



## Bacterial Co-Infections in COVID-19 Positive Patients in a Tertiary Care Hospital in Southern Assam

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### Abstract

*Owing to the limited therapeutic options, the current ongoing pandemic COVID-19 pandemic has raised concerns over secondary infections. Country and region-specific clinical data encompassing various infections are needed in guiding evidence-based treatment of COVID-19. To fill this major gap in our knowledge, we conducted a prospective study to ascertain the actual burden & molecular profile of pathogens causing bacterial co-infections in COVID-19 patients.*

*Out of 100 patients, 38 were admitted to ICU and 62 in wards. The outcome measure analysis was done in 24 patients whose clinical samples were culture positive. Blood was the predominant sample followed by urine. In blood, Klebsiella pneumoniae was the commonest isolate and was resistant to most antibiotics except colistin. Candida species was the predominant pathogen in urine.*

### Background

The current pandemic COVID-19 encompassed most countries of the world. Numerous emerging complications were reported which contributed greatly to the mortality and morbidity<sup>1,9</sup> of COVID-19 positive patients. Amongst these, co-infections played a crucial role, significantly affecting lives of these patients. Although the prevalence of co-infection was variable, higher proportion of co-infection was associated with non-survivor group as compared to survivor group. In wider date, there remains a paucity of information on frequency, nature and susceptibility profiles of the co-infecting pathogens and therefore this study was undertaken.

### Aims & Objectives

The present study was therefore undertaken to –

1. Determine the prevalence of bacterial co-infections in COVID-19 patients.
2. Identify the most common co-infecting organism.
3. Study their Antimicrobial susceptibility (AST) pattern.

### Methods

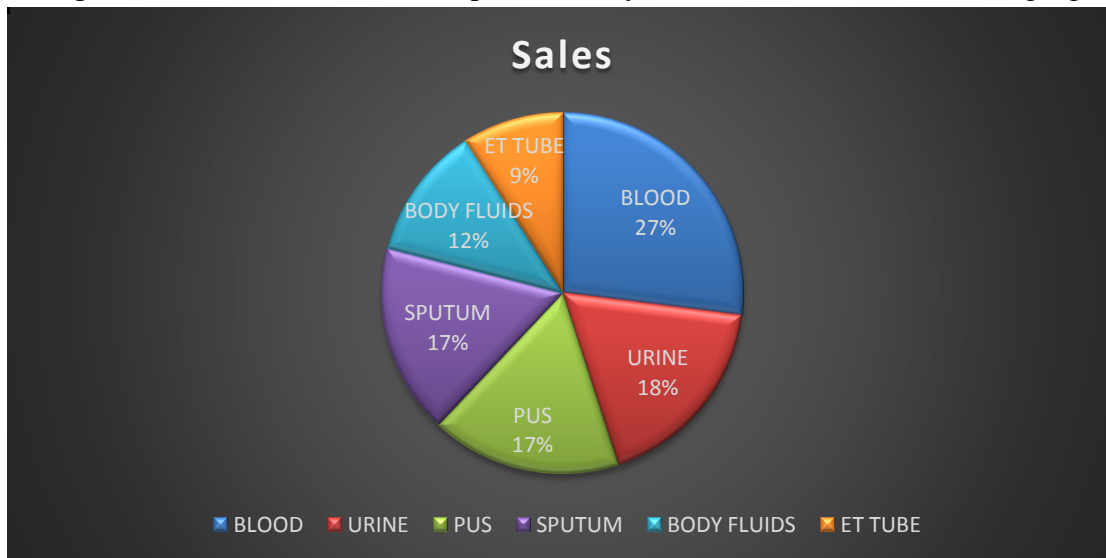
A monocenter prospective study was conducted in a tertiary care hospital in Southern Assam including 100 adult patients ( $\geq 18$  years old) from ICU and ward of COVID-19 positive patients. Samples collection was done with due adherence to standard infection control guidelines and

transported to the laboratory immediately using the shortest path. Direct microscopy followed by inoculation in different media at 37°C for 48 hours. Colonial growth was subjected to Gram

staining and biochemical identification. AST was performed on Muller-Hington Agar using disc diffusion technique using CLSI guidelines.

**Results**

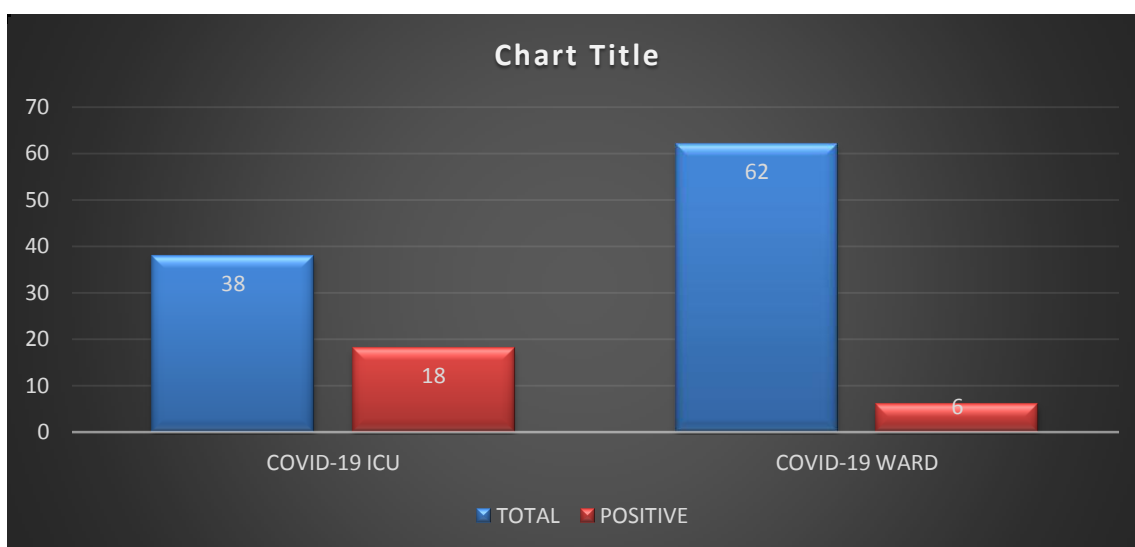
The various samples taken into account for the present study is enumerated in the following figure



Blood was the predominant sample (27%) and was followed by urine (18%). Body fluids were invariably sterile.

38 ICU patients and 62 COVID-19 ward patients were included in the study on random basis. The

outcome measure analysis was done in 24 (24%) patients whose clinical samples were culture positive. Out of 24 positive samples 18 were from COVID-19 ICU and rest 6 positive samples were from COVID-19 ward.

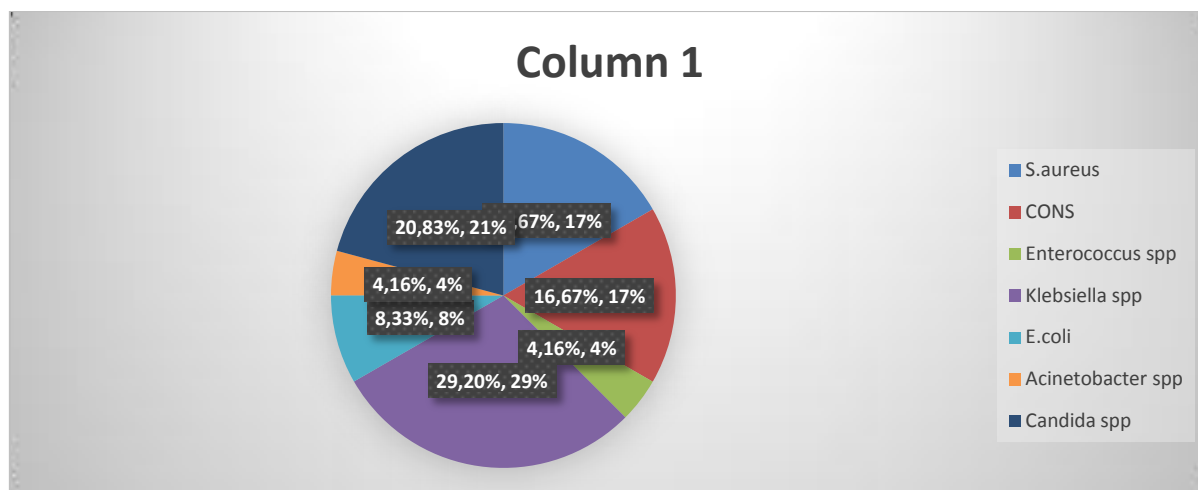


The organisms isolated from different specimen are enlisted in the following table

SL.NO	ISOLATES	BLOOD	URINE	PUS	SPUTU M	ET TUBE	BODY FLUID	TOTAL
1	Staphylococcus aureus	1(14.2%)	-	3(50%)	-	1(50%)	-	4(16.67%)
2	Coagulase negative staphylococcus	2(28.5%)	-	1(16.6%)	-	-	-	4(16.67%)
3	Enterococcus species	-	1(14.2%)	-	-	-	-	1(4.16%)
4	Klebsiella species	4(57.1%)	-	1(16.6%)	1(50%)	1-(50%)	-	7(29.2%)
5	Escherichia coli	-	1(14.2%)	-	1(50%)	-	-	2(8.33%)
6	Acinetobacter species	-	-	1(16.6%)	-	-	-	1(4.16%)
7.	Candida species	-	5(71.4)	-	-	-	-	5(20.83%)
	TOTAL	7	7	6	2	2	-	24

Overall, *Klebsiella pneumonia* (29.2%) was the most common isolate. Urine culture showed significant growth of *Candida* species (20.83%) Pus sample showed significant growth of

Methicillin Resistant *Staphylococcus aureus* (16.67%) was the predominant isolate in pus sample.



**ANTIMICROBIAL SUSEPTIBILITY PATTERN OF GRAM NEGATIVE BACTERIA ISOLATED FROM COVID POSITIVE PATIENTS**

BACTERIAL SPECIES	TOTAL ISOLATES	PATTERN	AMC	CPM	CIP	CL	NIT	PIT	IPM	MRP	AMP
Escherichia coli	2	S	1	2	1	2	1	1	2	2	1
		R	1	0	1	0		1	0	0	1
Klebsiella species	7	S	2	7	3	7		4	4	3	1
		R	5	0	4	0		3	3	4	6
Acinetobacter species	1	S	0	1	0	1	0	1	1	1	0
		R	1	0	0	0	0	0	0	0	1

**ANTIMICROBIAL SUSEPTIBILITY PATTERN OF GRAM POSITIVE BACTERIA ISOLATED FROM COVID POSITIVE PATIENTS**

BACTERIAL SPECIES	TOTAL ISOLATES	PATTERN	AZM	CX	COT	CD	CIP	GEN	VAN	LZ
Staphylococcus aureus	4	S	2	0	3	2	1	3	4	4
		R	2	4	1	2	3	1	0	0
Coagulase negative staphylococcus	4	S	1	1	2	1	2	3	4	4
		R	3	3	2	3	2	1	0	0
Enterococcus species	1	S	0	-	1	0	0	1	1	1
		R	1	-	0	1	1s	0	0	0

Majority of the pathogen isolated were multidrug resistant. Klebsiella was the commonest isolate and was resistant to almost all drugs except colistin. All isolates of *S. aureus* were methicillin resistant

### Discussion

The present study reports positivity of 24% for bacterial co infections in COVID-19 patients. Study by Lansbury et al<sup>2</sup> reports a positivity of 14%. Various other studies<sup>3,4,5,6,7</sup> showed bacterial coinfections are common among COVID-19 patients admitted to an ICU, occurring in 6–29% of these patients. As our knowledge of COVID-19 grows, understanding presenting factors associated with bacterial coinfection is essential so that empirical antibacterial therapy can be targeted to high-risk patients. Advanced age and other comorbidities, such as chronic kidney disease, diabetes, and chronic heart disease, have been associated with bacterial co-infections in some but not in other studies.<sup>(8)</sup>

### Conclusion

Identification of possible co-pathogens and the underlying molecular resistance mechanism is critical in developing diagnostics, appropriate curative and preventive interventions which are the need of the hour.

A high rate of secondary infections with resistant pathogens in COVID-19 patients highlights the importance of implementing antimicrobial stewardship programs. Adherence to the practice of initiating culture based guidance for antibiotic

and preventing irrational and over use of antimicrobial agents would be a rational approach.

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