

ORIGINAL RESEARCH

Antimicrobial resistance pattern of klebsiella isolated from various clinical samples in a tertiary care center, central India

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ABSTRACT

Background: Klebsiella pneumoniae (K. pneumoniae) is a common cause of health-care associated infections (HAIs) and has the emergence and spread of resistant strains of Klebsiella species a considerable threat to public health. **Objectives:** This study reveals the antibiotic sensitivity pattern of Klebsiella species isolated from various clinical samples in a tertiary care hospital. **Methods:** A total of 500 samples were tested during this period. The samples include urine, pus, BAL, ET aspirate, sputum and blood. Identification of Klebsiella species was done using colony characteristics and standard biochemical tests. Antimicrobial susceptibility testing was performed by modified Kirby-Bauer disc diffusion method as per CLSI M100 2022 guidelines. **Results:** Klebsiella species was isolated in 160 (32%) of specimen, among them Klebsiella pneumoniae was the predominant (81.2%). Among the positive cultures patients, 55.6% were female, most of the samples (80.6%) received from the IPD section. Maximum (38.1) samples were urine followed by pus samples (33.2%). Klebsiella spp. was 100% resistance to imipenem followed by Piperacillin-tazobactam (82.5%), Ciprofloxacin (75.6%), Amikacin (71.3%), Cotrimoxazole (66.3%), Levofloxacin (64.4%), Meropenem (63.2%) and Colistin (26.7%).

Conclusion:

Keywords: Klebsiella pneumoniae, Antibiotic sensitivity pattern, ICU, clinical samples

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INTRODUCTION

Antimicrobial Resistance (AMR) is a significant public health issue that threatens our ability to treat common infections. AMR often emerges in bacteria through upregulation of proteins that allow a subpopulation of resistant bacteria to proliferate through natural selection. Eight species of Klebsiella are identified. In that, K. pneumoniae, K. oxytoca, and K. granulomatis are associated with human illness. K. ozaenae and K. rhinoscleromatis are related to specific diseases [1]. Klebsiella pneumoniae is a gram-negative, encapsulated, a nonmotile bacterium that causes infection among hospitalized individuals who are immunocompromised [2]. It is responsible

for various infections, including urinary tract infections, pneumonia, bacteremia, meningitis, wound infections, and purulent abscesses [3]. Beyond human hosts, this bacterium finds its niche in a variety of environments, including animals, sewage, drinking water, surface waterways, polluted water, industrial effluents, and vegetation [4]. The widespread use of antimicrobials in clinical practice has led to the emergence of resistant bacterial pathogens contributing to the increased morbidity and mortality observed worldwide [5]. One study indicates that antimicrobial resistance level of the gram-negative bacteria ranges from 20 to 100% [6]. Resistant Klebsiella is one of the opportunistic pathogen

showing frequent acquisition of resistance to antibiotics accounting to about one-third of all Gram-negative infectious diseases [7, 8] such as bloodstream infection, pneumonia, urinary tract infections (UTI), nosocomial and community acquired infections [9]. As there is inappropriate use of antimicrobials, resistance is tremendously increasing and the therapeutic option has been significantly reduced [10, 11]. Ultimately, this increases cost of treatment and impedes the effective prevention and treatment outcomes in clinical settings [12, 13].

AIMS & OBJECTIVES

The current study is undertaken to know the prevalence of Klebsiella associated with infections and the antimicrobial sensitivity pattern of the isolates in our hospital.

MATERIALS AND METHODS

This cross-sectional observational study was conducted in the Department of Microbiology, MGM Medical College and associated M Y Hospital, Central India, from June 2021 to June 2022 (01 years). A total of 500 isolates were taken out of which 160 isolates found to be Klebsiella species were enrolled in this study.

INCLUSION CRITERIA

Klebsiella species isolated from clinical specimen received for culture and sensitivity and Patients those provide written informed consent for the study

EXCLUSION CRITERIA

Repeat isolation of Klebsiella species from the same patient and patients who not provide consent for the

study.

Urine, sputum, pus swab, and miscellaneous samples collected were inoculated on blood agar and MacConkey agar and incubated overnight at 37°C. Colonies were read after overnight incubation.

Isolation and identification of Klebsiella spp. was done using colony characteristics and standard biochemical tests.

Antimicrobial susceptibility testing was performed for all isolated organisms on Mueller-Hinton agar by the modified Kirby-Bauer disc diffusion method and for Colistin using broth dilution method as per CLSI M100 2022 guidelines.

The antibiotic discs with appropriate content were used and interpreted according to clinical and laboratory standards institute guidelines [14].

STATISTICAL ANALYSIS

The data were analysed using SPSS version 22. Frequencies and percentages were used to describe the categorical variables in this study. The results were presented as proportion ratios with a 95% confidence interval. Statistical significance was set if p-value <0.05.

RESULTS

In the 500 samples received during the study period, Klebsiella species was isolated in 160 (32%) of cases. Among the positive cultures patients, 89 (55.6%) were female and 71 (44.4%) was male. Most of the samples (80.6%) received from the IPD section.

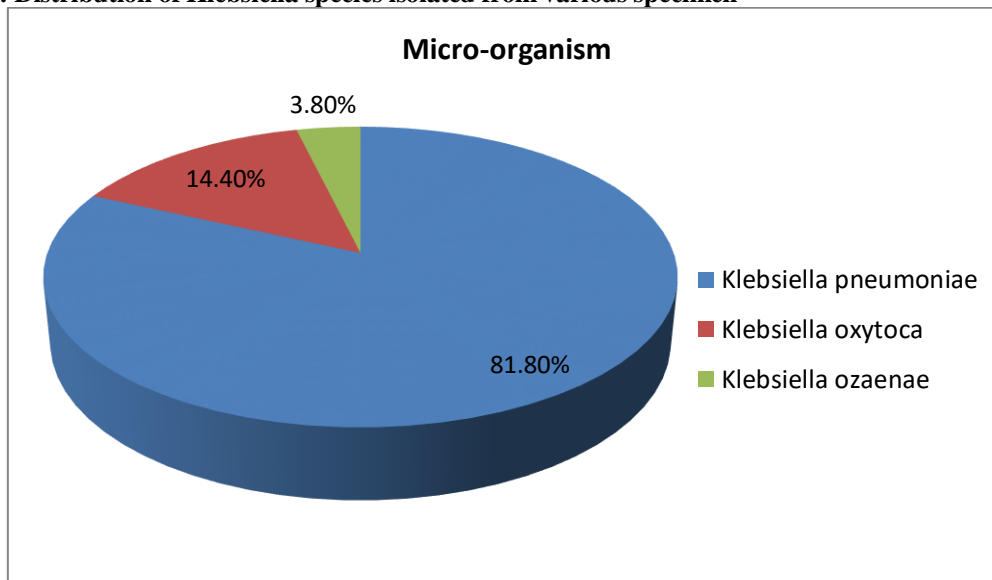
Among the positive culture, maximum (38.1) samples were urine followed by pus samples (33.2%). A detail was shown in table 1.

Table 1: Distribution of samples on the basis of gender, collection area and type of Specimen

Variables		Frequency (n=160)	Percentage
Gender	Male	71	44.4%
	Female	89	55.6
Collection area	IPD	129	80.6
	OPD	31	19.4
Specimen	BAL	11	6.9
	CSF	5	3.1
	ET	9	5.6
	PUS	53	33.2
	SPUTUM	13	8.1
	TROAT SWAB	8	5.0
	URINE	61	38.1

Among the Klebsiella species identified, *K. pneumoniae* was (81.8%) predominant followed by *Klebsiella oxytoca* (14.4%) and *Klebsiella ozaenae* (3.8%).

Figure 1: Distribution of Klebsiella species isolated from various specimen



Colistin Resistance pattern of the Klebsiella species were, 26.7%, 21.7% and 16.7% in Klebsiella pneumoniae, Klebsiella oxytoca and Klebsiella Ozaenae respectively.

Table 2: Distribution of Colistin MIC Test outcomes among different Klebsiella species

Colistin MIC Test	Klebsiella pneumoniae	Klebsiella oxytoca	Klebsiella Ozaenae
Intermediate sensitive	96 (73.3%)	18 (78.3%)	5 (83.3%)
Resistance	35 (26.7%)	5 (21.7%)	1 (16.7%)
Total	131 (100%)	26 (100%)	6 (100%)

Antibiotic sensitivity pattern of the Klebsiella isolated from various samples were depicted in Table 3. All Klebsiella were 100% resistance to imipenem. Resistance to Piperacillin –Tazobactam was higher (82.5%) followed by Ciprofloxacin was 75.6%, Amikacin(71.3%), Cotrimoxazole (66.3%), Levofloxacin (64.4%)and Meropenem(63.2%).

In urine culture Nitrofurantoin was resistance to 20.6% and Norfloxacin were 19.6%

Table 3: Antimicrobial susceptibility pattern of Klebsiella pneumoniae

Antibiotics	Susceptible	Resistance
Cotrimoxazole	50 (31.25%)	106 (66.25%)
Ciprofloxacin	36 (22.5%)	121 (75.6%)
Levofloxacin	55 (34.3%)	103 (64.4%)
Piperacillin –Tazobactam	26 (16.3%)	132 (82.5%)
Imipenem	0 (00%)	160 (100%)
Meropenem	58 (36.2%)	101 (63.2%)
Amikacin	45 (28.2%)	114 (71.3%)
Nitrofurantoin	29 (18.2%)	33 (20.6%)
Norfloxacin	31 (19.3%)	31 (19.3%)

DISCUSSION

Klebsiella species are responsible for a broad spectrum of clinical infections in immuno-competent or immunocompromised people. An extensive use of broad spectrum antibiotics in hospitalized patients has led to the increased prevalence as well as development of multidrug resistant strains of Klebsiella.

The incidence of Klebsiella isolates from various clinical samples in this study was 32%. It is similar to the Vijayashree V, et al [15] and Kashaf J, et al [16], isolation rate were 32% and 38% respectively.

Current study found slightly female predominance than male among culture positive patients, in contrast

to this other study conducted by PS Patil et al [17] and Biradar SK et al [18] reported male predominance.

A statistically significant difference observed between isolation of K. pneumoniae and gender of the patient in this study. Similar observation was noted in the study of Moiniet al [19].

In current study majority of the samples received from inpatients (IPD) section, in agreement with the study done by K Madhusudhan, et al [20].

In the present study the isolation of Klebsiella is maximum from urine samples followed by pus samples, in accordance with the Leavitt et al [21] and Parveen et al [22].

In our study Klebsiella pneumoniae was

predominantly isolated from various clinical samples followed by *K. oxytoca* and *K. ozaenae*, our results comparable with the Nirwati et al [23].

Present study found 26.7% *Klebsiella* was resistance to Colistin antibiotics, concordance to a study carried out by S Davoudabadi, et al [24] observed colistin resistance *Klebsiella* was 28.8%

In this study majority of the *Klebsiella* was multidrug resistance. The *Klebsiella* species were found 100% resistant imipenem and most resistance to Piperacillin-tazobactam, Ciprofloxacin, Amikacin, Cotrimoxazole, Levofloxacin and Meropenem (63.2%), similar results observed by many other researchers: Khan, R, et al [25], Gebremeskel et al [26] and Pavani G, et al [27].

CONCLUSION

We have concluded that *Klebsiella pneumoniae* was the predominant isolated micro-organism commonly resistance to a broad spectrum of drugs including beta-lactam antibiotics, carbapenemes, fluoroquinolones, and aminoglycosides. Hence, select appropriate antibiotics, prevent overuse & misuse of antibiotics and formulate antibiotic stewardship programme for preventing multidrug resistance *Klebsiella*.

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