



## RESEARCH ARTICLE

# Prevalence of secondary infections, antimicrobial susceptibility and predictors for mortality among critically ill COVID 19 patients admitted to an Intensive Care Unit in India

Dr BabySailaja. K<sup>1</sup>, Dr Renuka MK<sup>\*2</sup>, Dr Rathish Manimohan<sup>3</sup>, Dr Prasanth NVSN<sup>3</sup>

<sup>1</sup> Associate Professor, Department of Critical Care Medicine, Sri Ramachandra Institute of Higher Education and Research, Tamilnadu, India

<sup>2</sup> Professor, Department of Critical Care Medicine, Sri Ramachandra Institute of Higher Education and Research, Tamilnadu, India

<sup>3</sup> Senior Resident, Department of Critical Care Medicine, Sri Ramachandra Institute of Higher Education and Research, Tamilnadu, India

\* [renuka.mk@sriramachandra.edu.in](mailto:renuka.mk@sriramachandra.edu.in)



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**ABSTRACT**

**Background:** Critically ill COVID 19 patients requiring intensive care unit admission are at an increased risk of secondary infections owing to the need for invasive or non invasive oxygen therapy, prolonged indwelling catheters and long stay in intensive care unit. Secondary infections can further alter the clinical course and outcomes of these patients

**Aims:** In this study we aimed to investigate the prevalence, characteristics and factors associated with mortality in critically ill COVID 19 patients with secondary infections.

**Methods:** This was a single centre retrospective cohort study of adult critically ill COVID 19 patients admitted to the intensive care unit of a tertiary care hospital in India during one year period from May 2020 to April 2021.

**Results:** Among the 285 patients admitted to the intensive care unit 124 patients were identified with secondary infection. Out of the 250 isolates, 72.3% were gram negative bacilli with highest number of isolates recognised from blood (n=112, 44.8%). The most common organisms identified in our cohort were Klebsiella pneumoniae, Acinetobacter baumannii, Escherichia coli, Candida species and Enterococcus faecalis. Anti-microbial resistance was detected in 58.8% (n=147) of the isolates and majority of the patients received Carbapenem and Polymyxin. Patients with secondary infections were at increased risk of developing septic shock, acute kidney injury and also experienced higher mortality (50%, P-value <0.001). In our study cohort, increasing cumulative dose of steroids [OR 1.002, 95% CI: 1.001-1.004] and increasing length of intensive care unit stay [OR 1.071, (95% CI: 1.030-1.113)] were found to be predictive of mortality among patients with secondary infection.

**Conclusion:** Secondary infections were high among the critically ill COVID 19 patients with high antimicrobial resistance and lead to high mortality. This being a single centre retrospective study, prospective evaluation with proper anti-microbial stewardship is needed for more precise results.

**Keywords:** COVID 19, secondary infections, antimicrobial resistance, risk factors

## Introduction

During the pandemic with Corona virus (COVID 19 disease), the infection lead to a wide spectrum of disease. Patients were either asymptomatic, developed a simple upper respiratory infection or a viral pneumonia requiring hospitalisation. Some of them rapidly progressed to acute respiratory distress syndrome (ARDS) requiring intensive care unit (ICU) admission and invasive ventilation for severe hypoxemia.

Co-infections and secondary infections are a common association with severe viral infections of the respiratory tract which can lead to prolonged stay of ICU and hospitalisation and carries a risk of mortality.<sup>1,2</sup>

The prevalence pattern of secondary infections (SIs) in the COVID 19 patients was unknown due to the novelty of the disease. COVID 19 patients admitted to ICU were at a much higher risk of acquiring such infections due to various reasons. Firstly the virus can alter the immune response of the host to the SARS – Co V 2 infection in the form of a cytokine storm, reduced concentration of serum interferon gamma and alterations in the neutrophil and leucocyte characteristics.<sup>3,4,5</sup> Secondly, the ICU admitted patients are at increased need for invasive procedures and organ support. Thirdly, administration of dexamethasone as standard of care as put forth by the RECOVERY trial<sup>6</sup> and drugs like cytokine inhibitors to combat the dysregulated immune system will lead to immunosuppression predisposing them to infections.

Lack of knowledge of the etiology of these infections and their antimicrobial susceptibility in the COVID 19 patients led to inappropriate usage of prophylactic antimicrobials to the hospitalised COVID 19 patients. This poses a threat of developing high rates of antimicrobial resistance (AMR).<sup>7,8,9</sup> Development of AMR is associated with increased cost of hospitalisation and mortality owing to limited choice of antimicrobials and failure to treat even the common infections.<sup>10</sup> Furthermore an unparalleled increase in the need for ICU care as compared to staffing availability and personal protective equipment might magnify the situation by person to person transmission of these resistant pathogens.<sup>11,12</sup> There is a heterogenicity in the reported AMR among the COVID 19 patients across the globe because of the differences in the causative organisms and baseline AMR rate regionally. Furthermore, there are minimal studies highlighting the AMR among the Indian population as compared to other parts of the world. This is a much needed relevant data to substantiate the regional antimicrobial resistance and provide surveillance for the same.<sup>13,14</sup>

In this retrospective cohort study on COVID 19 patients admitted to a dedicated COVID ICU we aimed to investigate the prevalence of SIs, the causative pathogens, their antimicrobial resistance pattern and the prescribed antimicrobial therapy for these infections. We also evaluated the risk factors for developing infection and mortality in these set of patients.

## Study methods

This was a single centre retrospective cohort study performed in an ICU dedicated to COVID 19 patients of tertiary care hospital in India. The study was registered

under Clinical Trials Registry of India (CTRI) after obtaining ethical clearance from the institutional ethics committee. All adult patients above 18 years of age who were confirmed SARS COV-2 infection with real-time reverse transcription–polymerase chain reaction (RT-PCR) assay or nucleic acid amplification test (NAAT) and admitted to ICU during the one year period from May 2020 to April 2021 were included in the study.

Data extracted from the case records of these patients included demographic details, past medical history, clinical parameters, laboratory data, and APACHE II score at admission to ICU. Treatment details collected included need for mechanical ventilation with duration, vasopressor therapy received, corticosteroids and other immunosuppressive therapy given. Hospital and ICU length of stay (LOS), ICU outcome, development of shock and acute kidney injury (AKI) were recorded.

The primary outcome measured was presence of SIs in these patients. All the patients' case records were screened for SIs based on clinical signs, laboratory analysis and correlated with positive culture reports.

Blood stream infections (BSI) was identified if known pathogen was isolated from single positive blood culture or commensals were isolated from at least two positive blood cultures.

Secondary infection of the lower respiratory tract (sLRTI) or Ventilator associated pneumonia (VAP) was identified if clinical signs along with a positive culture for a significant pathogen from a mini broncho-alveolar lavage (BAL) sample were detected.

Catheter associated urinary tract infection (CAUTI) was identified if patients had an indwelling catheter for more than 48 hours and a positive urine culture defined as more than  $10^5$  colony forming units of one or two pathogens per millilitre of urine.

Patients in whom cultures were not sent were considered as not suspected to have a superadded infection. Further details were collected from the records of patients with suspected infection in whom samples from blood, BAL and urine were sent. This included date of first culture(s) and repeat cultures if any sent, site of sample, organism(s) isolated, their antimicrobial susceptibility, antibiotic(s) administered and the duration of therapy.

## STATISTICAL ANALYSIS:

Categorical data were expressed as number and percentage while continuous data as mean with standard deviation unless specified. P value was calculated by applying Mann Whitney U test and Chi square test for continuous and categorical values respectively. Binary and multivariable logistic regression analysis was conducted to identify association of risk factors for mortality and adjustment for confounders in patients with SIs

## Results

We identified a total of 285 COVID 19 confirmed patients who were admitted to our ICU during the one year period of the pandemic from May 2020 to April

Prevalence of secondary infections, antimicrobial susceptibility and predictors for mortality among critically ill COVID 19 patients 2021, of which 27 patients were excluded as they had an ICU stay of less than 48 hour and the remaining 258 patients were enrolled into the study. Cultures were raised in 146 patients out of whom 22 patients had been considered to have an insignificant growth or commensal.

Finally, 124 (48.06%) patients were identified with a clinically significant positive culture report and were considered to have developed secondary infection. The clinical characteristics, outcomes and complications of our study cohort is summarised in the Table 1.

**Table 1:** Characteristics of patients with COVID-19 disease admitted to ICU:

Parameter	Total (n=258)	With secondary infection (n=124)	Without secondary infection (n=134)	p-value
<b>Demographic Variables</b>				
Age (yr), mean(SD)	61.4 (±14.4)	63.3 (±11.7)	59.7 (±16.4)	0.118
Gender, Male, n (%)	182 (70.5)	84 (67.7)	98 (73.1)	0.342
<b>Comorbidities</b>				
Diabetes mellitus, n (%)	167 (64.7)	90 (72.6)	77 (57.5)	0.011*
Hypertension, n (%)	155 (60.1)	83 (66.9)	72 (53.7)	0.030*
Cardiac disease, n (%)	68 (26.4)	32 (25.8)	36 (26.9)	0.847
Respiratory disease, n (%)	22 (8.5)	13 (10.5)	9 (6.7)	0.279
Renal disease, n (%)	24 (9.3)	11 (8.9)	13 (9.7)	0.819
Neurologic disease, n (%)	18 (7.0)	8 (6.5)	10 (7.5)	0.750
<b>Inflammatory Markers</b>				
Ferritin, median (IQR)	420.3 (199.9-740.3)	410.5 (219.0-756.3)	428.5 (179.3-739.1)	0.866
CRP, median (IQR)	8.6 (3.1-14.3)	9.2 (3.8-14.1)	8.4 (2.6-14.9)	0.359
D dimer, median (IQR)	1.4 (0.6-3.8)	1.5 (0.6-3.9)	1.3 (0.7-3.7)	0.978
LDH, median (IQR)	477.0 (354.5-620.5)	507.0 (404.5-655.5)	440.0 (326.0-586.0)	0.007*
APACHE II, mean(SD)	13.0 (±5.7)	13.5 (±5.2)	12.5 (±6.1)	0.119
<b>Secondary Outcomes</b>				
Mechanical Ventilation, n (%)	94 (36.4)	76 (61.3)	18 (13.4)	<0.001*
Ventilator days, mean(SD)	9.6 (±7.2)	11.3 (±6.9)	2.4 (±1.4)	<0.001*
Vasopressor therapy, n (%)	96 (37.2)	76 (61.3)	20 (14.9)	<0.001*
Acute kidney injury, n (%)	54 (20.9)	36 (29.0)	18 (13.4)	0.002*
Septic shock, n (%)	71 (27.5)	61 (49.2)	10 (7.5)	<0.001*
ICU LOS, mean(SD)	9.7 (±7.0)	14.1 (±6.8)	5.6 (±4.1)	<0.001*
Hospital LOS, mean(SD)	13.0 (±5.7)	21.2 (±10.5)	12.7 (±7.9)	<0.001*
Mortality, n (%)	84 (35.3)	61 (50.0)	23 (19.8)	<0.001*

Our study cohort showed a male predominance with a mean age of 61.4(±14.4) years with no significant difference in age between patients with or without SIs. Diabetes mellitus followed by hypertension were the most common comorbid conditions present in these patients and were found to be risk factors for development of SIs.

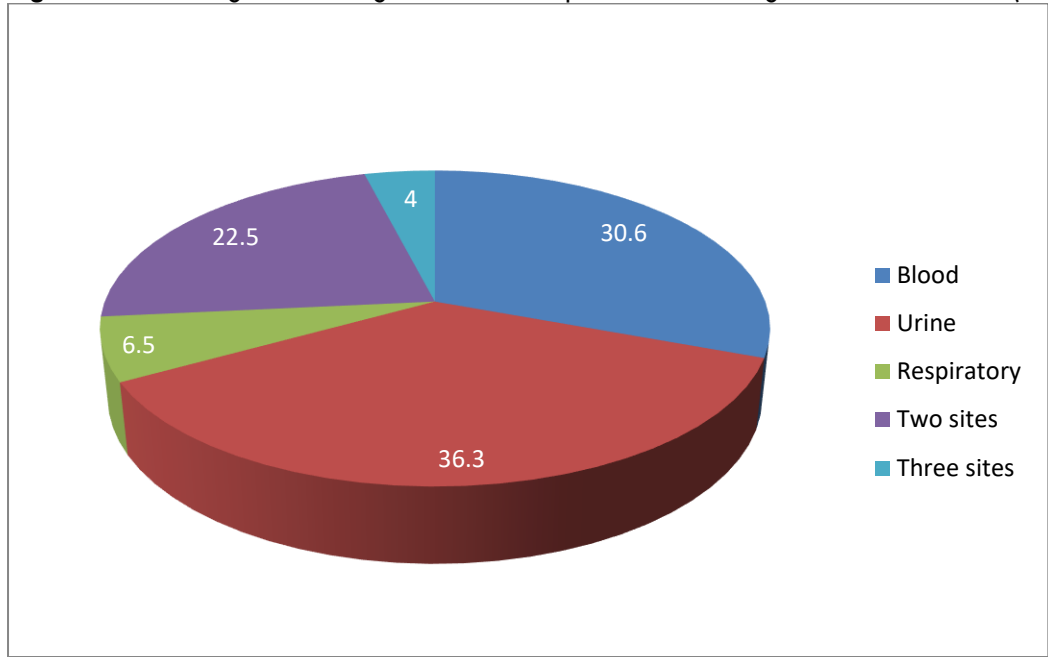
Other than a raised lactate dehydrogenase (LDH), neither elevated serum ferritin, d-Dimer, C-reactive protein (CRP) nor APACHE II score were found to be

significantly associated with development of SIs.

**PRIMARY OUTCOME:**

Clinically significant pathogens were isolated from 250 samples including blood, BAL and urine from 124 patients. We observed that the median day of first positive culture was day 5 of ICU stay (IQR 4 - 8). Thirty three patients developed an infection from multiple sites and few patients grew more than one organism. (Figure 1A)

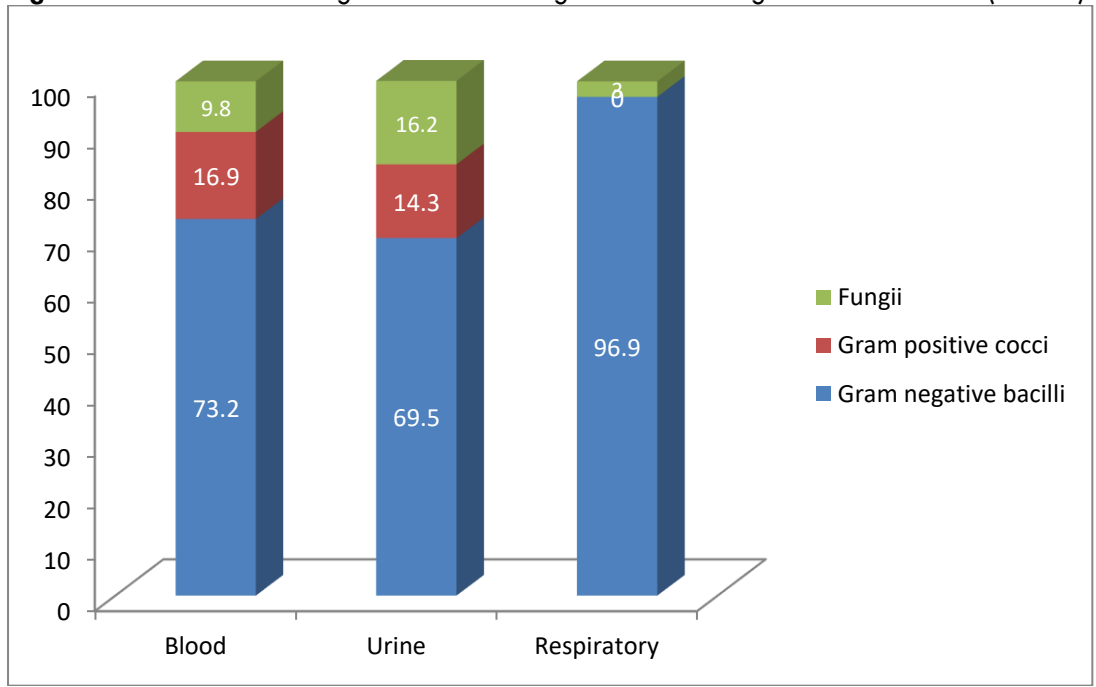
**Figure 1A:** Pie diagram showing distribution of patients according to sites of infection (n =124)



Recurrent infections in the form of a new pathogen or same pathogen with a different antimicrobial resistance were noted in 50 patients. The most frequently isolated

pathogens were gram negative bacilli (GNB) from all three sites with blood (n=112) being the predominant site followed by urine (n=105). (Figure 1B)

**Figure 1B:** Bar Chart showing distribution of organisms according to site of isolation (n=250)



The distribution of all identified pathogens from the study cohort was given in Table 2. Among the GNB, Klebsiella pneumoniae, Acinetobacter baumannii, Escherichia coli, Pseudomonas aeruginosa and Serratia marcescens were the predominant organisms. Acinetobacter baumannii and Klebsiella pneumoniae caused most BSI (41%). Serratia marcescens caused only bacteremia (n=18,

16%) whereas Escherichia coli bacteremia was noted in only 2 patients. Klebsiella pneumoniae, Acinetobacter baumannii, and Pseudomonas aeruginosa accounted for 97% of secondary pneumonia (sLRTI). Escherichia coli and Klebsiella pneumoniae were associated with almost 45% of CAUTI.

**Table 2:** Distribution of organisms by sites of infection

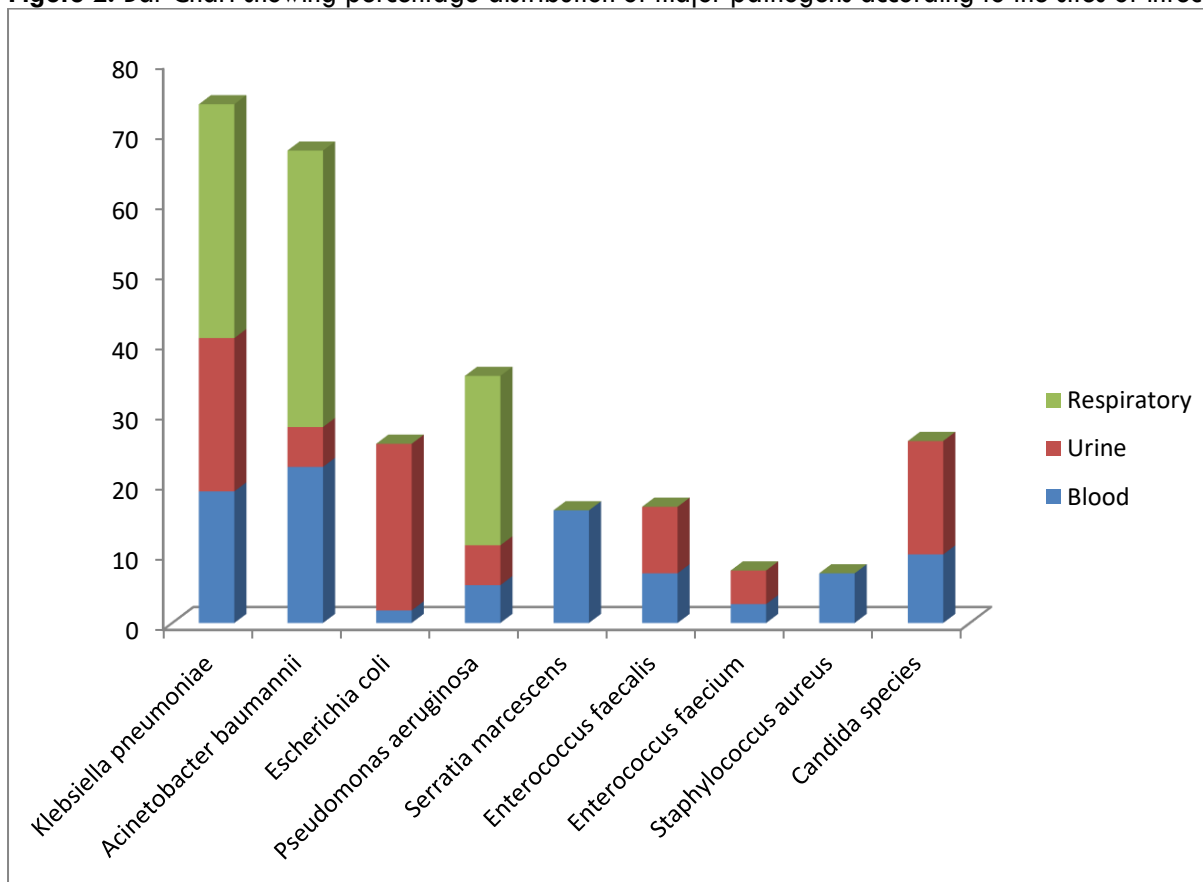
Organisms	Blood culture		Urine culture		MiniBAL culture	
	n=112	%	n=105	%	n=33	%
<b>Gram Negative Bacilli</b>						
Klebsiella pneumoniae	21	18.8	23	21.9	11	33.3
Acinetobacter baumannii	25	22.3	6	5.7	13	39.4
Escherichia coli	2	1.8	25	23.8	0	0

Organisms	Blood culture		Urine culture		MiniBAL culture	
<i>Pseudomonas aeruginosa</i>	6	5.4	6	5.7	8	24.2
<i>Serratia marcescens</i>	18	16.1	0	0	0	0
<i>Enterobacter species</i>	3	2.7	4	3.8	0	0
<i>Morganella morganii</i>	0	0	5	4.8	0	0
<i>Proteus. vulgaris</i>	0	0	3	2.9	0	0
<i>Burkholderia species</i>	2	1.8	0	0	0	0
<i>Ralstonia species</i>	2	1.8	0	0	0	0
<i>Providencia species</i>	1	0.9	1	1	0	0
<i>Citrobacter species</i>	1	0.9	0	0	0	0
<i>Stenotrophomonas maltophilia</i>	1	0.9	0	0	0	0
<b>Gram Positive Cocci</b>						
<i>Enterococcus faecalis</i>	8	7.1	10	9.5	0	0
<i>Enterococcus faecium</i>	3	2.7	5	4.8	0	0
<i>Staphylococcus aureus</i>	8	7.1	0	0	0	0
<b>Fungi</b>						
<i>Candida species</i>	11	9.8	17	16.2	0	0
<i>Aspergillus species</i>	0	0	0	0	1	3

Common gram positive cocci (GPC) isolated in our study were *Enterococcus faecalis* and *Enterococcus faecium* accounting for nearly 10% and 14% of BSI and CAUTI respectively followed by *Staphylococcus aureus* causing 7% bacteremia.

*Candida species* were responsible for 16.2% of CAUTI and 9.8% of BSI in our study cohort. Figure 2 highlights the major pathogens identified from all three sites.

**Figure 2:** Bar Chart showing percentage distribution of major pathogens according to the sites of infection



Almost 58.8% (n=147) of pathogens isolated from our study cohort exhibited antimicrobial resistance in the form of multi drug resistance (MDR) and extensively drug resistance (XDR). *Acinetobacter baumannii* showed the highest resistance with 59 % (n=26) Carbapenem resistant strains followed by *Klebsiella pneumoniae* with 54.5% (n=30) Carbapenem resistant strains. Majority of the *Escherichia coli* isolates (33.3%) of our study cohort

were resistant to third generation Cephalosporins [extended spectrum beta lactamases (ESBL)]. One Vancomycin Resistant *Enterococcus faecium* (VRE) and three Methicillin resistant *Staphylococcus aureus* (MRSA) were recognised. About 27.6% (n=8) *Candida* isolates were fluconazole resistant. The antimicrobial susceptibility of commonly isolated pathogens of our study was shown in Table 3.

**Table 3:** Distribution of the major organisms by their antimicrobial susceptibility pattern

Organism	No of pathogens	Antibiotic susceptibility (n %)			
		BL-BLI	ESBL	MDR	XDR
<b>Gram negative organisms</b>					
Acinetobacter baumannii	44	13(29.5)	5 (11.4)	13(29.5)	13(29.5)
Klebsiella pneumoniae	55	17(30.9)	8(14.5)	6 (10.9)	24(43.6)
Pseudomonas aeruginosa	20	1(5.0)	16 (80.0)	1 (5.0)	2 (10.0)
Serratia marcescens	18	18(100.0)	0	0	0
Escherichia coli	27	11 (40.7)	9 (33.3)	4 (14.8)	3 (11.1)
<b>Gram positive organisms</b>		<b>Ampicillin Sensitive</b>	<b>MDR</b>	<b>MRSA</b>	<b>VRE</b>
Enterococcus faecalis	18	8 (44.4)	10 (55.6)	0	0
Enterococcus faecium	8	2 (25.0)	5 (62.5)	0	1 (12.5)
Staphylococcus aureus	8	5 (62.5)	0	3 (37.5)	0
<b>Fungi</b>		<b>Fluconazole Sensitive</b>	<b>Fluconazole Resistant</b>		
Candida species	29	21 (72.4)	8 (27.6)		

The most commonly prescribed antibiotics for gram negative infections in our study cohort were Meropenem (39.9%) followed by Polymyxins (Polymyxin B and Colistin) in 29.5% of infections. Fifty percent of gram positive pathogens required Vancomycin. About 34.5% of Candida infections were treated with Caspofungin and 20.7% of fungal isolates were untreated as the patients died before cultures were available.

#### Secondary outcomes:

Patients with SIs had a significant and prolonged requirement for mechanical ventilation, longer length of stay in ICU and hospital. These patients also had a significant risk of developing shock which was requiring vasopressor therapy probably secondary to sepsis and increased risk of acute kidney injury. The overall mortality of our study population was 35.3% (84/ 238) with a significantly higher mortality in patients who developed SIs compared to patients with no SIs (50% vs. 19.8%, p value <0.001).

When we assessed the risk factors for mortality in patients with SIs by conducting binary logistic regression, increasing age [OR -1.054, (95% CI:1.031-1.078)], development of AKI [OR 4.156, (95% CI: 2.162-7.989)], development of septic shock (OR 9.474,(95% CI: 4.965-18.076)], increasing cumulative dose of steroids [OR 1.002, 95% CI: 1.001-1.004]] and increasing length of ICU stay [OR 1.071, (95% CI: 1.030-1.113)] were found to be significantly associated with mortality among patients with secondary infection in COVID-19.

However, only increasing age [AOR 1.074, (95% CI-1.030-1.121)], development of septic shock (AOR 10.647, (95% CI: 3.838-29.538)] and incremental cumulative dose of steroids [AOR 1.003, (95% CI: 1.001-1.005)] were predictors of mortality in these patients after adjustment with other confounding parameters. (Table 4)

**Table 4:** Binary and multivariable logistic regression analysis to identify factors associated with mortality among patients with secondary infection in COVID-19

Risk factor	OR (95% CI)	p-value	AOR (95% CI)	p-value
Age	1.054 (1.031-1.078)	<0.001*	1.074 (1.030-1.121)	0.001*
Diabetes	1.311 (0.744-2.310)	0.349	0.652 (0.238-1.784)	0.405
Acute kidney injury	4.156 (2.162-7.989)	<0.001*	1.752 (0.640-4.793)	0.275
Septic shock	9.474 (4.965-18.076)	<0.001*	10.647 (3.838-29.538)	<0.001*
Cumulative dose of steroids	1.002 (1.001-1.004)	0.002*	1.003 (1.001-1.005)	0.004*
ICU LOS	1.071 (1.030-1.113)	<0.001*	0.991 (0.919-1.069)	0.811

#### Discussion:

In this retrospective study we investigated the prevalence of secondary infections in COVID 19 positive patients admitted to ICU as they are at high risk of developing SIs and mortality similar to other respiratory viral pandemics

like Influenza A (H1N1)<sup>1</sup> and Middle East Respiratory Syndrome (MERS).<sup>2</sup> A meta-analysis by Sands KE et al.<sup>12</sup> showed that hospital acquired infections in ICU was common in COVID 19 patients compared to non covid patients. Out of the 124 patients with an identified

**Prevalence of secondary infections, antimicrobial susceptibility and predictors for mortality among critically ill COVID 19 patients**  
infection 250 pathogens were isolated from blood, urine and respiratory samples of our study cohort.

In a systematic review and meta-analysis of 138 studies on the prevalence of co-infections and secondary infections, Bradley J. Langfold et al<sup>13</sup> identified that admission to ICU was by itself associated with the development of infection (Odds ratio of 7.52) as compared to patients admitted to ward.(4.9% and 8.4% vs. 8.4% and 39.9% of co-infections and secondary infections respectively). In our study the incidence of SIs was as high as 48%. However, reports from similar studies in the past were highly variable both globally<sup>15-20</sup> and in India.<sup>21, 22, 23</sup>

The most common comorbid conditions associated with our study population were diabetes and hypertension and were similar to that observed by Karuna et al<sup>23</sup> and Yadav et al.<sup>24</sup> This was in contrast to the observation from the multicentre study of 269 UK hospitals, the ISARIC WHO CCP UK study where hypertension and cardiac diseases predominated their population.<sup>17</sup>

De Bruyn et al<sup>20</sup> and Haque et al<sup>22</sup> observed that diabetes was one of the risk factors for SIs in their patients which were similar to our study as well. Corticosteroid therapy as a primary variable associated with SIs was noted in the study cohort of Afnan et al,<sup>18</sup> de Bruyn et al<sup>20</sup> and Haque et al.<sup>21</sup> But we could not establish the same because all our patients were treated with steroids as a standard protocol in our ICU.

Highest number of organisms isolated from blood stream infections in our study was in concordance with the study by Vijay et al<sup>25</sup> and Khurana et al<sup>22</sup> from India and Ripa et al<sup>26</sup> from Italy. This was in contrast to that reported from China,<sup>16,19</sup> UK,<sup>17</sup> Belgium,<sup>20</sup> Italy<sup>27</sup> and India<sup>22, 24</sup> where secondary pneumonia was the commonest. A multicentre study from 6 ICUs (OUTCOMEREA) by N. Buetii<sup>15</sup> showed that ICU admitted COVID 19 patients were at higher risk for BSIs than non covid patients as ICU stay prolonged more than 7 days. In our study the prolonged ICU stay (9.7 ±7.0 days) could be a reason for the higher occurrence of BSIs.

There was a high incidence of CAUTIs in our study population. Multiple reasons could be cited, firstly, prolonged mechanical ventilation including prone position leading to prolonged need for indwelling catheter. Secondly, due to the impact of the pandemic an unparalleled increase in ICU beds compared to facilities and trained staff availability might be another burden. Thirdly poor hand hygiene practices because of the isolation policies like wearing gloves giving a false assurance of sterility might have increased our CAUTI rates.<sup>12</sup>

In contrast to this, we observed a low rate of secondary pneumonia. Though 76 patients identified with SIs were on invasive mechanical ventilation, only 20 patients developed a secondary pneumonia with 33 isolates (13.2%) identified. In contrast to our finding, studies by Li et al,<sup>16</sup> Russell et al,<sup>17</sup> Haque et al<sup>22</sup> and Liana et al<sup>27</sup> showed a high incidence of secondary pneumonia. The possible explanation for this low incidence of secondary pneumonia in our study could be the usage of closed

suction devices for all our patients on invasive ventilation. This might have reduced the number of ventilator disconnections and hence the contamination with pathogens and colonisation of breathing circuits. A systematic review and meta-analysis by Sanaie et al<sup>28</sup> supported our study in that closed tracheal suction device usage was associated with reduced VAP rates.

The top list of pathogens in our study cohort correlated with the World Health Organisation (WHO) priority pathogens<sup>29</sup> and was comparable with previously reported observations. GNB were responsible for majority of BSI in our study population similar to reports from other studies.<sup>16, 18, 19,21, 22, 25</sup> In contrast to our findings, European studies from France<sup>15</sup> UK,<sup>17</sup> Belgium<sup>20</sup> and Italy<sup>26, 27</sup> showed a higher prevalence of gram positive bacteremia. The predominance of GNB in causing secondary pneumonia in our study was in concordance with findings from across the world.<sup>16-27, 30</sup> Marco ripa et al<sup>26</sup> compared the antimicrobial resistance pattern during pre-pandemic and pandemic era and found increased resistance among Acinetobacter and Enterococcus faecium post Covid pandemic. In their study by Anahita et al,<sup>30</sup> they observed decreased multi drug resistance among organisms causing VAP in COVID 19 patients compared to non covid patients. In the study by Li et al<sup>16</sup> from China, Carbapenem resistance was detected in 91.7% and 76.6% of Acinetobacter baumannii and Klebsiella pneumoniae. Also 75% of extended spectrum beta lactamase producing E.coli were isolated from urine in their study.

We also observed a high rate of antimicrobial resistance among our study pathogens. Nearly 66% of our GNB were resistant to third generation Cephalosporins and Carbapenems and sensitive only to Polymyxins. Similarly among the GPC, 55% of Enterococcus faecalis and 62.5% Enterococcus faecium were resistant to Ampicillin. Among the fungal pathogens, 28% of Candida species showed Fluconazole resistance. In the study by Vijay et al,<sup>25</sup> 47% of the pathogens were multidrug resistant with 92.6% Acinetobacter baumannii and 72.8% Klebsiella pneumoniae resistant to carbapenems and 32% Vancomycin resistant Enterococci. Overall, 64-69% of GNB with third generation Cefalosporins and Carbapenem resistance were detected in the study by Khurana et al.<sup>21</sup>

Despite the detection of high MDR, Vijay et al<sup>25</sup> observed that a greater percentage of their study population received Beta lactum-Beta Lactamase Inhibitors (BL-BLI) compared to carbapenems, however Polymyxin and Meropenem were the most commonly prescribed antibiotic in our study cohort.

The RECOVERY trial<sup>6</sup> showed reduced 28 day mortality in patients requiring mechanical ventilation and oxygen support, but did not evaluate the association between steroid therapy and secondary infections. Ritter et al,<sup>31</sup> addressed the impact of steroids on secondary infections and all-cause mortality without studying the association of steroids with mortality among patients with secondary infections alone. In the study by Liana et al,<sup>27</sup> however the unadjusted mortality was high in patients on longer duration of steroid. In contrast with their findings, we observed an association of steroids with high mortality in our patients who developed secondary infections.

This study had several limitations. Firstly, it was a single centre retrospective study with a small sample size. Secondly, due to the retrospective correlation of clinical signs of infection with microbiological culture reports differentiation between true infection and colonisation may not be accurate.

## Conclusion

High incidence of secondary infections was observed in critically ill COVID 19 patients and carried a significant mortality risk. Majority of these infections were caused by the organisms recognised by WHO as 'critical' and 'high priority' pathogens exhibiting resistance which

translated to treatment failure. This will add on to the threat of increasing antimicrobial resistance in the community at large. Therefore appropriate selection and timing of antimicrobials is the cornerstone to treat such infections when suspected.

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