

Profile of Bacterial Infections and Antimicrobial Resistance in Patients with Covid-19 in a Tertiary Care Hospital

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ABSTRACT

Purpose: This study was done with the purpose of detecting the effect of misuse of antibiotics while treating COVID-19 infections. We aim at detecting and monitoring the resistance profile against antibiotics in patients positive for COVID-19. Materials and methods: This study was conducted for a period of 4 months from March ,2021 to June ,2021 which included

patients confirmed as COVID-19 positive by RT-PCR for whom clinical samples were sent suspecting secondary bacterial infection .This is a retrospective study done by collecting data from samples including blood , urine, respiratory samples and others . A total of 56 samples were collected and the data was analysed.

Results: A total of 56 samples from patients confirmed as COVID-19 positive by RT-PCR for whom clinical samples were sent suspecting secondary bacterial infection. The organisms were isolated only in samples of urine and blood. A total of 12 organisms were isolated out of the 56 samples collected, with a majority of gram negative organisms. The MBL production was observed in 22.2% and ESBL production was observed in 55.5% of the gram negative bacilli isolated. Out of all the organisms isolated, 9 were multidrug resistant (81.8%).

Conclusion: The rampant use of empiric antibiotic therapy for the treatment of COVID -19 has led to the increase of the already challenging issue of antimicrobial resistance. An institution catered antimicrobial stewardship programme is crucial at this juncture, to ensure the sustainability of these precious lifesaving antibiotics.

Key words: Secondary bacterial infection, COVID 19, MBL, ESBL

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INTRODUCTION

The SARS coronavirus 2 (COVID 19) pandemic has emerged as one of the biggest threats to mankind, affecting over 3 crore people and causing over 3 lakh deaths in India. Several treatment protocols have been used to treat the infection but no treatment could guarantee complete resolution of the illness. This lead to the rampant use of antibiotics and hence emergence of multidrug resistant bacteria producing secondary infections thereby worsening the prognosis of infection [1]. Bacterial infections in severe influenza and other viral infections lead to a worse prognosis in these patients [2]. Studies done in the 1918 influenza pandemic suggests that bacterial infections secondary to viral infection can be a major cause of increase in mortality in infected patient which was further confirmed in the 2009 H1N1 influenza pandemic [3,4].

MATERIALS AND METHODS

This retrospective study was conducted for a period of 4 months from March ,2021 to June ,2021.The study included patients confirmed as COVID-19 positive by RT-PCR for whom clinical samples were sent suspecting secondary bacterial infection .The data from all samples including blood, urine, respiratory samples and others were included in the study. The samples from patients that were not sent to the laboratory were excluded from the study. A total of 56 samples including blood, urine, pus and respiratory specimens were processed using standard Microbiological procedure. The culture of the samples was performed using conventional methods and sensitivity was performed using Kirby Bauer Disk diffusion method and evaluated as per CLSI 2020. The antibiotics tested for Gram negative bacteria included Meropenem, Imipenem, Amoxicillin clavulanate, Amikacin, Gentamicin, Ciprofloxacin, Ceftriaxone, Cefotaxime, Cefixime, Ceftazidime, Cefazolin, Aztreonam and Ampicillin. Gram positive organisms were tested for sensitivity to Penicillin, Cefoxitin, Cotrimoxazole, Ciprofloxacin, Gentamicin, Rifampicin, Chloramphenicol, Erythromicin, Vancomycin and Linezolid.

RESULTS

A total of 56 samples from patients confirmed as COVID-19 positive by RT-PCR were collected for a period of 4 months from March 2021 to June ,2021.The clinical samples were sent suspecting secondary bacterial infection The samples included blood, urine, sputum and pus collected and processed using standard microbiological procedure.

Out of the 56 samples, majority of the samples were collected from urine and the least number of samples were collected from sputum. A total of 11 samples (19.6%) showed significant growth of pathogenic organisms, amongst which were *Escherichia coli* (56%), *Klebsiella pneumoniae* (27.2%), *Staphylococcus aureus* (18.1%) and *Enterococcus species* (9%).

A total of 12 organisms (21.4%) from urine and blood samples were isolated. The sputum and pus samples did not show any culture positivity. The majority of pathogens isolated were Gram negative organisms. Amongst the Gram negative organisms isolated, Metallobetalactamase production was observed in 2 organisms (22.2%) and Extended spectrum beta lactamase production was observed in 5 organisms (55.5%).

Amongst the blood samples collected, 2 Staphylococcus aureus were isolated both of which were Methicillin Resistant Staphylococcus aureus(MRSA) .The Enterococcus species isolated from urine was resistant to Tetracycline, Ampicillin, High level Gentamicin and Penicillin but was sensitive to Vancomycin and Linezolid.

The organisms isolated from these patients in general showed higher resistance profiles including ESBL, MBL and MRSA.2 patients who had secondary bacterial infection in blood, with ESBL producing Klebsiella pneumoniae and MBL producing Escherichia coli succumbed to the infection (Tables 1 to Table 4).

Table 1: Demographic distribution of patients.

Age	Male	Female
30-39 years	1	0
40-49 years	3	2
50-59 years	9	7
60-69 years	16	8
Total	39	17

Table 2: Profile of bacterial infections observed in confirmed COVID-19 patients.

Urine (n=22)	Blood (n=18)	Sputum (N=7)	Pus (N=9)
3	2	0	0
2	1	0	0
0	1	0	0
0	2	0	0
1	0	0	0
	Urine (n=22) 3 2 0 0 1	Urine (n=22) Blood (n=18) 3 2 2 1 0 1 0 2 1 0 1 0	Urine (n=22) Blood (n=18) Sputum (N=7) 3 2 0 2 1 0 0 1 0 0 2 0 1 0 0 1 0 0 1 0 0

Table 3: Resistance profiles of gram negative organisms isolated.

	URINE (n=22)	BLOOD (n=18)
Meropenem	0	2
Imipenem	0	2
Pipercillin Tazobactam	0	2
Amikacin	1	1
Gentamicin	1	1
Ceftriaxone	3	2
Ceftazidime	3	2
Aztreonam	3	2

Ampicillin	4	4
Amoxicillin clavulanic acid	3	4
Doxycycline	0	1
Chloramphenicol	0	1
Ciprofloxacin	3	2
Cotrimoxazole	1	1

Table 4: Resistance profiles of gram positive organisms isolated.

	Urine (n=22)	Blood (n=18)
Linezolid	0	0
Vancomycin	0	0
Clindamycin	NA	0
Rifampicin	NA	0
Ciprofloxacin	0	0
Cefoxitin	NA	2
Erythromycin	0	2
Tetracycline	1	0
Amikacin	NA	0
Gentamicin	NA	0
Cotrimoxazole	0	2
Penicillin	1	2
High level Gentamicin	1	NA
Ampicillin	1	NA

DISCUSSION

COVID-19, the life-threatening infectious disease has forced the entire world into a standstill. It is the need of the hour to gain as much knowledge as possible regarding the pathogenesis and the progression of the disease to ensure treatment with positive outcomes [5].

The recent data from areas having a high burden of COVID 19 suggests that secondary bacterial infections are very common, especially amongst patients who are admitted for prolonged periods of time. In the present study, out of the 56 patients who were tested, 12 patients (21.4%) showed presence of bacterial infection along with COVID-19 infection. Amongst the 12 culture positive patients, majority of the samples were from blood followed by urine. This is similar to the study by Khurana et al where out of 290 culture positive specimens the maximum number of samples were from blood followed by urine [4]. In the present study, MBL production was observed in 22.2% and ESBL production was observed in 55.5% of the gram negative bacilli isolated. Out of all the organisms isolated, 9 were multidrug resistant (81.8%). This is in higher than observed in the study by Khurana et al [4] where around 60% of organisms isolated were multidrug resistant (MDR).

CONCLUSION

The rampant use of empiric antibiotic therapy for COVID-19 has led to the increase of the already challenging issue of antimicrobial resistance. This study throws light on the status of antimicrobial resistance in secondary bacterial infections in COVID-19 positive patients. An institution catered antimicrobial stewardship programme is crucial at this juncture, to ensure the sustainability of these precious lifesaving antibiotics.

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