

Evaluation Of Antimicrobial Resistance Among Clinical Isolates Of *Klebsiella* Spp From A Tertiary Care Center.

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Abstract: In recent years, due to the inappropriate use of antibiotics, drug resistance has increased in Gram negative bacilli, including *Klebsiella pneumoniae*. Drug resistance is associated with an increase in mortality and therapeutic costs. Therefore, determination of an antibiotic resistance pattern for choosing the appropriate treatment for infections caused by this bacterium seems necessary. In the present study all *Klebsiella* isolated during study period from Pus, CSF, ET tube. Urine, Sputum etc were evaluated for their antimicrobial sensitivity pattern. 160 *Klebsiella* isolated from various clinical specimen were processed for antimicrobial sensitivity using disc diffusion method as per CLSI guideline. Maximum resistance was found for Piperacillin-tazobactam (74%). Most of the *Klebsiella* found resistant to commonly used antibiotics. 36% of isolated were found Multidrug resistant (MDR). Among tested antimicrobials highest sensitivity was found for carbapenem group of antibiotics.

Key Words: Antibiotic, Resistance, *Klebsiella*

Introduction:

Klebsiella is a Gram-negative, encapsulated, a non-motile bacterium that causes various infection among hospitalized individuals. It may cause various infections, including urinary tract infections, pneumonia, bacteremia, meningitis, wound infections, and purulent abscesses. Its pathogenicity is related to many virulence factors, including its ability to acquire resistance against multiple antibiotics. *Klebsiella* is known for its high frequency and diversity of antimicrobial resistance genes. The worldwide emergence of multi-drug resistant (MDR) strains of *Klebsiella pneumoniae* is a growing public health issue for developing nations.(1)

Globally, antimicrobial resistance (AMR) is one of the most serious threats to public health. Infections produced by *K. pneumoniae* have grown over the past decade and constitute a particular concern to immunocompromised individuals. Increased healthcare costs, prolonged hospitalization, untreated infections, and mortality rates are the consequences of this situation (2)

The 2022 GRAM Global Burden Report, calculated AMR to be associated with 4.95 million deaths in 2019, 1.27 million attributable deaths, placing AMR as a leading cause of mortality globally. Performing antimicrobials susceptibility testing and resistance pattern identification plays an important role in treating patients since these isolates showing multidrug resistance are of great concern for the treating physician and it plays a significant role in the mortality of the patient. The detection of multidrug resistance is, however, a primary step in effectively controlling antibiotic-resistant bacterial infections that can lead to clinical failure and additional antibiotic resistance. Increased global infections by multidrug-resistant bacteria closely associated with limited drug

treatments imply the failure of empirical treatments and strengthen the need for antibacterial therapies based on antimicrobial sensitivity tests [3, 4, 5]

Several studies have demonstrated outbreaks in hospitals due to *K. pneumoniae* resistant to cephalosporins, aminoglycosides and quinolones of third generation [Enzymatic modification (β-lactamases), reduced permeability (selective blockage), increased membrane transport (efflux pumps), altered binding site (specific receptors) and metabolic bypass are the mechanisms of antibiotic resistance in bacteria (6)

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 [6, 7]. 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 Previous studies have indicated *Klebsiella*'s resistance to antibiotics reaching 68.3% in south Africa , 54% in India [1], and 97.17% in Equatorial Guinea. *Klebsiella* species are able to develop cross resistance; and the treatment failure is also high [7]

Aim:

Present study was aimed to evaluate antimicrobial resistance pattern of *Klebsiella* spp isolated from various specimen of a tertiary care center.

Material & Methods:

It was a prospective cross sectional study conducted in the Department of Microbiology of a tertiary care hospital over a period of 1 year from June 2021 to June 2022. Study was conducted on sample received in Bacteriology lab for Culture and Sensitivity testing. *Klebsiella* spp isolated from various specimen Pus, sputum, BAL, CSF, Urine and Endotracheal tube were included in the study. All samples were inoculated on Blood agar and MacConkey agar and incubated at 37°C for 24 hrs. Culture growth was examined after 24 and 48hrs and Isolation and identification of *Klebsiella* spp. was done using, Colony morphology, Gram staining morphology, Motility testing and standard biochemical tests. Antimicrobial sensitivity testing of isolated *Klebsiella* spp was done using Kirby Bauer disc diffusion method as per CLSI M100 2022 guidelines. Study was approved from Institutional Ethics committee.

Result and Discussion:

Antibiotics are now widely utilized, and new antibiotics are constantly being developed for the treatment of illnesses. The widespread use of Beta-lactam antibiotics in hospitals and the community “has resulted in increased morbidity, mortality, and health-care costs.

Klebsiella infections are a major opportunistic GNB in health-care settings, posing a global health-care concern. Its importance has grown as a result of its stability to survive in a variety of environments the development of drug resistance mechanisms, and the rise of multidrug and pandrug resistant strains.” The isolation, identification and performing antimicrobial susceptibility testing of *Klebsiella* infection to find the resistance patterns aids in the selection of appropriate antibiotic and it plays the important role in lowering patient mortality and morbidity and reducing the spread of resistant strains in the community.

In the present study 160 *Klebsiella* isolates were recovered from various specimens . Out of 160 isolates 89 (55.6%) isolates are from female patients whereas 71 (44.4%) isolates were from male patients. Females are more commonly affected compared to males in our study. However, this was in contrast with other studies done by SR amyetal.[8], P S Patil et al.[9] Biradar SK et al.[10] & Bashir et al.[11] who stated males are more commonly affected compared to female which may be due to increased “prevalence of alcoholism and smoking” among males.

Among 160 isolates, the isolated *Klebsiella* spp. were found to be *Klebsiella pneumoniae* (131/81.9%) followed by *Klebsiella oxytoca* (23/14.4%) and minimum were *Klebsiella ozaenae* (6/3.8%) (Table-1). The results were in concurrence with study done by S Ramya et al. [8], Sandeep vasikar et al., [12] & Asmaa (2012) [13]. SR amya et al., stated that among 366 isolates, the isolated *Klebsiella* spp. were found to be *Klebsiella pneumoniae sub spp pneumoniae* (89%), *Klebsiella oxytoca* (7%), *Klebsiella pneumoniae subsp aerogenes* (4%). Similar results were suggested by Sandeep vasikar et al., (2017).

Klebsiella pneumoniae is one of the leading causes of nosocomial infections seen world wide causing pneumonia, blood stream infections, urinary tract infections, surgical site infections and meningitis (Peleg and Hooper, 2010) [14].

Sensitivity testing for various antibiotics were performed as per local requirement and availability of antibiotic following CLSI guidelines. In our study we have found maximum resistance for Piperacillin–Tazobactam 89.9% whereas Parama Aminul et al reported 51.2% and Barakzahiet al 48.3% resistance to same antibiotic .

In our study very high level of resistance was shown by all tested antibiotics .Most of the *Klebsiella* showed resistance to Cotrimoxazole, Ciprofloxacin, Amikacin, Imipenem and Meropenem .(Table 2 & 3). Paroma et al and Barakzahiet al [15] also reported high level resistance towards ceftriaxone, ceftazidime, gentamicin, amikacin, and meropenem (72.8%, 75.3%, 60.3%, 50.3%, and 44.7%, respectively) and (73%, 72%, 58%, 63%, and 43.4%, respectively) [26]

Out of 160 *Klebsiella* 59 (36%) isolates were found to be MDR showed resistance to 3 classes of antibiotics . Paramaaminul et al reported 82% MDR *Klebsiella* in their study.

Conclusion:

In this study majority of the isolated *Klebsiella pneumoniae* were found to be multidrug-resistant. Therefore, there are very few therapeutic options for treating MDR *Klebsiella pneumoniae*, portraying a gloomy picture for hospital infection management in Bangladesh, suggesting that a proper surveillance system should be implemented to prevent an impending healthcare management disaster. Due to the high prevalence of resistance in *Klebsiella* isolates, there is a need for strict measures in the administration of antibiotics. Antibiotic resistance can also be reduced by choosing the appropriate antibiotic for treatment and by taking antibiotic susceptibility tests.

Table 1. Isolation of Different *Klebsiella* spp

ORGANISM	Frequency	Percent
<i>Klebsiella oxytoca</i>	23	14.4
<i>Klebsiella ozaenae</i>	6	3.8
<i>Klebsiella pneumoniae</i>	131	81.9
Total	160	100.0

Table-2 Antimicrobial Susceptibility pattern of *Klebsiella pneumoniae*

Total Tested	Antibiotic	R	%	S	%
131	Piperacillin tazobactam	106	80.9	25	19.1
131	Ciprofloxacin	97	74.0	34	26.0
131	Amikacin	93	71.0	38	29.0
131	Cotrimoxazole	85	64.9	46	35.1
131	Levofloxacin	85	64.9	46	35.1
131	Imipenem	84	64.1	47	35.9
131	Meropenem	84	64.1	47	35.9
51	Norfloxacin	26	51.0	25	49.0
51	Nitrofurantoin	25	49.0	26	51.0

Table-3 Antimicrobial Susceptibility pattern of Other *Klebsiella* spp

Total Tested	Antibiotic	R	%	S	%
29	Piperacillin tazobactam	26	89.7	3	10.3
29	Ciprofloxacin	24	82.8	5	17.2
29	Amikacin	21	72.4	8	27.6
29	Cotrimoxazole	21	72.4	8	27.6
29	Levofloxacin	18	62.1	11	37.9

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