

Secondary Bacterial Infection in Patients with COVID 19 Infections Attending a Tertiary Care Hospital in Ahmedabad

Urvesh V. Shah*, Ayushi K. Patel**, Urvashi S. Rana**

Abstract :

Introduction: The COVID-19 disease caused by SARS COV -2 is highly contagious. Many bacterial infections were found among patients with COVID 19 infection. **Aim:** To estimate the prevalence of secondary bacterial infections in patients infected with COVID 19 infection attending a tertiary care hospital. **Methods:** Various samples were collected from COVID 19 positive patients showing signs and symptoms of bacterial infection and were subjected to culture examination. **Results:** In the present study, 47 (6.48%) out of total 725 COVID positive patients were positive for secondary bacterial infections. Klebsiella species followed by Escherichia coli were the most commonly isolated organisms. Pneumonia followed by Urinary tract infection were the most commonly encountered infections in our study. **Conclusion:** Prevalence of secondary bacterial infections in patients with COVID-19 infection attending our hospital is low. Majority of secondary bacterial infections were seen among admitted patients attributable to longer hospital stays, use of steroid and invasive procedures in such patients.

Keywords: Bacterial infections, COVID-19, Culture examination

Introduction:

Bacterial co-pathogens are commonly identified in viral respiratory tract infections such as influenza and are an important cause of morbidity and mortality, necessitating timely diagnosis and antibacterial therapy.⁽¹⁻³⁾ Bacterial co-infection in patients with severe influenza has been reported to be as high as 20–30%^(3,4) and is associated with a greater severity of illness, greater use of healthcare resources, and increased risk of death.⁽⁵⁾ Though a high heterogeneity has been reported in this rate in different studies varying from 2% to 65%. The prevalence, incidence and characteristics of bacterial infection in patients infected with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is not well understood and has been raised as an important knowledge gap.^(6,7)

Despite of absence of role of antibiotics in treatment of COVID-19, they are prescribed in patients with suspected or documented COVID-19 for a variety of reasons. This includes difficulty in ruling out bacterial co-infection on presentation, but also the possibility of bacterial secondary infection during the course of the illness. Extrapolating from concerns of an increase in mortality in patients with bacterial superinfection during influenza pandemics, several guidelines advocate the use of empirical antibiotics for patients with severe COVID-19.^(8,9) However, this assumption raises concerns of antibiotic overuse and subsequent harm associated with bacterial resistance. Understanding of the proportion of COVID-19 patients with acute bacterial and fungal co-infection, and the culprit pathogens, is crucial for treating patients with COVID-19. This will help to ensure responsible use of antibiotics and hence minimize negative consequences of overuse.⁽⁶⁾ Apart from that, this knowledge could have a marked influence in refining empirical antibiotic management guidelines for patients with COVID-19.

* Professor and Head

** Resident,
Department of Microbiology,
GCS Medical College,
Ahmedabad, Gujarat, India

Correspondence : Dr. Ayushi Patel

E-mail : ayushipatel1995123@gmail.com

We performed a review to determine the prevalence of bacterial and fungal infection in patients with COVID-19 and to identify the most common co-infecting organisms in COVID-19 patients.

Materials and Method :

We conducted a retrospective study including all patients tested positive for COVID 19 RTPCR coming to GCSMCHRC from 1st March 2021 to 15th January, 2022. This included both, patients admitted in wards and ICU and patients attending OPD. All types of samples were collected including blood, urine, tracheal aspirate, sputum, pus, tissue etc. These samples were cultured on appropriate culture media. Bacteria and fungi were identified on basis of staining, colony morphology and biochemical tests. Antimicrobial susceptibility testing was performed by disk diffusion method according to CLSI guidelines.

Results:

In this study, 725 RTPCR tested COVID-19 positive patients were included. 471 patients were from outpatient department (OPD). 254 patients were admitted in wards and ICUs. Bacterial and fungal culture results showed that 47 out of 725 patients (6.48%) were positive for bacterial infections and 6 out of 725 patients (0.8%) had only fungal infection. The median age of patients was 51 years (range of age 25–86 years), and 43 (81%) patients were Males. Majority of infections were seen in 40 to 60 years of age (40%) followed by 20-40 year (31%), 40-60 year (13%), >80 year (9%). Out of 725 patients, 207 patients were suspected to have secondary infection. Among these 207 samples collected for microbiological culture, 47(22%) and 6 (2.8%) samples were positive for bacterial and fungal growth respectively. Out of the total 53 patients showing positive cultures, 48(90.57%) were admitted to either wards or ICU whereas 5 (9.43%) attended on the Out-patients basis. Out of the total 110 respiratory specimens [endotracheal aspirate, sputum and

bronchoalveolar lavage (BAL)], 20 were positive (18%) *Klebsiella pneumoniae* was the most common pathogen (40%) followed by *Acinetobacter baumannii* (30%). Other pathogens were *Escherichia coli* (10%), *Candida species* (10%) and *Pseudomonas aeruginosa* (10%). Out of the 35 urine samples, 12 were positive (34%) *Escherichia coli* was leading pathogen (50%) followed by *Enterococcus species* (33%) and *Candida species* (16%). Out of 34 blood samples, 10 were positive (29%). *Klebsiella species* was most common agent causing blood stream infection. Other pathogens were *Escherichia coli* (20%), *Candida species* (20%), and *Coagulase negative Staphylococcus* (20%). Out of 28 wound samples, 11 were positive (39%). Pathogens in wound infections were *Klebsiella species* (63%), *Escherichia coli* (18%) and *Pseudomonas aeruginosa* (18%). According to culture results, the commonest pathogens identified were mainly Gram negative bacteria (GNB), including *K. pneumoniae* (n = 19), *E. coli* (n = 12), *Acinetobacter baumannii* (n=6) and *Pseudomonas aeruginosa* (n=4). Among Gram-positive bacteria, *Enterococcus species* (n=4) and *Coagulase negative Staphylococcus* (n=2) were isolated. Mixed infection with more than one organism from the same site was seen in 3.7% of total culture positive patients. In this study, pneumonia was the most commonly reported infection (n=20, 37%) followed by urinary tract infections (n=12, 23%), wound infection (n=11, 21%) and blood stream infection (n=10, 19%).

Fig. 1 : Types of infections

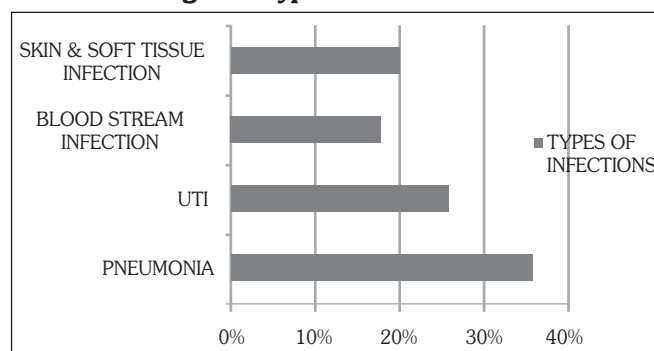


Fig. 2 : Types of infections

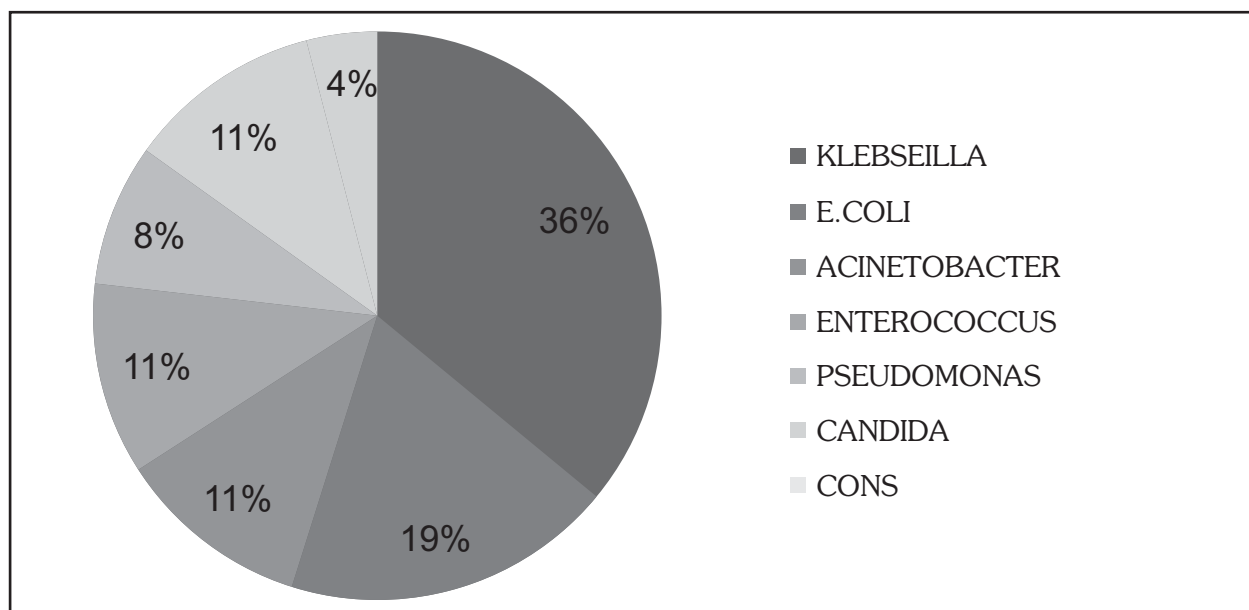


Table 1 : Antimicrobial Susceptibility

	Klebseilla species	Acinetobacter baumannii	Escherichia coli	Pseudomonas aeruginosa
Ampicillin	0%	0%	20%	0%
Cefuroxime	0%	0%	40%	0%
Ceftazidime	-	-	-	50%
Ceftriaxone	0%	0%	40%	0%
Cefepime	0%	0%	40%	50%
Ampicillin Sulbactam	11%	0%	40%	0%
CefoperazoneSulbactam	43%	0%	80%	100%
PiperacillinTazobactam	46%	0%	80%	100%
Imipenem	81%	37%	0%	100%
Amikacin	79%	0%	0%	100%
Ciprofloxacin	37%	0%	40%	100%
Levofloxacin	48%	67%	60%	100%
Doxycyclin	37%	67%	80%	0%
Cotrimoxazole	27%	0%	40%	0%
Colistin	100%	100%	100%	100%
Fosfomycin (Urine sample only)	100%	-	100%	-
Nitrofurantoin(Urine sample only)	100%	-	100%	-
Tigecycline	100%	100%	100%	0%

Discussion:

There is a shortage of data to make a certain estimate on the exact prevalence of bacterial or fungal co-infections in COVID-19 patients, since most studies being retrospective, suffer greatly from selection bias. But from the emerging data, it is clear that the bacterial co-infection rate is lower than seen in patients with influenza H1N1 and H3N2.^(10,11) According to two meta-analyses published so far, bacterial co-infection rates were 3.5% and 7%, respectively.^(12,13) The overall prevalence of secondary infections in our study was found to be 6.48%. The predominance of infection with gram negative pathogens in the patients included in our study reflects the profile of secondary infections which matches quite less with the typical picture of community-acquired infections. In our study the most common sites of secondary infection in COVID-19 patients were found to be respiratory and urinary sites. Gram-negative pathogens were predominant in causing infections. In our study, out of total 53 patients positive for culture, 48 (90.57%) were admitted to either wards or ICUs, suggesting prolonged hospital stay to be the predisposing factor for co-infections in COVID patients. It is well known that most hospitalized moderate or severe COVID-19 patients have been prescribed steroids, undergo invasive procedures, and sometimes have a prolonged hospital stay, rendering them vulnerable to HAIs. Invasive device-associated infections during hospitalization due to mechanical ventilation and central venous catheter implantation in these patients may be the reason of predominance of Gram negative pathogens. Among co-infections in patients with COVID-19, *Klebsiella* (36%) and *Escherichia coli* (19%) constituted more than 50% of the isolates. This correlates with ICMR data published in the last few years, wherein *Klebsiella* and *E. coli* were the most commonly isolated pathogen.^(14, 15) High isolation rates along with reduced susceptibility of *Klebsiella* to drugs like piperacillin-tazobactam (54% isolates show resistance), cefoperazone sulbactam (57% isolates show resistance) and carbapenems (19%

isolates show resistance) are alarming and need urgent containment measures through appropriate infection control and antimicrobial stewardship interventions.⁽¹⁶⁾

Conclusion:

Prevalence of bacterial and fungal co-infections in patients with COVID-19, admitted to our hospital or attending our OPD is low; however, when such infections are present, they cause severe disease with worst outcomes, as most co-infections are nosocomial and due to XDR pathogens. These data were captured when COVID-19 cases were on the rise, and the findings suggest that a lot of overprescribing of antimicrobials happened during that time. Additionally, the overuse of broad-spectrum antimicrobials and poor infection control are fostering the development of highly drug-resistant pathogens in the future. Therefore, all efforts should be made to improve infection control practices (such as hand hygiene/glove hygiene, device bundle compliance, and air quality). This will help in reducing the incidence of secondary infections, particularly those of nosocomial origin. The strict practice of antimicrobial stewardship will help in reducing drug pressure, which is a key driver of drug resistance.

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