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Multidrug Resistant *Klebsiella* Species from Clinical Isolates from Medical Emergency Unit of a Tertiary Hospital in South Eastern Nigeria

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Abstract

Background: The rising global prevalence of multidrug-resistant *Klebsiella* species poses a significant public health concern. Infections caused by these resistant bacteria are linked to high levels of morbidity and mortality, with mortality rates reported to be over 60% in affected individuals. This study aimed to assess the prevalence of multidrug resistant *Klebsiella* species isolated from patients attending the Adult Emergency Unit of Alex Ekwueme Federal University Teaching Hospital, Abakaliki (AEFUTHA). **Methods:** This was a hospital-based cross-sectional study involving consenting patients who presented to the Adult Medical Emergency Unit of AEFUTHA. Clinical specimens were obtained from patients showing signs of infection. The collected samples were processed in the laboratory, and relevant data were analyzed using SPSS version 25. **Results:** A total of 146 (11.7%) *Klebsiella* isolates were recovered from the clinical specimens analyzed. *Klebsiella pneumoniae* was

the most frequently identified species, accounting for 58.9% of isolates, while *Klebsiella oxytoca* constituted the remaining isolates. Most isolates demonstrated susceptibility to piperacillin-tazobactam and meropenem. Among the multidrug-resistant strains, extended-spectrum beta-lactamase (ESBL) production was identified in 32.6% of *K. pneumoniae* and 31.7% of *K. oxytoca* isolates. Carbapenemase production was detected in 19.8% of *K. pneumoniae* and 10% of *K. oxytoca* isolates. **Conclusion:** A high burden of *Klebsiella* infections was observed among patients in the emergency unit of AEFUTHA. The majority of the isolates were multidrug-resistant organisms, including ESBL-producing and carbapenemase producing strains.

Keywords

Klebsiella, *Klebsiella pneumoniae*, *Klebsiella oxytoca*, Infection, ESBL, Carbapenemase, Multidrug Resistant

1. Introduction

Multidrug resistance (MDR) is recognized as one of the greatest threats to global public health by the Infectious Diseases Society of America (IDSA) [1]. MDR is defined as the resistance of a bacterial isolate to at least one antimicrobial agent in three or more antimicrobial classes. Extensively drug-resistant (XDR) organisms are susceptible to only one or two antimicrobial classes, whereas pan drug-resistant (PDR) organisms are resistant to all agents in every antimicrobial class [2]. Previous studies have reported a steady global rise in the prevalence of multidrug resistant *Klebsiella* species, creating a major public health concern. Infections caused by these resistant *Klebsiella* species are linked to significant morbidity and mortality, with mortality rates reported to be greater than 60% among affected patients [3].

Multidrug-resistant (MDR) *Klebsiella* species are widely distributed across the globe. In Asia, the pooled prevalence of MDR *Klebsiella* infections has been estimated at approximately 55%. Likewise, studies conducted in low- and middle-income countries in Africa have shown that the prevalence of MDR bacterial infections ranges between 29% and 51%, with *Klebsiella* species ranking among the most commonly isolated Gram-negative pathogens [4] [5].

In Nigeria, the prevalence of multidrug-resistant *Klebsiella* species, particularly *Klebsiella pneumoniae*, remains alarmingly high, especially in hospital-acquired infections, where rates frequently exceed 50% to 70%. Many of these isolates are associated with a high prevalence of extended-spectrum beta-lactamase (ESBL) production. MDR *Klebsiella* species are responsible for several clinically important infections, including urinary tract infections (UTIs), septicemia, respiratory tract infections, and wound infections. The increasing burden of these infections is largely attributed to significant resistance to commonly used antibiotics such as cephalosporins and fluoroquinolones, alongside the growing emergence

of carbapenem resistance [6]. Furthermore, a study conducted in southeastern Nigeria found that about 55% of *Klebsiella* isolates recovered from clinical specimens were multidrug resistant [7].

Klebsiella species have acquired resistance to multiple classes of antibiotics, thereby posing major challenges to treatment and infection control strategies. Among these organisms, *Klebsiella pneumoniae* is recognized as a leading cause of healthcare-associated infections, particularly among immunocompromised patients and individuals with underlying comorbid conditions [8] [9].

Multidrug-resistant (MDR) strains of *Klebsiella pneumoniae* possess a wide range of resistance genes that compromise the effectiveness of commonly used antimicrobial agents. The emergence and spread of these resistant strains are influenced by several factors, including the inappropriate and excessive use of antibiotics, poor infection prevention and control measures, and genetic mutations. In addition, the organism's capacity to rapidly acquire and transfer resistance determinants through mobile genetic elements greatly facilitates the spread of antimicrobial resistance.

Infections caused by multidrug-resistant (MDR) *Klebsiella pneumoniae* are linked to increased morbidity and mortality, especially among critically ill patients and individuals undergoing invasive medical procedures. The most frequently reported clinical manifestations include pneumonia, urinary tract infections, and bloodstream infections.

The emergence of antibiotic resistance in bacterial species is driven by several genetic mechanisms, including plasmids, transposons, and integrons, which promote the acquisition and horizontal transfer of resistance genes [10] [11]. To survive the action of antimicrobial agents, bacteria utilize various adaptive mechanisms such as activation of efflux pumps, decreased outer membrane permeability particularly within the lipopolysaccharide (LPS) layer production of antibiotic inactivating enzymes, and alteration of antimicrobial target sites [12].

Furthermore, the growing prevalence of antibiotic resistance is fueled by multiple factors, including the indiscriminate and inappropriate use of antibiotics, overdependence on broad-spectrum antimicrobial agents, and the limited availability of effective targeted antimicrobial therapies [13].

Common resistance genes identified in *Klebsiella* species include *blaCTX-M*, *blaSHV*, and *blaTEM*, which encode extended-spectrum β-lactamases (ESBLs) capable of hydrolyzing a wide variety of β-lactam antibiotics [14]. Furthermore, the emergence of carbapenemase-producing strains has significantly limited available treatment options. Among the most important of these are *Klebsiella pneumoniae* carbapenemase (KPC) and New Delhi metallo-β-lactamase-1 (NDM-1), both of which confer resistance to carbapenems, antibiotics that are often considered drugs of last resort [15] [16].

In Ebonyi State, particularly at Alex Ekwueme Federal University Teaching Hospital Abakaliki, the largest tertiary healthcare institution in the state, there is paucity of data on the prevalence of multidrug-resistant (MDR) *Klebsiella* infec-

tions. This lack of information poses a major challenge to the development and implementation of effective antimicrobial stewardship programmes as well as targeted infection prevention and control measures.

To bridge this knowledge gap, the present study sought to determine the prevalence of multidrug-resistant *Klebsiella* species isolated from patients receiving care in the adult emergency unit of Alex Ekwueme Federal University Teaching Hospital Abakaliki.

2. Methods and Materials

2.1. Study Design

This study was a cross-sectional study of all the patients at both male and female adults in the medical emergency unit of Alex-Ekwueme Federal University Teaching Hospital Abakaliki, Ebonyi State. The clinical diagnosis of infection was made by the emergency physician and casualty officers working in emergency unit. Samples were collected from patients based on the diagnosis and site of infection before administration of antibiotics. Clinically relevant specimens were collected from the participants that consented to be part of the study. The specimens were analyzed according to the microbiological standard protocol. Multidrug resistant phenotypes were determined using double disc synergy test and modified carbapenemase inactivation method (MCIM) for extended spectrum beta-lactamase and carbapenem resistance respectively. The data collected were analyzed using SPSS version 25.

2.2. Study Area

This study was conducted at the medical emergency units of the Alex-Ekwueme Federal University Teaching Hospital Abakaliki (AEFUTHA), Ebonyi State. The hospital is the largest tertiary hospital in the Southeast of Nigeria. Ebonyi State is one the states in Southeast Nigeria, has Enugu and Benue towards north and southern border with Imo, Abia and Cross River.

2.3. Type of Samples Collected

Clinically relevant samples including blood, urine, wound swab, wound biopsy, sputum was collected based on the nature and sites of infection in order to increase the chances of isolating the pathogen of interest.

2.4. Recruitment of Patients

Adults on admission in emergency unit were recruited for this study after informed consent. Demographic data and clinical information of patients was obtained from the patient' medical record file.

2.5. Sample Size

All eligible patients in admitted in emergency unit were included in the global point prevalence survey. While the sample size for the cross-sectional study was

calculated based on the formula:

$$N = Z^2 \frac{pq}{d^2}$$

N = the desired sample size;

Z = the standard normal deviation, usually set at 1.96 corresponding to 95% Confidence interval;

p = the prevalence;

$q = 1 - p$;

d = the standard error (margin of error) set at 0.05.

Where prevalence rate of *Klebsiella* species infection is 16% in study done by Mike-Ogburia *et al.* (2025) [6]. The sample size was calculated using the formula above where: $z = 1.96$; $p = 0.16$; $q = 1 - p = 0.84$.; $d = 0.05$.

$N = (1.96)^2 \times 0.16 \times 0.84/(0.05)^2$

$$= 3.8416 \times \frac{0.1344}{0.0025}$$

= 207 isolates

2.6. Inclusion Criteria

All patients with clinical diagnoses of infections were enrolled into the study.

2.7. Exclusion Criteria

Patients without clinical evidence of infection and those who were critically ill were excluded from the study.

2.8. Questionnaire

A structured questionnaire was administered to patients to obtain demographic and medical record review which captured data on age, sex and clinical symptoms and length of hospitalization of the patients.

2.9. Sample Collection and Transportation

Blood culture bottle was given to the attending physicians to collect blood sample from adults on admission following examination by the attending physicians. Sterile bottle was given to patients with urinary tract infections for urine sample collection. Wound swabs were collected from patients with any form of skin and soft tissues infections, pus, cerebrospinal fluid and all samples collected were transported to the Microbiology laboratory of the Alex-Ekwueme Federal University Teaching Hospital Abakaliki Research Laboratory.

2.10. Quality Control

Quality control strains were obtained from Department of Medical Microbiology, AEFUTHA. Quality control of Antimicrobial Susceptibility Testing was carried out according to the clinical Laboratory Standards Institute (CLSI) guidelines using ATCC 43300 *S. aureus* as control strain [17].

2.11. Screening and Sampling Techniques

Consecutive Sampling technique was used to select patients that met the eligibility criteria, subsequently patients with identified *Klebsiella* pathogens were recruited into the study. Non duplicate *Klebsiella* species isolates were used in the study.

2.12. Laboratory Specimen Processing

Sputum, Wound Biopsy, Urine, Wound Swab Specimen Processing

Specimens were inoculated on blood agar (incubated for 24 hours) and MacConkey agar (incubated under 37˚C for 24 hours).

2.12.1. Blood Culture Processing

Incubated the blood culture bottles in the BACT ALERT machine at 37˚C, subcultured broth from a positive flagged on chocolate (incubated under 5% carbondioxide for 24 hours) and macconkey agar (incubated under 37˚C for 24 hours).

2.12.2. Gram Stain and Biochemical Identification of the Isolates

The isolates were Gram stained and Gram negative bacilli were selected for further identification. *Klebsiella* species were biochemically identified using chromogenic sugar fermentation method.

Microbact 20A/E (Oxiod) identification profile was used in identification of Gram-negative organisms to species level according to the manufacturer's instruction. Oxidase test was used to select the type of microbact kit used for each of the isolate. Microbact 20A/E was used for oxidase negative Gram negative bacilli (*Klebsiella* spp.).

Principle: microbat 20A/E has commercially prepared reagents and biochemical sugars embedded on the wells of the kit. The organisms either ferment, or oxidize the sugar which leads to colour change seen after 24 hours incubation.

Procedure: the isolate was used to make a broth suspension of equal turbidity with 0.5 McFarland standards. The suspension was also used to fill the micro wells in the microbact kit. This was incubated for 18 hours in an ambient air between 35˚C to 37˚C. The manufacturer's instruction was followed strictly and color changes read with the corresponding guide.

Result: the organism was identified with the codes generated using the microbact software.

2.12.3. Antibiotic Susceptibility Testing

Antibiotic susceptibility testing was done using Modified Kirby-Bauer disc diffusion method.

Principle: modified Kirby-Bauer disc diffusion relies on diffusion of the antibiotics impregnated in the disc into the agar to inhibit the bacterial growth and it is measured under standard conditions.

Procedure: an overnight growth and pure culture was used to make a suspension of equivalent turbidity with 0.5 McFarland standards. Mueller Hinton agar was used. The suspension of the organism was inoculated on the agar using sterile

swab. The number of antibiotics disc used were maximum six discs in a 100 mm agar plate. The agar was incubated at 35˚C to 37˚C for 18 hours in an ambient air and the zone diameter (zone of inhibition) was measured using ruler.

Result: the zone of inhibition was interpreted as sensitive, intermediate (the intermediate category implies clinical efficacy in the body sites where the drugs are physiologically concentrated and also include a buffer zone for inherent variability in test methods) or resistant according to Clinical Laboratory Standards Institute (CLSI) standards [17].

Choice of antibiotics: antibiotics used for different organisms were chosen based on CLSI and the antibiotics commonly prescribed in medical ward. Two Mueller Hinton agar plates were used for each isolate and maximum of six antibiotic discs were placed in 100 mm agar plate. The selected antibiotics for each of the organisms according to CLSI were as follows:

The Gram negative isolates such as *Klebsiella* spp.: gentamicin (10 µg), amikacin (30 µg), ciprofloxacin (5 µg), levofloxacin (5 µg), cefuroxime (30 µg), cefotaxime (30 µg), ceftriaxone (30 µg), cefepime (30 µg), piperacillin-tazobactam (100/10µg), amoxicillin-clavulanate (20/10µg), and meropenem (10 µg).

2.13. Definition of MDRO and Specific MDROs

Multidrug Organism (MDRO): can be defined as resistance to at least one in three different classes of antibiotics. There are specific of multidrug resistance organism with enzymes that confer them ability to resist most classes of antibiotics such as carbapenemase producing Enterobacteriaceae (CPE), extended spectrum beta-lactamase (ESBL) and others [18] [19].

2.13.1. Antibiotic Resistance Testing

The common resistance phenotypes tested on *Klebsiella* species were as follow: extended spectrum *β*-lactamase producer and carbapenemase producing *Klebsiella*.

2.13.2. Phenotypic Detection and Confirmation of Extended Spectrum *β*-Lactamase (ESBL) Producing *Klebsiella* spp. Using CLSI Break Point and Double Disc Synergy Test

ESBLs are enzymes produced by some *Klebsiella* spp. which hydrolyze most penicillin and cephalosporin up to fourth-generation as well as aztreonam.

Principle: the confirmation test for ESBL producing *Klebsiella* example double disc synergy test evaluates the synergy between an oxyimino cephalosporin and an inhibitor like clavulanic acid. The clavulanic acid inhibits ESBL and allows the third generation cephalosporin to inhibit the growth of the organism in that direction therefore forming a dome bell shape.

Screening: the *Klebsiella* isolates were screened for ESBL production by using disc diffusion of ceftazidime (30 µg) and cefotaxime (30 µg) placed on inoculated plate containing Muller Hinton agar according to CLSI recommendation. The zone diameter of ≤22 mm and ≤27 mm for ceftazime and cefotaxime respectively were indicated as suspected ESBL production. The positive isolates were subjected to confirmatory test using double disk synergy test.

Procedure of the confirmatory test: double disc synergy test (DDST) was used to test for presence of ESBL in *Klebsiella*. Discs containing cephalosporin (cefotaxime and ceftazidime) were placed next to a disc with clavulanic acid (amoxicillin-clavulanic acid). The distance between the discs was 20 mm centre to centre. The agar was incubated at 35˚C to 37˚C for 18 hours in an ambient air.

Result: positive result was indicated by augmenting of zone of inhibition towards the direction of the amoxicillin-clavulanic acid with dumb-bell or keyhole appearance.

Quality Control

Klebsiella pneumoniae ATCC 700603 was used as positive control organism.

Escherichia coli ATCC 25922 was used as negative control organism [17].

2.13.3. Phenotypic Screening and Confirmation of Carbapenemase Production in *Klebsiella* spp.

Carbapenemases are β-lactamases that hydrolyze penicillin, in some cases cephalosporin, monobactams and carbapenems. The technique used to screen for carbapanemase production in enterobacteriaceae was the result of the disc diffusion test of the isolates on carbapenems (meropenem) and confirmation was done using Modified Carbapenem Inactivation Method (mCIM).

Principle: modified carbapenem inactivation method uses the principle of detection of enzymatic hydrolysis by incubating a carbapenem with a bacterial suspension. The principle involves incubation of carbapenem disc for four hours in an aqueous suspension of a carbapenemase-producing *Klebsiella* spp., the carbapenem in the disc is degraded by the carbapenemase; as against, if the test organism does not produce carbapenemase, the carbapenem retains its antimicrobial activity after incubation in the bacterial suspension. The disc is removed from the suspension and placed on a Mueller Hinton agar swabbed with indicator organism; following overnight incubation, the zone of inhibition is measured to determine if the carbapenem have been hydrolyzed.

Screening: the *Klebsiella* isolates were screened for carbapenemase production by using disc diffusion of meropenem (10 µg) placed on inoculated plate containing Muller Hinton agar and the isolate according to CLSI recommendation. The isolates that were either resistant or intermediate for meropenem or that is with zone diameter ≤ 23 mm (equivalent of 2 - 4 µg/l MIC) for meropenem were subjected to confirmatory test using modified carbapenem inactivation method.

Procedure of the confirmatory test: the isolate to be tested was emulsified in 2 ml tryptic soy broth (TSB) and vortex for 15 seconds. The carbapenem (meropenem) disc was added to the TSB tube using sterile forcep and incubated for four hours at 35˚C to 37˚C in ambient air. The standardized inoculum of the indicator organism (*E. coli ATCC 29522*) was used to inoculate on Mueller Hinton agar. The meropenem was removed from the TSB using 10 µL loop by placing the flat side of the loop against the flat edge of the disc and carefully placed on the inoculated Mueller Hinton agar (MHA). The MHA plate was incubated at 35˚C to 37˚C

in ambient air for 18 - 24 hours. Following incubation, the zone of inhibition was measured.

Result: carbapenemase production was indicated when the zone diameter is 6 - 15 mm or presence of colonies within a 16 - 18 mm zone and was reported as carbapenemase detected. It is indicated as negative, if the zone is ≥19 mm and was reported as carbapenemase not detected.

Quality Control: *K. pneumoniae* ATCC BAA-1705 was used as positive control, *K. pneumoniae* ATCC BAA-1706 as negative control and *E. coli* ATCC 25922 served as indicator organism [17].

2.14. Data Analysis

The statistical analysis software version 25 (SPSS) was used for data analysis.

The data were entered into Excel Microsoft and statistical analysis was done using Social Sciences (SPSS) software, version 25. The variables were expressed in percentages and frequency tables.

2.15. Ethical Approval

The ethical approval for the study conduction was obtained from Alex-Ekwueme Federal University Teaching Hospital Abakaliki Research Ethical Committee (HREC). The study was conducted according to declaration of Helsinki. Both verbal and written informed consents were obtained from all the participants after the detail of the study was explained to them.

3. Result

One thousand two hundred and fifty (1250) clinical samples were submitted to the laboratory for bacterial culture between first January, 2025 to 31st December, 2025. Of the 1250 clinical specimens, three hundred and thirteen (313) were culture positive for bacterial pathogens and 146 (11.7%) were identified as *Klebsiella* specie from non-duplicate specimens. One hundred and forty-six of the participants were enrolled into the study. Eighty two (56.2%) of them were females and sixty-four (43.8%) were males. The mean age of the participants was 43 ± 5 years (Table 1). The predominant infection was respiratory tract infection (34.2%), followed by urinary tract infection (27.4%) (Table 2).

Table 1. Baseline characteristics of patients.

Variable	Frequency (n = 146)	Percentage
Sex		
Females	82	56.2
Males	64	43.8
Age group (Years)		
≤20	14	9.6

Continued

21 - 30	20	13.7
31 - 40	42	28.8
41 - 50	34	23.3
51 - 60	27	18.5
≥61	9	6
Mean Age (yrs)	43 ± 5 year	

Table 2. Types of sites of infection.

S/n	Site of Infection	Frequency	Proportion (%)
1	Respiratory tract infection	50	34.2%
2	Urinary tract infection	40	27.4%
3	Blood stream infection	27	18.5%
4	Wound infection	17	11.6%
5	Others	12	8.2%
		146	100%

Klebsiella pneumoniae 86 (58.9%) was the most frequently identified species while *Klebsiella oxytoca* was 60 (41.1%) (**Table 3**). Over 60% of *Klebsiella pneumoniae* were sensitive to gentamicin, levofloxacin, piperacillin tazobactam and meropenem. While majority of *Klebsiella pneumoniae* were resistant to ciprofloxacin, cefuroxime, ceftriaxone, amoxicillin clavulanate and trimethoprim sulphamethoxazole. *Klebsiella oxytoca* were 80%, 79%, 57%, and 50% resistant to trimethoprim sulphamethoxazole, cefuroxime, cefuroxime, ceftriaxone, and ciprofloxacin respectively while majority (91%) of *Klebsiella oxytoca* were sensitive to meropenem (**Table 4**).

Table 3. Different *Klebsiella* species isolated from various specimens.

S/N	Specimen (n)	*Klebsiella pneumoniae*	*Klebsiella oxytoca*	Total
1	Sputum (50)	33 (38.4%)	17 (28.3%)	50 (34.2%)
2	Blood (27)	19 (22%)	8 (13.3%)	27 (18.5%)
3	Urine (40)	18 (20.9%)	22 (36.7%)	40 (27.4%)
4	Wound (17)	10 (11.6%)	7 (11.7%)	17 (11.6%)
5	Ascitic fluid (7)	4 (4.7%)	3 (5%)	7 (4.8%)
6	Others (5)	2 (2.3%)	3 (5%)	5 (3.4%)
	Total	86	60	146 (100%)

Table 4. Antibiotics Susceptibility Testing (AST).

S/N	Organisms	Gentamicin	Ciprofloxacin	Levofloxacin	Cefuroxime	Ceftriaxone	Amoxicillin Clavulanate	Piperacillin Tazobactam	Trimethoprim Sulphamethoxazole	Meropenem
1	*Klebsiella pneumoniae* (86)	60%	48%	62%	24%	40%	58%	74%	19%	84%
		52	41	53	21	34	50	64	16	72
2	*Klebsiella oxytoca*	58%	50%	65%	21%	43%	51%	72%	20%	91%
		35	30	39	13	26	31	43	12	55

Table 5 shows multidrug resistant phenotypes tested which included extended spectrum beta-lactamase (ESBL) and carbapenemase producer among *Klebsiella* species. There were 32.6% (28/86) *Klebsiella pneumoniae* that showed extended spectrum beta-lactamase enzyme (ESBL) production while 31.7% (19/86) of *Klebsiella oxytoca* were ESBL producers. Carbapnem resistant phenotypes were also identified among *Klebsiella* species, 19.8% (17/86) were *Klebsiella pneumoniae* and 10% were *Klebsiella oxytoca*.

Table 5. Antibiotic resistance phenotypes.

S/N	Organism	Number	ESBL Positive	ESBL Negative	CRE Positive	CRE Negative
1	*Klebsiella pneumoniae*	86	28 (32.6%)	58 (67.4%)	17 (19.8%)	69(80.2%)
2	*Klebsiella oxytoca*	60	19 (31.7%)	41 (68.3%)	6 (10%)	54 (90%)
	Total	**146**	**47 (32.2%)**	**99 (67.8%)**	**23 (15.8%)**	**123 (84.2%)**

4. Discussion

In the present study, *Klebsiella* species were isolated from 146 (11.7%) out of 1250 clinical specimens analyzed. The majority of the isolates were identified as *Klebsiella pneumoniae*, accounting for 59% (86/146) of the total isolates. This finding is consistent with the report by Emilia and Florence, who documented a prevalence of 54.1% in Cameroon [20]. Similarly, a previous clinical study conducted in southeastern Nigeria reported a prevalence of 64.3%, which closely aligns with our findings [7]. In contrast, much higher prevalence rates have been documented in India (98%) and the United Kingdom (76%) [21] [22]. The predominance of *Klebsiella pneumoniae* observed in this study may be attributed to its recognized role as a major causative agent of both community acquired and hospital acquired infections.

Respiratory tract infections were the most common type of infection identified in this study, followed by urinary tract infections and bloodstream infections. The majority of *Klebsiella* species, including both *Klebsiella pneumoniae* and *Klebsiella oxytoca*, were isolated from respiratory and urinary tract specimens, respectively. This observation is consistent with findings from previous studies that identified sputum and urine as the major sources of *Klebsiella* isolates [23] [24]. *Klebsiella pneumoniae* demonstrated low susceptibility to ciprofloxacin (48%), ceftriaxone (40%), cefuroxime (24%), and trimethoprim sulphamethoxazole (19%). Similarly, most *Klebsiella oxytoca* isolates were resistant to cefuroxime (71%), ceftriaxone (57%), and trimethoprim sulphamethoxazole (80%). These findings are comparable to reports by Bright and colleagues [7] [25].

Overall, a substantial proportion of *Klebsiella* isolates exhibited resistance to third-generation cephalosporins, ciprofloxacin, amoxicillin clavulanate, and trimethoprim sulphamethoxazole. These antibiotics are commonly prescribed empirically for the treatment of both hospital-acquired and community-acquired infections, including pneumonia, urinary tract infections, and other severe bacterial infections. The high level of resistance observed in this study is in agreement with findings from previous studies [26] [27].

A high prevalence of multidrug resistance was observed among the *Klebsiella* species isolated in this study. Of the 146 *Klebsiella* isolates, 32.6% of *Klebsiella pneumoniae* and 31.7% of *Klebsiella oxytoca* were identified as extended-spectrum β-lactamase (ESBL) producers. These findings are consistent with previous studies that reported ESBL prevalence rates of 29.5% in Lagos and 30% in Maiduguri [28] [29]. However, the prevalence observed in the present study is lower than the rates of 68.2% and 70% reported in Uganda and Ethiopia, respectively [24] [30]. The high prevalence of ESBL-producing isolates recorded in this study may be attributed to the selective pressure resulting from the extensive use of third-generation cephalosporins, as documented in previous studies [31] [32].

Carbapenems are considered reserve antibiotics for the treatment of infections caused by extended spectrum β-lactamase (ESBL)-producing organisms. In the present study, the prevalence of carbapenemase production was 19.8% among *Klebsiella pneumoniae* isolates and 10% among *Klebsiella oxytoca* isolates. Overall, the cumulative prevalence of carbapenemase producing *Klebsiella* species was 15.8%, which is comparable to rates of 12.8% and 23.2% reported in studies conducted in Kenya [33] [34].

The increasing emergence of carbapenemase producing pathogens is of significant public health concern because of the limited therapeutic options available for treating these infections. This trend may also be linked to inadequate regulation and unrestricted use of antibiotics, prevention and control practices within healthcare facilities may be a major contributing factor to the growing prevalence of carbapenem-resistant pathogens.

5. Conclusions

Klebsiella pneumoniae was the predominant species isolated in this study, while

respiratory tract infection was the most frequently encountered infection in the emergency unit. Most *Klebsiella* isolates demonstrated high susceptibility to piperacillin tazobactam and meropenem.

Nevertheless, multidrug-resistant phenotypes, including extended-spectrum β-lactamase (ESBL) and carbapenemase-producing strains, were detected among many of the *Klebsiella* isolates responsible for severe and life-threatening infections.

The high burden of multidrug resistant *Klebsiella* infections observed in this study underscores the need for strengthened surveillance of antimicrobial resistant pathogens. In addition, improved infection prevention and control measures are strongly recommended.

6. Limitation

The finding from this study is very important but cannot be applied generally because it is a single center study and the resistance was detected only using phenotypic method. Therefore, further study with larger sample size, multicenter and molecular analysis will be recommended.

Author Contributions

The concept and study framework was designed by Nweke Chinedu Idakari. Sample collection, specimen analysis, data processing and manuscript writing were done by all the authors. All the co-authors read and approved the final manuscript.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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