

Assessing Common Etiologic Agents of Blood Stream Infections in COVID-19 Patients Admitted to ICU: An Observational StudyAlpana Singh¹, Ajay Kumar²¹Tutor, Department of Microbiology, Government Medical College, Bettiah, Bihar, India²Professor, Department of Microbiology, Government Medical College, Bettiah, Bihar, India

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Conflict of interest: Nil

Abstract**Aim:** The aim of the present study was to find the common causative agents of blood stream infections in Covid 19 patients admitted to ICU of tertiary care hospital.**Methods:** The present cross-sectional study was carried out at department of Microbiology for the period of 12 months. 200 patients were included in the study.**Results:** Out of 200 samples, we got growth in 48 (24%) samples and no growth in 152 (76%) samples. There were 62.50% gram negative bacteria followed by 29.16% gram positive bacteria. The predominance of male gender (77%) of patients were affected, where 23% female were affected. The *Staphylococcus hemolyticus* and *enterococcus faecium* was the most common Gram positive bacterial isolates in patients. *E. coli* was the most common Gram negative bacterial isolates in patients. 8.33% were *Candida tropicalis* in the study.**Conclusion:** Covid 19 has complex disease pathogenesis. Patients on immunosuppressive therapy are at risk of developing secondary blood stream infections. Initially most of the secondary BSI were endogenous as *Enterococcus spp* was most prevent organisms. Patients admitted to the ICUs are also at risk of developing nosocomial infections. The patients on mechanical Ventilator are at risk of Ventilator associated infections.**Keywords:** AST, BSI, COVID- 19, SARS- CoV- 2

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Introduction

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was first identified in Wuhan, China, in December 2019. [1] Intensive care unit (ICU) admission is required for 20% of patients with coronavirus disease 2019 (COVID-19) due to acute respiratory distress syndrome (ARDS) or other complications. [2-4] The incidence of blood stream infections (BSIs) among non-COVID-19 patients with infection is high. [5] The immune dysregulation induced by severe SARS-CoV-2 infection and the immunosuppressive agents used for treatment can predispose patients to concurrent infections. Studies detected a reduction in both CD4+ T and CD8+ T lymphocyte counts, an increase in neutrophils, a reduction in interferon gamma (IFN- γ) serum concentrations, and a cytokine pattern characterized by excess pro-inflammatory molecules. [6-8] Moreover, the need for vasopressors, renal replacement therapy (RRT), or sometimes extracorporeal membrane oxygenation (ECMO) may increase the risk of developing infectious complications.

There are reports that the incidence of BSIs is higher for COVID-19 patients in comparison with non-

COVID-19 patients [9] during the ICU stay. However, there is scarce data regarding secondary infections in patients with severe COVID-19 [10-12], especially for those admitted to the ICU who receive invasive mechanical ventilation. There is also limited evidence on how secondary infections and especially BSIs affect patients' outcomes, such as mortality, duration of mechanical ventilation, or length of stay. The mechanisms are mainly related to physical barriers, immune responses, and flora imbalance. There are many clinical risk factors for clinical secondary infections, such as older age (>60 years) and underlying conditions such as hypertension, diabetes, obesity, and hemodialysis.5,7 The developments of SBI is closely associated with immunosuppressive therapy (long-term and high-dose glucocorticoid use), invasive procedures (e.g., endotracheal intubation, tracheotomy) and use of broad-spectrum antimicrobial agents. [13,14]

The aim of the present study was to find the common causative agents of blood stream infections in Covid 19 patients admitted to ICU of tertiary care hospital.

Materials and Methods

The present cross-sectional study was carried out at department of Microbiology, Government Medical College, Bettiah, Bihar, India for the period of 12 months. 200 patients were included in the study.

Blood culture and Antibiotic susceptibility of all age group patients RT PCR/Antigen positive for Covid-19 was considered which are performed at central laboratory of PSH. The blood culture specimens were collected from two different sites at an interval of minimum of 1 hour. Blood cultures are done as

standard protocol on automated blood culture system, Bact/Alert for continuous monitoring. The culture medium used in blood cultures system supports growth of aerobic bacteria as well as fungi. The positive blood culture was inoculated on different media as standard protocol. Identification and antimicrobial susceptibility of isolates was performed on automated system-VITEK 2.

Results

Table 1: Culture positivity

Total number of samples	Growth	No growth
200	48 (24%)	152 (76%)

Out of 200 samples, we got growth in 48 (24%) samples and no growth in 152 (76%) samples.

Table 2: Group of pathogens with respect to culture positivity

Pathogens	N	%
Gram negative bacteria	30	62.50
Gram positive bacteria	14	29.16
Candida Spp.	4	8.34

There were 62.50% gram negative bacteria followed by 29.16% gram positive bacteria.

Table 3: Gender distribution

Gender	N	%
Male	154	77
Female	46	23
Total	200	100

The predominance of male gender (77%) of patients was affected, where 23% female were affected.

Table 4: Gram positive organisms isolate from blood culture

Organisms isolated	No. of isolates	Percentage (%)
<i>Staphylococcus hemolyticus</i>	11	22.91%
<i>Enterococci feceum</i>	11	22.91%
<i>Enterococci fecalis</i>	6	12.50%
<i>Enterococci gallinarum</i>	2	4.16%
Total	30	62.50%

The *Staphylococcus hemolyticus* and *enterococcus feceum* was the most common Gram positive bacterial isolates in patients.

Table 5: Gram negative organisms isolate from blood culture

Organisms isolated	No. of isolates	Percentage (%)
<i>Klebsiella pneumonia</i>	3	6.25%
<i>Acinetobacter spp</i>	2	4.16%
<i>Escherichia coli</i>	4	8.33%
<i>Pseudomonas spp</i>	1	2.08%
<i>Acromobacter xylosoxidaus</i>	2	4.15%
<i>Aerococcusviridance</i>	1	2.08%
<i>Kocuriarosea</i>	1	2.08%
Total	14	29.16

E. coli was the most common Gram negative bacterial isolates in patients.

Table 6: Yeast isolated from blood culture

Organisms isolated	No. of isolates	Percentage (%)
Candida Tropicalis	4	8.33%
Total	4	8.33%

8.33% were candida tropicalis in the study.

Discussion

The global COVID-19 pandemic is currently ongoing, with more than 130 million infections and nearly three million deaths worldwide. [15] Mortality in critically ill patients is 22.9% to 61.5%. [16,17] In critically ill patients with COVID-19, the presence of acute respiratory distress syndrome (ARDS) is an important risk factor for secondary bloodstream infection (SBI) because of a prolonged stay in the intensive care unit (ICU), with approximately 13.5% SBI reported. [18]

Out of 200 samples, we got growth in 48 (24%) samples and no growth in 152 (76%) samples. There were 62.50% gram negative bacteria followed by 29.16% gram positive bacteria. There are several studies on secondary infections in COVID-19 patients. Most of them include several types of infections, such as BSIs or infections of the respiratory tract. The populations included were usually mixed in terms of severity (hospitalizations both in ICUs and medical wards). Even in studies conducted in ICUs, patients may be under invasive mechanical ventilation or other forms of respiratory support, such as high flow oscillatory ventilation (HFOV) or non-invasive mechanical ventilation (NIV). [19-22]

The predominance of male gender (77%) of patients were affected, where 23% female were affected. The *Staphylococcus hemolyticus* and *enterococcus faecium* was the most common Gram positive bacterial isolates in patients. *E. coli* was the most common Gram negative bacterial isolates in patients. 8.33% were candida tropicalis in the study. The incidence, type, and etiology of co-infections and superinfections in patients hospitalized for COVID-19 during the first epidemic periods have been summarized in two large systematic reviews, showing a prevalence of superinfections up to 41% in critically ill COVID-19 patients requiring ICU assistance. [23,24]

The results for the impact on secondary infections of immunosuppressive agents administered for the treatment of COVID-19 disease are inconclusive. There are studies where these agents are independently associated with increased nosocomial infections [21] and others that indicate no correlation. [22] Vandsala Baskaran found limited evidence for community-acquired bacterial co-infection in hospitalised adults with COVID-19, but a high rate of Gram-negative infection acquired during ICU stay, consisting largely of Gram-

negative bacteria, particularly *Klebsiella pneumoniae* and *Escherichia coli*. [25] Bacterial, fungal and viral co-infections and superinfections in hospitalized patients with COVID-19 are low; however, when present, they may cause severe diseases with worse outcomes. *S. pneumoniae* and *S. aureus* are the most common pathogens to cause community-acquired pneumonia co-infections. In our area, *P. aeruginosa* and *E. coli* were frequent bacteria that caused hospital-acquired superinfections. [26]

Conclusion

Covid 19 has complex disease pathogenesis. Patients on immunosuppressive therapy are at risk of developing secondary blood stream infections. Initially most of the secondary BSI were endogenous as *Enterococcus* spp was most prevent organisms. Patients admitted to the ICUs are also at risk of developing nosocomial infections. The patients on mechanical Ventilator are at risk of Ventilator associated infections.

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