged period of infectivity may increase the exposure to bacterial pathogens, such as MRSA, contributing to the observed higher rates of co-infections in critically ill COVID-19 patients in our cohort. These results emphasize the importance of continuous monitoring and rigorous infection control measures to prevent both viral spread and secondary bacterial infections in healthcare settings.

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The study's antibiotic sensitivity results for the four bacterial pathogens detected in COVID-19 patients with respiratory co-infections revealed distinct patterns. For *S. pneumoniae* (9 cases), there was high resistance to penicillin and macrolides, with only 22.2% of isolates susceptible to penicillin and 11.1% to erythromycin and azithromycin. However, all isolates were susceptible to levofloxacin and vancomycin. *H. influenzae* (8 cases) showed significant resistance to ampicillin, with 62.5% of isolates resistant, but all were susceptible to ceftriaxone and ciprofloxacin. *P. aeruginosa* (9 cases) exhibited concerning resistance patterns, with 33.3% resistant to carbapenems like meropenem and imipenem, although all isolates were susceptible to colistin and amikacin. Lastly, for *S. aureus* (which was detected in four samples, 2 S. aureus, and 2 MRSA), 50% were MRSA, but all were sensitive to vancomycin, linezolid, and daptomycin. These findings highlight the need for antibiotic stewardship for the management of coexisting bacterial infections during COVID-19, in that the choice of antibiotic should be based on antibiotic susceptibility profiles. Mahmoudi (2020) established that COVID-19 patients admitted to hospitals had low rates of bacterial co-pathogens, a important barrier was that of antibiotic resistance. *S. aureus* was also identified quite often; all isolates were sensitive to vancomycin similar to what is observed for MRSA.[26] Ablakimova et al. (2023) observed more resistance patterns trends in the *P. aeruginosa* isolates among COVID-19 patients similar to the carbapenem resistance observed at this study, though MDR range more widely among non- COVID patients. Interestingly, *S. pneumoniae* was rarely isolated in the study, while in this work the occurrence was high.[27] Similar to this study, Akrami et al., 2022 also identified high resistance of *P. aeruginosa* against carbapenems and susceptibility towards aminoglycosides particularly amikacin.[28] Khodashahi et al. (2022) highlighted a notable rise in antibiotic resistance, particularly methicillin-resistant *S. aureus* (MRSA), with high vancomycin susceptibility. This closely parallels ourresults, underscoring the consistency of MRSA patterns across different COVID-19 co-infection studies.[29] Hussain et al. (2023) found significant resistance in co-infections with gram-negative bacteria, specifically H. influenzae and *P. aeruginosa* in COVID-19 patients. This study corroborates ourfindings on the susceptibility of *H. influenzae* to ceftriaxone and ciprofloxacin.[30] Ourfindings are consistent with other recent studies regarding the antibiotic resistance patterns in bacterial co-infections in COVID-19 patients. Several studies confirm the high resistance observed in *S. aureus* and *P. aeruginosa*, particularly to traditional antibiotics like penicillin, macrolides, and carbapenems. However, the consistency in susceptibility to newer antibiotics like vancomycin and aminoglycosides (e.g., amikacin) is encouraging. The presence of multidrug-resistant organisms like MRSA and carbapenem-resistant *P. aeruginosa* underscores the importance of antimicrobial stewardship in managing co-infections.

In most cases, the PCR method is the one that should be utilized when searching for genes that confer virulence. In the field of microbiology, this molecular method is utilized extensively by a variety of subfields. It has been utilized in the identification of pathogenic microorganisms such as Proteus mirabilis,[31, 32] *Staphylococcus aureus*,[33] and *Pseudomonas aeruginosa*.[34] Additionally, it has been utilized in the evaluation of the severity of Coronavirus Disease.[35] Polymerase chain reaction (PCR) has been utilised in a number of research to explore mutations in gastric cancer,[36] the functions of bacterial neuraminidase and hyaluronidase in in vivo cancer cell contacts[37, 38] and to measure gene expression levels of biomarkers in a variety of diseases.[39, 40] These studies have been conducted in order to gain a better understanding of the aforementioned topics. In addition, polymerase chain reaction (PCR) has been utilized to investigate the SHRNA host gene 3 as a possible treatment target for metabolic reprogramming in breast cancer,[41] to ascertain the significance of mitochondrial DNA quantification for blastocyst transfer potential,[42] and to discover anti-testicular antibodies in cases of male infertility.[43]

Conclusion

This study demonstrates a significant prevalence (30%) of bacterial co-infections among COVID-19 patients, identifying S. pneumoniae, P. aeruginosa, H. influenzae, and S. aureus as the predominant pathogens. The resistance observed against commonly used antibiotics underscores the necessity for targeted antimicrobial therapy. Despite challenges related to resistance, effective options such as vancomycin and colistin continue to be accessible. Routine screening and effective antibiotic stewardship are crucial for directing suitable treatment and mitigating antimicrobial resistance.

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