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Antibiotic Resistance Pattern of Klebsiella pneumoniae in Clinical Sample of Patients Attending Aisha Muhammadu Buhari General Hospital Jega, Kebbi State, Nigeria

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Abstract

Klebsiella pneumoniae is known as an agent of nosocomial, and community acquired infections, basically because of its broad spectrum antibiotic resistance, and is of great concern to patient treatment outcome. The pathogen showcase public health significance as its incidence and resistance profile is rapidly increasing, it's consequently turned out to be among the major public health issues, from a global perspective. The study aimed to determine the antibiotic resistant pattern of K. pneumoniae in a clinical sample of patients attending General Hospital Jega, Kebbi State, North-West, Nigeria. A sample comprised of sputum, blood and urine was aseptically collected and analyzed using standard microbiological techniques and molecular method, Antibiotic Sensitivity Testing (AST) was carried out using modified Kirby-Bauer disk diffusion method, and Extended Spectrum Beta-Lactamase production (ESBL) by Double Disk Synergy Test (DDST). Out of the total 138 samples that were analyzed during the course of the present study, 13/138 (9.42%) yielded positive for Klebsiella pneumoniae, sputum samples recorded the highest prevalence rates of 15/27 (5.66%), followed by urine 9/27 (3.40%), and blood 3/27 (1.13%) respectively. The AST study reveals that a significant number of the isolates are resistant, and the highest percent recorded in Cefepime (92.30%), and Cefoxitin (92.30%), followed by Ceftazidine (84.61%), Cefpodoxime (84.61%), then Tetracycline (76.92%), Cefotaxime (61.53%) respectively. Furthermore, Imipenem (69.23%), was recorded as the least resistant drug followed by Meropenem (61.53%), Augumentin (53.84%), and Ciprofloxacin (46.15%) respectively. Our present study, reveals that ESBL phenotypes were only observed in 10/8 (80%), out of 10 (100%) of suspected ESBL producers screened isolates. During the molecular analysis, out of the total isolates analyzed by Polymerase Chain Reaction, 4/8 (50%) isolates were amplified with the BlaTEM gene. The research concludes that K. pneumoniae harbor genes that confer the ability of antibiotic resistance. Furthermore, the study highlighted resistance issues and the necessity for coordinated action to address them.

Keywords: Klebsiella pneumoniae, Antimicrobial resistance, Blood, Urine and Sputum samples

INTRODUCTION

Klebsiella pneumoniae, was initially discovered in 1875 by Theodor Albrech Edwin Klebs, a German physician and bacteriologist, from the respiratory tract of a dying patient, diagnosed with pneumonia. Later in 1882, Carl Friedländer provided a comprehensive description of the microorganism, resulting in its temporary designation as Friedlander's bacillus (Chang et al., 2021). Furthermore, in 1885, Trevisan V. paid tribute to Theodor Albrech Edwin Klebs by naming the genus as Klebsiella (Ning et al., 2022). The genus Klebsiella encompasses a group of immotile members of the enterobacteriaceae family, traditionally classified into Klebsiella pneumoniae, K. ozaenae, and K. rhinoscleromatis (Saif et al., 2020).

The bacterial species Klebsiella pneumoniae is distinguished by its encapsulated Gram-negative nature. It is known to colonize the skin, dental cavity, respiratory tract, and gastrointestinal tract of human beings. (Badger-Emeka et al., 2021). In terms of its dimensions, this species typically measures between 1-2 µm x 0.5-0.8 µm, and it thrives under normal conditions at a temperature of 37ºC for a duration of 18-24 hours. When cultivated on MacConkey Agar, the colonies of Klebsiella pneumoniae display a distinctive appearance, being both large and mucoid, with a color ranging from pink to red (Grover et al., 2022). The organism is widely recognized for its exploitative nature, is an important cause of hospital and community acquired infections, including but not limited to pneumonia, infections of the urinary system, infections in the bloodstream meningitis, and liver abscess among others. (Medrzycka-Dabrowska et al., 2021). Klebsiella pneumoniae exerts a significant impact on the healthcare sector because it is one of the species recognized as part of ESKAPE group of organisms, associated by their characteristic potential to escape or evade the action of antimicrobial agents (WHO, 2017). Furthermore, in light of the growing worldwide issue of antimicrobial resistance, the World Health Organization prioritizes research and development of novel antibiotics, upon listing K. pneumoniae among the bacteria species of the group (WHO, 2017). And also According to a global antimicrobial resistance surveillance report conducted by the World Health Organization, K. pneumoniae is one of the nine bacteria implicated in antibiotic resistance (WHO, 2014). K. pneumoniae has demonstrated resistance against several third-generation cephalosporin antibiotics, notably cefotaxime, ceftazidime, and ceftriaxone (Effendia et al., 2018).

K. pneumoniae uses multiple types of resistance mechanisms, involving target site alteration, drug deactivation, lower cell permeability, and stimulation of efflux pumps, to survive the deadly effects of antibiotics. (Ferreira et al., 2019). Nevertheless, some strains of K. pneumoniae can produce extended-spectrum beta-lactamase (ESBL) enzymatic agents which allow them to withstand and even outlive the toxic effects of β-lactam pharmaceuticals by virtues of destroying the active site, “Beta-lactam ring”. Cephamycins and carbapenems are among the β-lactam antibiotics that these ESBLs can hydrolyze and deactivate. (Jalal et al., 2023). And thus, the impact of ESBL enzymes can be surmounted by β-lactam inhibitors, such as clavulanic acid (Ferreira et al., 2019). ESBLs are coded by transferable plasmid-mediated genes, including TEM, SHV, and CTX-M (Jalal et al., 2023). The burden of infection caused by K. pneumoniae, as a consequence of its ability to withstand the impact of antimicrobial medications, is highly correlated with elevated morbidity and mortality, a correlation that may be attributable to the large number of resistance genes harbored by the bacteria (Orole et al., 2020). The bacterium adheres to host cells using fimbriae and adhesins, thereby facilitating tissue infection. Prolonged hospital stays, prior antibiotic usage, and the type of ventilation are risk factors associated with colonization and infection by K. pneumoniae (Orole et al., 2020).

In Kebbi State, however, there is paucity of data on the prevalence and antibiotic resistant pattern of K. pneumoniae and other some bacteria pathogens

(Danlami et al., 2019 ; Kalgo et al., 2022), and most of the few research data available, are established, based on phenotypic methods. Given that, this study was designed to use molecular methods to ascertain the prevalence, antibiotic resistance profile, genetic diversity, and spread of extended-spectrum-β-lactamases in K. pneumoniae isolated from clinical source of patients attending Aisha Muhammadu Buhari general hospital Jega (AMBGHJ) of Kebbi State, North-West, Nigeria.

MATERIALS AND METHODS

Study area

This study was carried out at Jega Local Government Area of Kebbi State, which was situated at latitude of 12.3667° N and a longitude of 4.6333° E, encompassing a land area of 891km2. The population of this area is roughly 200,000 (NPC, 2006).

Figure 1, Map of Kebbi State showing the research study area; Jega Local Government, accessed 15/12/2023 (https://www.KebbiState.gov.ng).

Study Design

This is a descriptive hospital-based study were clinical samples were gathered from Aisha Muhammadu Buhari General Hospital Jega. The samples then were handled at the Department of Microbiology of the Postgraduate Laboratory at Kebbi State University of Science and Technology (KSUSTA), Aliero. And Subsequent molecular analyses were also carried at the Molecular Biology Laboratory, Faculty of Agriculture, KSUSTA.

Sample Collection and Ethical Consideration

A total of 138 clinical specimens comprised of sputum, blood, and urine were procured from the Aisha Muhammadu Buhari General Hospital Jega,

located in Kebbi State. The prevalence rate was assessed to be 10% according to Danlami et al. (2019). Before data collection, ethical approval was sought from the Kebbi State Health Research Ethics Committee (KSHREC). The corresponding reference number for ethical approval was MOH/KSREC/VOL I/56, and the KSHREC registration number was 107:017/2023.

Inclusion and Exclusion Criteria

Samples were obtained from consented inpatients and outpatients of both sexes and those of age that range between ≥ 10 and ≤ 90 were included. Those who patients didn't give their consent and who were on antibiotics treatments two weeks before sample collection, were excluded from the study participate.

Isolation and Identification

The clinical samples were all subjected to inoculation on MacConkey agar plates using the streaked plate method. Subsequently, they were incubated at 37°C under aerobic conditions for a duration of 24 hours, facilitating the growth of distinct colonies. Then the colonies were subjected to phenotypic identification, whereby their characteristics such as colony morphology, staining behavior, and biochemical properties (including Oxidase, Urease, MR-VP, Simon citrate, and Indole) were carefully observed and recorded (Cheesbrough, 2010).

Determination of Antibiotic Resistance Profile of Klebsiella pneumoniae Isolates

The antibiotic resistance pattern of Klebsiella pneumonia isolates was determined through the modified Kirby-Bauer disk diffusion method on Mueller-Hinton agar. This determination was carried out according (CLSI, 2020).The antibiotics employed in this study included Tetracycline (TTR 30 µg), Augmentin (AMC 30 µg), Ciprofloxacin (CIP 5 µg), Cefepime (FEP, 30 µg), Cefotaxime (CTX 30 µg), Ceftazidime (CAZ 10 µg), Cefpodoxime (CPD 10 µg), Cefoxitin (CFT 30 µg), Imipenem (IMP, 10 µg), and Meropenem (MEM 10 µg). The test isolates were prepared as a suspension and adjusted to 0.5 McFarland turbidity standards. These suspensions were then aseptically inoculated onto Muller-Hinton agar plates using sterile swab sticks, and the antibiotic discs were subsequently applied. Within 15 minutes of inoculation of plates, then the Plates was incubated at 37ºC for 18 to 24 hrs. Following incubation, the clear zone diameter surrounding the disc was measured using transmitted light, and the results were interpreted in line with (CLSI, 2020).

Screening Tests for extended spectrum β-lactamases (ESBL) Production

According to CLSI guidelines CLSI, (2020), an isolate was identified as a potential ESBL producer if it demonstrated resistance to two or more third-generation cephalosporin antibiotics and had a zone size of less than 17 mm for Cefpodoxime, 22 mm for Ceftazidime, and 27 mm for Cefotaxime. This identification was established through a confirmatory test procedure.

Confirmatory Tests for (ESBL) Production

After adjusting the suspension of test isolates to 0.5 McFarland turbidity standards and using sterile swab sticks for aseptic inoculation on Muller-Hinton agar plate, the isolates that were resistant to two or more beta lactam antibiotics were considered potential ESBL producers and subjected to phenotypic confirmation by Double Disk Synergy Test (DDST). Augumentin (AMC 30 µg), disk was placed at the center of the plate and Cefpodoxime (10µg), Cefotaxime (30µg) and Ceftazidime (30µg), were placed each on either sides of the central disk Augumentin (AMC 30 µg), at a distance of 15 mm apart and the plates were incubated for 18 to 24 h at 37°C. After 18 to 24 hours of incubation, an isolates that produce zone of inhibition ≥ 5 mm of any of the cephalosporins tested toward the central disk Augumentin (AMC 30 µg), was considered ESBL

producer and positive for the test (Aljanaby et al., 2016)

Molecular Identification of K. pneumoniae Isolates by PCR

DNA Extraction

DNA was extracted by boiling method, briefly; three to five (3-5) pure and fresh colonies was introduce into a sterile micro centrifuge tube containing 1ml of distilled water, then the cells were lysed by heating in the water bath at 100°C for 20 minutes, immediately the cells were placed into ice for 30 min and the other cellular components were removed by centrifugation at 8500 rpm for 10 min. Finally, the supernatant was used as the DNA template for PCR or stored at −20°C for further analysis (Aljanaby et al., 2016).

Determination of Extracted DNA Concentration

The amount of light DNA absorbed at ~260 nm (A260) was ascertained using a spectrophotometer to determine the concentration of DNA. DNA was considered pure when the ratio of (A260/A280) fell between ~1.8 and 2.0 for dsDNA, while a ratio of less than 1.7 will indicate protein or RNA contamination. (Gupta, 2019).

Amplification of blaTEM Gene: Polymerase Chain Reaction

The amplification was performed from protocol adapted by Effendia et al. with little modifications, using Master Mix ready to load (Solis Biodyne, Estonia) with pure genomic DNA of K. pneumoniae as template, and primers, Table 1. PCR reactions was achieve by 20µl total volume, encompasses with 4µl of Solis Biodyne Master Mix ready to load (Solis Biodyne, Estonia), 0.6µl of forward and reverse primer, 1µl of template DNA, and 13.8µl of molecular grade water making 20µl of PCR solution. The temperature and time conditions of the amplification involved initial steps denaturation process at 95°C for 15 min, 30 cycles denaturation at 95°C for 30 sec, annealing at 54°C for 30 sec, extension at 72°C for 4 min followed by the final extension on temperature of 72°C for 10 min. (Effendia et al., 2018). Furthermore following the final PCR cycle, the products was stored at -20°C temperature for other analysis (Dalia, et al., 2020).

Table 1: Primer used for amplification of extended spectrum beta-lactamase ESBL BlaTEM gene

Gene	sequence	Amplicons bp	References
BlaTEM	Forward; (5'-TCGCCGCATACACTATTCTCAGAATGA-3) Reverse; (5'-ACGCTCACCGGCTCCAGATTTAT-3')	445	Effendia *et al*., 2018

Electrophoresis of PCR Products

The amplication product was separated base on the protocol adapted by Effendia et al. (2018) with little modifications briefly as follows; ten microliter 10µl of the PCR products and 10µl DNA ladder ready to load (Solis Biodyne, Estonia) was used, then were analyzed by electrophoresis on 1.5% agarose gel containing 10µl of SYBR dye, pipetted into well created with comb. Electrophoresis was run at 90 volts for 30 minutes, after which DNA amplicon were then viewed on a UV trans-illuminator (Effendia et al., 2018).

STATISTICAL ANALYSIS

The data obtained during the course of the study were analyzed using Microsoft Office Excel (2013), then the data was presented by frequency tables, and charts

RESULT

Samples and Patient Demographics

Out of the total 138 clinical samples collected from patients attending Aisha Muhammadu Buhari General Hospital Jega (AMBGHJ), upon obtaining informed consent and have met the selection criteria. The age of the patients was from 10 to 90 years, and the study participants were majorly Males 78/138 (56.52%). The highest sample is urine with 48 (34.78%), then followed by sputum at 46 (33.33%), and blood samples at 44 (31.88%) respectively.

Table 2. Prevalence of Klebsiella pneumoniae infection to sex and age of patients attending Aisha Muhammadu Buhari General Hospital Jega

Variables	Negative samples (%)	Positive Samples (%)	Total samples (%)
Sex			
Male	70 (56)	8 (61.54)	78 (56.52)
Female	55 (44)	5 (38.46)	60 (43.47)
Age			
10-25	38 (30.4)	2 (15.38)	40 (33.58)
26-41	32 (25.6)	7 (53.85)	39 (29.43)
42-57	31 (24.8)	3 (23.08)	34 (22.64)
58-73	20 (24.8)	1 (7.69)	21 (11.32)
74-90	4 (3.2)	0 (0)	4 (3.01)
Total	**125 (90.58)**	**13 (9.42)**	**138 (100)**

Prevalence of K. pneumoniae infection among patients attending General Hospital Jega

Out of one hundred and thirty eight (138) clinical samples that were collected from patients attending (AMBGHJ). The significant number of Klebsiella pneumoniae was observed in 13/138 (9.42%). However, the prevalence of Klebsiella pneumoniae was highest in the adolescent age group ranging from 26–41 with 7/13 (53.85%) as compared to the lowest value of 1/13 (7.69%) in the age group of 58-73 Table 2. Klebsiella pneumoniae infections were highest in males with 8/13 (61.54%) as compared to females with 5/13 (38.46%) Table 3. The sputum sample had the highest yield with 8/13 (61.54%), then followed by Urine samples with 3/13 (23.08%) while the lowest value was observed in Blood with 2/13 (15.38%).

Table 3. Prevalence of Klebsiella pneumoniae infection in relation to Sample and gender of patients attending Aisha Muhammadu Buhari General Hospital Jega General Hospital Jega

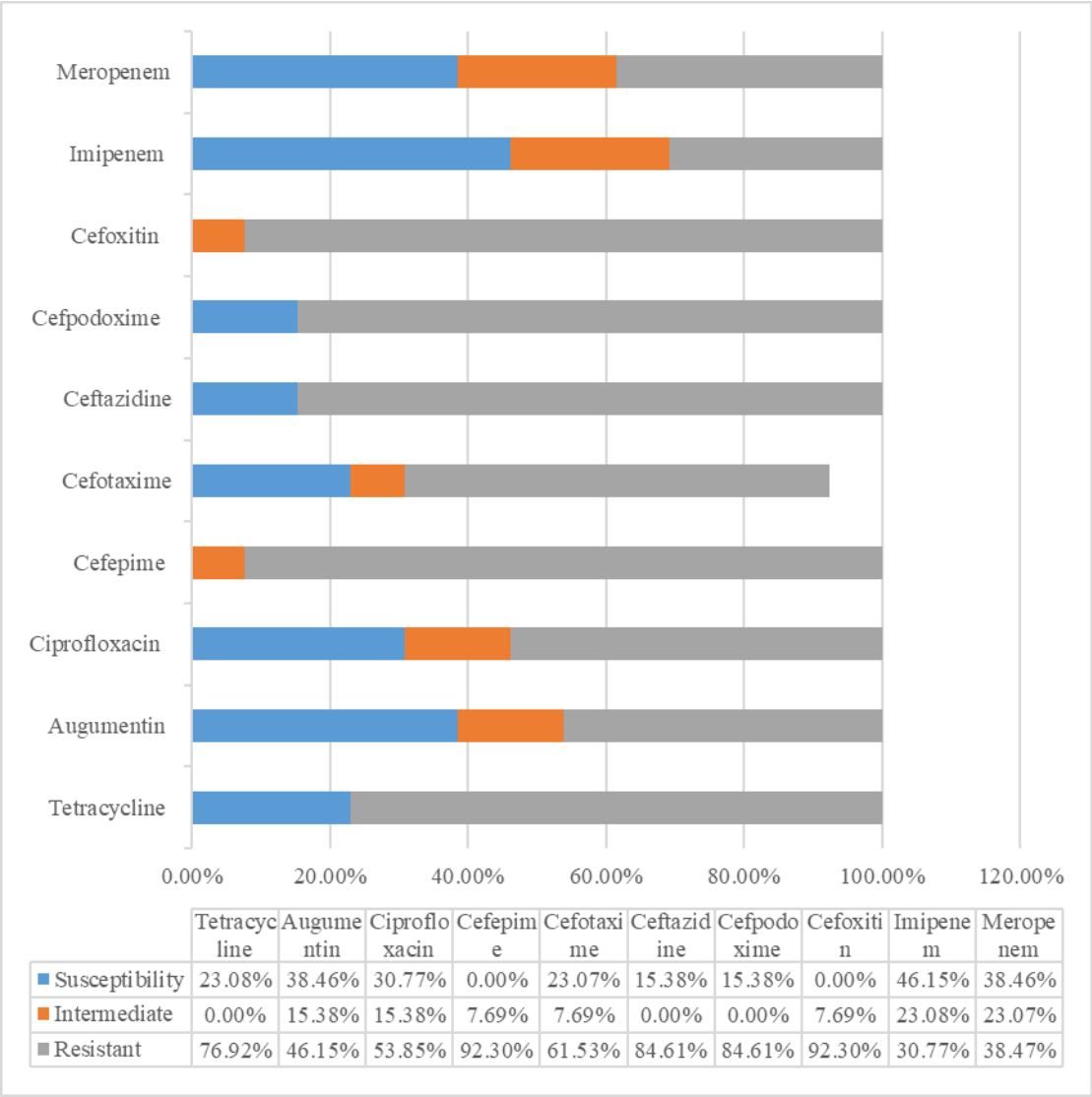
Sample	Male, n (%)	Female, n (%)	Total, n (%)
Sputum	5 (38.46)	3 (23.08)	8 (61.54)
Blood	2 (15.38)	0 (0)	2 (15.38)
Urine	1 (7.70)	2 (15.38)	3 (23.08)
Total	**8 (61.54)**	**5 (38.46)**	**13 (100)**

Screening of Antibiotic Resistance Profile of Klebsiella pneumoniae Isolates

The antibiotic resistance profile of Klebsiella pneumoniae isolates was determined using nine (10) different antibiotics as depicted in Table 4. Cefepime 12/13 (92.30%), and Cefoxitin 12/13 (92.30%), followed by Ceftazidine 11 (84.61%), and Cefpodoxime 11/13 (84.61%), then Tetracycline 10/13 (76.92%), Cefotaxime 8/13 (61.53%). While Imipenem 9/13 (69.23%), was the most sensitive drug then followed by Meropenem 8/13 (61.53%), Augumentin 7/13 (53.84%), and Ciprofloxacin 6/13 (46.15%)

Table 4. Screening of Antibiotic Resistance Profile in K. pneumoniae isolated from a patient in Aisha Muhammadu Buhari General Hospital and Jega.

Antibiotics	Disc potency (µg) Number of isolates (n=13)	Susceptible, n (%)	Intermediate, n (%)	Resistant, n (%)
Tetracycline	30	2 (15.38)	1 (7.69)	10 (76.92)
Augumentin	30	4 (30.77)	2 (15.38)	7 (53.85)
Ciprofloxacin	5	3 (23.08)	4 (30.77)	6 (46.15)
Cefepime	30	1 (7.69)	0 (0)	12 (92.30)
Cefotaxime	30	3 (23.08)	2 (15.38)	8 (61.53)
Ceftazidine	10	1 (7.69)	1 (7.69)	11 (84.61)
Cefpodoxime	10	2 (15.38)	0 (0)	11 (84.61)
Cefoxitin	30	1 (7.69)	0 (0)	12 (92.30)
Imipenem	10	6 (46.15)	3 (23.08)	4 (69.23)
Meropenem	10	7 (53.85)	1 (7.69)	5 (38.46)



	Tetracycline	Augumentin	Ciprofloxacin	Cefepime	Cefotaxime	Ceftazidine	Cefpodoxime	Cefoxitin	Imipenem	Meropenem
Susceptibility	23.08%	38.46%	30.77%	0.00%	23.07%	15.38%	15.38%	0.00%	46.15%	38.46%
Intermediate	0.00%	15.38%	15.38%	7.69%	7.69%	0.00%	0.00%	7.69%	23.08%	23.07%
Resistant	76.92%	46.15%	53.85%	92.30%	61.53%	84.61%	84.61%	92.30%	30.77%	38.47%

Figure 2. Resistant pattern of K. pneumoniae isolated (n=13)

Phenotypic Screening and Confirmation of Extended Spectrum Beta-Lactamase production (ESBLs) among K. pneumoniae isolates n=13, by Double Disk Synergy Test (DST)

Out of ten (10) Klebsiella pneumoniae isolates that are resistant to more than two drugs in third-generation cephalosporin antibiotics upon routing antibiotic susceptibility testing out of the total 13 Klebsiella pneumoniae isolates, that were isolated during the present study in (AMBGJ). The 10 suspected isolated were further subjected to phenotypic screening and a confirmation test, were revealed that only 8 (80%) out of the total 10 isolates was confirmed positive for ESBLs enzymes producing Klebsiella pneumoniae isolates, while 2 (20%), were ESBLs enzymes producing negative as shown in Table 5.

Table 5. Phenotypic Tests of ESBLs production of K. pneumoniae isolates n=13, based on by (DDST) Test

Number of suspected ESBLsp (%)	Number of confirmed ESBLsp negative (%)	Number of confirmed ESBLsp positive (%)
10 (100)	2 (20)	8 (80)

Detection of ESBL BlaTEM Gene

Out of 8 phenotypically confirm positive ESBL producing isolates only 4/8 (50%) isolates amplified the BlaTEM gene among the 8 K. pneumoniae isolates respectively.

DISCUSSION

Thirteen (13.0) K. pneumoniae isolates was yield during the present study course, from the whole (138), clinical samples that were cultured, which comprised sputum, urine, and blood samples that were aseptically collected from Aisha Muhammadu Buhari General Hospital Jega (AMBGHJ) respectively. The prevalence rate in this report was recorded as (9.42%) as shown in Table 2. A comparatively similar study was reported from Enugu State, Nigeria with a prevalence rate of (10.47%) by (Aneke et al., 2022), and is in line with findings reported from Niger State, with a prevalence rate of (13.07%) which yielded various clinical samples (Oyedum et al., 2022). And consequently, this study is partially similar to our reports but a little bit higher to a study done at a Tertiary Care Hospital in Bangladesh where the isolates are yielded from various clinical specimens of urine, wound swab, sputum, endotracheal aspirates, and blood, (15%) (Sonia et al., 2020). However this report is contrary to our study, (34%) (Orole et al., 2020), and to a study conducted at Tertiary Care Hospital, Jaipur, Rajasthan, India (30.15%) (Ashina et al., 2021), and another report was K. pneumoniae accounted for (14.5%) (Asati et al., 2013). Furthermore, this study, however, recorded a prevalence rate lower than our study (6.85%) (Zaharaddin et al., 2023) and a previous study reported from Kaduna with a lower rate (4.21%) isolated from different clinical samples by (Iliya et al., 2021), and with a report conducted among of Federal Polytechnic Bida, Niger State Nigeria with (5.7%) (Alfa et al., 2022). And our study is contrary to a study reported from Osun State Southwestern Nigeria, where K. pneumoniae isolates were yielded from various clinical samples with a prevalence rate of (5.87%) (Akingbade et al., 2019). These variations and differences in terms of lower or higher rates of isolation may be due to the sample size variation or differences in geographical locations.

The isolates of Klebsiella pneumoniae identified in clinical cultures of patients attending (AMBGHJ) exhibited varying levels of resistance to the antibiotics tested as shown in Table 4 and Figure 2. The highest resistance was recorded in Cefepime (92.30%), and Cefoxitin (92.30%), followed by Ceftazidine (84.61%), and Cefpodoxime (84.61%), then Tetracycline (76.92%), Cefotaxime (61.53%). On the other hand, some drugs exhibited lower resistance rate Imipenem was the lowest (69.23%), followed by Meropenem (61.53%), Augumentin (53.84%), and Ciprofloxacin (46.15%) as indicated in Table 4 respectively, this study is comparatively similar with findings from Kebbi State, about Cefotaxime (74%) and Ceftazidine (66%) (Kalgo et al., 2022), and with a report from Nasarawa State were Cefexime (46.9%) Cefotaxime (53.0%) Ciprofloxacin (65.3%) Ceftazidime (55.1%) (Ngwai et al., 2023). And with a study, reported the resistance rate to Cefotaxime as 54(72.00%), Ceftazidime (74.67%), Ciprofloxacin (89.33%) (Sonia et al., 2020). However, the resistance rate recorded from our present study toward tetracycline (77.78%), confer corroborates findings a result by (Olusola et al., 2013) where they recorded Tetracycline with the resistance of (75.20%) and (65.2%) were also reported by (Orole et al., 2022) respectively, a similar study was also reported from Anyigba, in Dekina, Kogi State, Nigeria concerning Cefoxitin (62.5%), Cefotaxime (100%), Ceftazidime

(41.7%), and Ciprofloxacin (75.0%) by (Mofolorunsho et al., 2021). Study conducted at Nnamdi Azikiwe University among the students residing in the university campuses located along Agulu, Mbaukwu and Awka, Anambra State, Nigeria also recorded similar result with regard to Cefpodoxime (100%), and Tetracycline (85.0%) which was reported by (Chidimma et al., 2018).

Furthermore, this study is in agreement with a previous study reported from Lafia, Nasarawa State, with respect to Imipenem as the most sensitive drugs with (83.67%), while its differ in terms of Augumentin with (36.73%) (Ngwai et al., 2023), also similar with a study reported from Tertiary Care facility located at Bangladesh were recorded Imipenem and Meropenem with equal percentage as the most sensitive with (62.66%) then consequently followed by Augumentin with (25.33%) which differ from our report (Sonia et al., 2020) These antibiotics can consider as alternative options for empirical therapy for K. pneumoniae infections. However comparatively different results were reported with a percentage of susceptibility to Meropenem (25%) and Imipenem (18.75%) (Aljanaby & Alhasani, 2016) and another result reported Meropenem (88%) and Imipenem with (90%) followed by Augumentin (48%) (Sharanya et al., 2018). Consequently, our present differs from a report conducted at kano Metropolis, Nigeria where they recorded (100%) resistant isolates in Cefotaxime, Ceftazidime and Augumentin toward 10 clinical isolated of K. pneumoniae from patient suspected of urinary tract infections by (Muhammad et al., 2019), also with a report from Kebbi were Ciprofloxacin (0%), and Ceftazidime (80.0%) recorded as such by (Danlami et al., 2019), and with a study conducted at Ahmadu Bello University Teaching Hospital, Zaria, they recorded resistance of tetracycline, with (50%), ciprofloxacin, (50%) to and amoxicillin-clavulanate (42%), cefotaxime (30%), and Ceftazidime (30%) respectively which is contrary to our present findings (Abdulfatai et al., 2023).

These observed differences could be due to regional and attitudinal behavior towards the prescription and consumption of antibiotics especially the cephalosporins in both hospital and community settings or this alarming resistance may be due to indiscriminate use of these antibiotics in the study location. And as a result of the ability of bacteria isolates to produce Beta-lactamase which can hydrolyse the ring Beta-lactam, there by inactivating the drugs, primarily third generation cephalosporins drugs (Ali et al., 2014). Prevalence of ESBLs-Producing K. pneumoniae was asses, however the occurrence of ESBLs amidst of isolates varies greatly worldwide, and is rapidly changing over time (Turugurwa et al., 2019). The rate of percentage in ESBL production in different K. pneumoniae isolate was cleared in Table 5, in our present study, ESBL phenotypes were found to be positive in 8/10 (80%), out of 10 K. pneumoniae isolates, this demonstrating a high prevalence of ESBL production, our study is partially similar with a study reported by (Zaghloul et al., 2021) with (56.3%) and another reported from Latin America were ESBL producing K. pneumoniae was recorded as (54.4%) (Aminazadeh et al., 2008). However differs with study conducted at Zaria which reported (40%) prevalence of ESBL producing isolates (Giwa et al., 2018) and (40.7%) different results was reported from Port Harcourt Southern, Nigeria (Lawson et al., 2021) And also with a report of (26.5%) has been reported in Ilorin, which quite differ with our report by (Fadeyi et al., 2016). These observed differences could be due to regional and attitudinal behavior towards prescription and consumption of antibiotics especially the cephalosporins in both hospital and community settings.

Molecular analysis using polymerase chain reaction showed that most of the isolates possess BlaTEM gene 4/8 (40%), after subjecting all ESBL positive upon screening and confirmatory test by DDST respectively. Our report is comparatively similar with a study were recorded 24 (48.5%) (Orole et al., 2020),

and with another research conducted in in Egypt, with (67. 6%) (Ahmed & Shimamoto, 2011). However this report varies from a study conducted at Sokoto, in which out of 36 clinical isolates 19 (14.7%) was detected with BlaTEM gene (Olowo-okere et al., 2020) and also with another work reported that (93.75) (Aljanaby & Alhasani, 2016).

CONCLUTION

The prevalence of K. pneumoniae in our facility was 9.42% and found to be resistant to many antibiotics, also possessed resistance gene. Therefore, it is imperative that all laboratories develop sound antibiotic policies and identify drug resistance mechanisms. It is necessary to implement an appropriate antibiotic stewardship program. This will aid in the detection and eradication of newly emerging strains of multidrug resistance.

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AUTHOR'S CONTRIBUTION

Muhammad, S., Bagudo, A. I., Manga, S. S., Aliero, A. A., Jibo, G. G., and Muhammad, U. conceived the study and participated in its design and coordination. Muhammad, S., Bagudo, A. I., Muhammad, U., and Mohammed, S. performed sample collection and analysis. Muhammad, S., Bagudo, A. I., and Manga, S. S., analyzed the results. Muhammad, S., and Bagudo, A. I., drafted the manuscript.

CONFLICT OF INTEREST

All authors have no competing interests.

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DISCLOSURE OF CONFLICT OF INTEREST

We hereby declare that there is no competing interests as the authors of this paper.

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