

Phenotypic Characterization and Resistance Trends of *Klebsiella pneumoniae* from Selected Hospitals in Ilorin, Kwara State Nigeria

*¹Abdulmalik Aliyu, ¹Susan M. David, ¹Ronke H. Bello, ¹Haisat Y. Olufadi-Ahmed, ¹Muhammed A. Sani, ²Lateef A. Akinpelu, ¹Ummkhair O. Abdussalam, ¹Oyinnoza Mamman, ¹Oluwapelumi M. Gbade, ¹Islamiyat O. Salman, ³Mohammed Naibi ⁴Abiodun O. Shittu, ⁵Ngaistad S. Njinga.

¹Department of Pharmaceutical Microbiology & Biotechnology, University of Ilorin, Ilorin, Nigeria

²Department of Pharmacology and Toxicology, University of Ilorin, Nigeria.

³Department of Microbiology, Federal University Gusau, Gusau, Nigeria

⁴Department of Pharmaceutics & Industrial Pharmacy, University of Ilorin, Ilorin, Nigeria

⁵Department of Pharmaceutical & Medicinal Chemistry, University of Ilorin, Ilorin, Nigeria

*Corresponding Author's Email & Phone No.: alivu.a@unilorin.edu.ng, +2348037553870

Received on: April, 2025

Revised and Accepted on: May, 2025

Published on: July, 2025

ABSTRACT

Klebsiella pneumoniae has emerged as a formidable pathogen, complicating the treatment of infections in healthcare settings. In this study, we examined the phenotypic characteristics and resistance trends of *K. pneumoniae* isolates from 150 clinical samples - including urine, blood, and deep throat sputum - collected from selected hospitals in Ilorin, Nigeria. Forty-nine isolates were recovered, with a predominance among female patients and individuals aged 18 - 40 years. Identification and antimicrobial susceptibility testing were performed using standard bacteriological methods and a modified Kirby-Bauer disc diffusion technique. The findings revealed a concerning level of resistance to cephalosporins and beta-lactam/β-lactamase inhibitor combinations, whereas aminoglycosides, carbapenems, and fluoroquinolones demonstrated relatively higher susceptibility rates. Notably, the majority of the isolates exhibited multidrug resistance, with several showing high Multiple Antibiotic Resistance Index values that underscore the significant antibiotic pressure in the clinical environment. These results highlight the urgent need for enhanced antibiotic stewardship and continuous surveillance to inform targeted treatment strategies. The insights gained from this study provide crucial data for developing effective interventions aimed at curbing the spread of multidrug-resistant *K. pneumoniae* and ultimately improving patient outcomes in resource-limited settings.

Keywords: Antibiotic Resistance, *Klebsiella pneumoniae*, β-Lactamase, MARI, MDR

1.0 INTRODUCTION

1.1 Background Information

The overuse and misuse of antibiotics have given rise to microorganism strains that are resistant to available antibiotics creating 'superbugs' that are constituting a menace to the global health (Salam *et al.*, 2023). In 2019, antimicrobial resistance (AMR) was reported to have caused an estimated 4.95 million deaths globally (Murray *et al.*, 2022). The increase in resistance to antimicrobial agents among common bacteria is jeopardizing the successful clinical outcomes that was attributed to antibiotic therapy. Additionally, the rate at which resistance to antibiotics is developing and spreading globally exceeds the strategies in place to alleviate the crisis (Iskandar *et al.*, 2022). This has led to the listing of antibiotic resistance among the three most important public health threats of the 21st century (Salam *et al.*, 2023). Antibiotics are antimicrobial agents used to combat bacterial infections but unfortunately, these organisms has developed the ability to withstand the presnce of these agents leading to resistance (Muteeb *et al.*, 2023). Antibiotic resistance (AMR) occurs as a result of natural biological phenomenon that occurs among

these organisms in order to safeguard the lethal selection pressure (Peterson and Kaur,2018). One of the most successful bacterial strategies to evade the action of antibiotics is the inactivation of the antibiotic molecule by production of enzymes that inactivate the drug (Munita & Arias, 2016). These enzymes can 1) chemically alter the antibiotics as seen in aminoglycoside modifying enzymes or 2) destroy the antibiotic molecule itself (Munita & Arias, 2016; Peterson and Kaur, 2018). *K. pneumoniae* has a number of mechanisms to counteract the effects of antibiotics among which are possession of efflux pump genes, which alter membrane porosity, the production of inactivating enzymes, and modifications to the target site (Li *et al.*, 2023). Two major enzyme-mediated mechanisms involved in resistance that have been demonstrated in *Klebsiella pneumoniae* are the β-lactamases-production and carbapenemases production, infections caused by these strains are associated with higher morbidity and mortality rates than non-resistant strains (Karampatakis *et al.*, 2023). Aminoglycoside modifying enzymes have also been reported in *Klebsiella pneumoniae* (Essalhi *et al.*, 2024). In recent is the emergence of virulence strains of *Klebsiella* which are

attributed to capsules in encapsulated strains, lipopolysaccharide, siderophores and fimbriae. (Karampatakis *et al.*, 2023). The spread and circulation of these AMR phenomenon is facilitated by biological determinant which involves both horizontal and vertical transfer of resistant genes as well as human determinant such as over use of antibiotics in agriculture and healthcare sector, migration and globalization (Salam *et al.*, 2023).

1.2 Statement of Problem

Antibiotic resistance among the Enterobacteriaceae is a common phenomenon particularly with the β -lactams antibiotics have been documented by several researchers especially common among *Escherichia coli* and *Klebsiella pneumoniae* that are important causes of several systemic infections (Peterson and Kaur, 2018; Lynch *et al.*, 2021; Rong *et al.* 2023) . *Klebsiella pneumoniae* is a Gram-negative encapsulated, sessile bacterium from the family Enterobacteriaceae, it is one of the main pathogens responsible for pneumonia infection and is found in soil, surface waters, human stool, gastrointestinal tract of patients, hospital environment and can be responsible for nosocomial infection (Ashurst & Dawson, 2023). In addition to pneumonia, *Klebsiella pneumoniae* can invade other tissues and can cause various infections such as cellulitis, meningitis, urinary tract infections, liver abscesses, blood infections, skin and wound infections. *Klebsiella pneumoniae* has become notorious for causing serious and increasingly life-threatening infections that are not responsive to antibiotics treatments, this is due to the widespread of hypervirulent and resistant strains and thus Multi-drug resistant (MDR) *K. pneumoniae* has increasingly been a major public health threat (Shah *et al.*, 2025), leading to high human and economic burden as a result of increased morbidity, prolong hospital stay, high cost of treatment and in extreme cases mortality (Itani *et al.*, 2024).

1.3 Relevance of the study

Globally, several studies has reported antibiotic resistance among *Klebsiella pneumoniae* isolated from a wide range of clinical sources (Giubelan *et al.* 2021; Oladipo *et al.* 2021) there is still need for continuous surveillance of antimicrobial resistance among *Klebsiella pneumoniae* through the collection of valid antimicrobial resistance information which will aid the understanding of their antibiogram profile to develop strategies to curb the widespread dissemination and provide effective empirical therapy to alleviate human burden and suffering.

1.4 Objective of the study

This study aim to investigate the antibiogram profile of characterized *Klebsiella pneumoniae* isolates associated

with varying clinical samples within two selected hospitals in Ilorin with the aim to design an effective intervention strategies in order to improve wellbeing.

2.0 MATERIALS AND METHOD

2.1 Materials

Nutrient Agar (NA), MacConkey Agar (MCA), Muller Hinton agar (MHA), and oxidase strips were obtained from Oxoid, England. Analytical Profile Index (API 20E) kit, selected antibiotics discs (Mast Group Ltd), sterile antibiotic disc dispenser (Mast Group Ltd in Merseyside, UK).

2.2 Ethical Consideration

The ethical approval was issued by the State Ministry of Health, Ilorin with the approval number ERC/MOH/2023/03/095 after careful consideration of the study protocol.

2.3 Sample Collection

A total of 150 samples were were collected from a hospital in Ilorin. The type of samples collected from patients were urine (77), blood (51) and deep throat sputum (22) were collected from the Pathology Unit, Microbiology Laboratory of the two selected hospitals from April, 2023 to June, 2023.

2.4 Isolation and Identification of *Klebsiella* isolates

Isolation of *Klebsiella* species were carried from collected samples using standard bacteriological protocols as described by Cheesbrough (2006). Samples were cultured on MacConkey Agar and incubated 37°C for 24 hours. Post 24 hours incubation, plates that yielded distinct pink mucoid colonies due to their ability to ferment lactose were deemed as presumptive *Klebsiella* isolates. These isolate were purified by repeated subculturing and preliminarily identified using Gram reaction, and oxidase.

Further confirmatory identification was carried out on the isolates using Analytical Profile Index (API 20E) kit and the octal codes generated were interpreted using the software as described by the manufacturer. Finally, pure and identified *Klebsiella pneumoniae* were maintained on sterile nutrient agar slants, and stored in the refridgerator at 4°C until needed.

2.5 Determination of Antibiotic susceptibility testing for *Klebsiella pneumoniae* isolates

The antibiotic susceptibility testing of confirmed *Klebsiella pneumoniae* isolates was determined using modified Kirby-Bauer disc-diffusion technique as described by Ndzime *et al.* (2023) . Ten (10) pannel of antibiotics of antibiotics including Ceftriaxone (5 μ g),

Cefepime (30µg), Cefotaxime (5µg), Amoxicillin/Clavulanic acid (30µg), Ceftazidime (10µg), Tobramycin (10µg), Imipenem (10µg), Levofloxacin (5µg), Kanamycin (30µg), and Ampicillin/Sulbactam (20µg) were used.

Standardized inoculum of 0.5 McFarland turbidity containing 1.5×10^8 CFU/mL of freshly subcultured test bacteria were inoculated by swabbing using sterile cotton swab on the surface of MHA and left to dry for 5 minutes. Aseptically, selected antibiotic discs were placed on the MHA using a sterile antibiotic disc dispenser. Subsequently, the plates were incubated at 37°C for 18 hours, and the inhibition zone diameter for each antibiotic was measured in millimeter using a meter rule and interpreted using the EUCAST, 2022 interpretative chart which allows the classification of isolates as sensitive “S” or resistant “R”.

2.5.1 Determination of Multiple Antibiotic Resistance Index

The Multiple Antibiotic Resistance (MAR) Index was determined according to the protocol of by Ndzime *et al.* (2023). It was obtained by taking the ratio of the number of antibiotics to which the *Klebsiella pneumoniae* isolates exhibited resistance (*a*) to the total number of antibiotics tested against the organism (*b*).

Given as;

$$\text{MAR Index} = a/b$$

2.5.2 Determination of Antibiotic Resistance phenotypes

The Multiple Antibiotic Resistance (MAR) Index was determined according to the protocol of by Konaté *et al.* (2017). It was obtained by taking the combination of antibiotics to which the *Klebsiella pneumoniae* isolates exhibited resistance hence the determination of their resistant phenotypes.

2.5.3 Determination of Antibiotic Resistance category

The Antibiotic Resistance category was determined according to the protocol of by Magiorakos *et al.* (2011) which classify it the *Klebsiella pneumoniae* isolates as Multidrug resistant (MDR), Extensive Drug Resistant (XDR) or Pandrug-resistant (PDR) Isolates.

2.6 Data Analysis

All data obtained were organized and analysed using frequency, percentages, bar chart and tabular presentations.

3.0 RESULT

3.1 Isolation and Identification of *K. pneumoniae* isolates

From the 150 non-duplicate samples collected and 49 *Klebsiella pneumoniae* isolates were identified from urine 25 (51%), deep throat 21 (32.7%), and blood 8 (16.3%) with an overall isolation rate of 32.67 % as shown in Table 1. The highest (77.6%) number of *Klebsiella pneumoniae* isolates were obtained from female patients within the age range of 18- 40 years yielded the highest number of 21 (42.9%) of isolates as presented in Table 2.

Table 1: Distribution of *Klebsiella pneumoniae* Isolates by specimen

Isolate Source	No of Samples collected (n=150)	<i>Klebsiella pneumoniae</i> (n=49) No (%)
Urine	77	25 (51.0)
Blood	51	8 (16.3)
Deep throat sputum	22	16 (32.7)
Total	150	49 (32.67)

Table 2: Percentage Distribution of *Klebsiella pneumoniae* isolates among age-group and gender

Age range (years)	Subjects harboring <i>Klebsiella pneumoniae</i> isolates		Total (%)
	Male (%)	Female (%)	
0 – 17	2 (4.1)	7 (14.3)	9 (18.4)
18 – 40	6 (12.2)	21 (42.9)	27 (55.1)
41 and above	3 (6.1)	10 (20.4)	13 (26.5)
Total	11 (22.4)	38 (77.6)	49 (100)

3.2

Antibiotic Susceptibility Testing and Multiple Antibiotic Resistance Index (MARI) of *K. pneumoniae* Isolates

The *Klebsiella pneumoniae* isolates exhibit high resistance to cephalosporins, with cefotaxime,

ceftazidime, cefepime, and ceftriaxone showing resistance rates above 70%. Beta-lactam/β-lactamase inhibitor combinations (amoxicillin/clavulanic acid and ampicillin/sulbactam) also demonstrate limited effectiveness, with over 60% resistance and a notable

proportion of intermediate responses. These findings indicate that cephalosporins and β -lactam inhibitors may not be the best treatment choices for infections caused by these isolates.

Among the tested aminoglycosides, tobramycin appears to be the most effective, with 63.3% susceptibility, while kanamycin shows moderate activity (42.9% susceptibility). Carbapenems (imipenem) and fluoroquinolones (levofloxacin) also demonstrate relatively higher susceptibility rates (57.1% and 61.2%, respectively) as shown in Table 3, making them more promising options. However, their intermediate and resistance rates still highlight the need for careful selection based on susceptibility testing.

The phenotypic resistance pattern of *Klebsiella pneumoniae* isolates indicates varying levels of resistance to multiple antibiotics. The resistance profiles range from non-multiple antibiotic resistance index (MARI) isolates to those exhibiting high (\geq) MARI values as indicated in Table 4. The increasing MARI values among 91.8 % isolates suggest significant antibiotic pressure and the potential spread of resistant clones. The presence of

resistance to last-resort antibiotics (IMI, K, LEV) is alarming (Table 4) and highlights the need for stringent antibiotic stewardship. The most resistant isolates (4.1%) displayed resistance to nearly all tested antibiotics, including β -lactams, carbapenems, aminoglycosides, and fluoroquinolones.

3.3 Antibiotic Resistance category of *Klebsiella pneumoniae* isolates

The distribution of *Klebsiella pneumoniae* isolates based on antimicrobial resistance (AMR) levels is categorized into non-multidrug-resistant (non-MDR), multidrug-resistant (MDR), extensively drug-resistant (XDR), and pandrug-resistant (PDR) groups. The majority of isolates fall into the MDR category (59.2%), with a substantial proportion exhibiting resistance to at least three antibiotic classes. A smaller percentage of isolates are classified as XDR (6.1%), demonstrating resistance to nearly all tested antibiotic categories except for one. Meanwhile, PDR (4.1%) isolates, which are resistant to all tested antibiotics as shown in Figure 1, are the least common but present a significant clinical challenge.

Table 3: Overall Antibiotic Susceptibility and Resistance Profile of *K. pneumoniae* Isolates

Antibiotic Discs	Number and percentage (%) of Susceptible Isolates	Number and percentage (%) of Resistant Isolates	Number and percentage (%) of Intermediate Isolates
Cefotaxime (5 μ g)	2 (4.1)	46 (93.9)	1 (2.0)
Ceftazidime (10 μ g)	1 (2.0)	42 (85.7)	6 (12.2)
Cefepime (30 μ g)	2 (4.1)	36 (73.5)	11 (22.4)
Ceftriaxone (5 μ g)	3 (6.1)	39 (79.6)	7 (14.3)
Amoxicillin/Clavulanic Acid (30 μ g)	5 (10.2)	30 (61.2)	14 (28.6)
Ampicillin/ Sulbactam (20 μ g)	4 (8.2)	30 (61.2)	15 (30.6)
Kanamycin (30 μ g)	21 (42.9)	13 (26.5)	15 (30.6)
Tobramycin (10 μ g)	31 (63.3)	13 (26.5)	5 (10.2)
Imipenem (10 μ g)	28 (57.1)	14 (28.6)	7 (14.3)
Levofloxacin (5 μ g)	30 (61.2)	9 (18.4)	10 (20.4)

Table 4: Phenotypic Resistance Pattern of *Klebsiella pneumoniae* Isolates

ISOLATE CODE	NO. OF ORGANIS		PHENOTYPIC RESISTANCE PATTERN	MARI
	M			
CP020	1		CAZ	Non-MARI
AU013	1		CTX, AUG	Non-MARI
GB069	1		CTX, CAZ	Non-MARI
GB 029	1		CTX, SAM	Non-MARI
CP039	1		CAZ, CPM, CRO	0.3
AU035, AU045	2		CRO, AUG, TN	0.3
AU024, GB 066, CP017	3		CTX, CAZ, CPM, CRO	0.4
GB 018	1		CTX, SAM, CAZ, AUG	0.4
CP031	1		CTX, CAZ, AUG, SAM, LEV	0.5
F026	1		CTX, CAZ, CPM, AUG, SAM	0.5
AU040, CP40	2		CTX, CAZ, CPM, CRO, AUG	0.5
F007, M022	2		CTX, CAZ, CPM, CRO, LEV	0.5
F008	1		CTX, CAZ, CPM, CRO, SAM	0.5
CP029	1		CTX, CAZ, CPM, CRO, TN	0.5
AU010	1		CTX, CAZ, CRO, SAM, AUG	0.5
CP048	1		CTX, CAZ, CRO, SAM, K	0.5
GB052	1		CTX, CPM, CRO, AUG, SAM	0.5
GB 051	1		CTX, LEV, SAM, CAZ, AUG	0.5
AU022, GB 050, F027, F017	4		CTX, CAZ, CPM, CRO, AUG, SAM	0.6
CP019	1		CTX, CAZ, CPM, CRO, K, LEV	0.6
GB076	1		CTX, CAZ, CPM, CRO, K, TN	0.6
AU008	1		CTX, CAZ, CPM, CRO, SAM, K.	0.6
F036	1		CTX, CAZ, K, TN, IMI, LEV	0.6
CP008	1		CTX, CPM, CRO, SAM, K, LEV	0.6
AU016	1		CTX, CAZ, CPM, CRO, AUG, K, TN	0.7
F021, F040, M030, M047	4		CTX, CAZ, CPM, CRO, AUG, SAM, LEV	0.7
AU027, AU005, GB077, CP035	4		CTX, CAZ, CPM, CRO, SAM, AUG, IMI	0.7
CP011	1		CTX, CAZ, CRO, AUG, SAM, LEV, IMI	0.7
GB031	1		CTX, CPM, CRO, AUG, SAM, K, TN	0.7
GB055, GB006	2		CTX, CAZ, CPM, CRO, AUG, SAM, K, TN	0.8
F004	1		CTX, CAZ, CPM, CRO, AUG, SAM, K, TN, LEV	0.9
AU039	1		CTX, CAZ, CPM, CRO, SAM, AUG, K, TN, IMI	0.9
CP005, AU019	2		CTX, CAZ, CPM, CRO, AUG, SAM, K, TN, LEV, IMI	1.0
TOAL	49			

Key; CTX- Cefotaxime, CAZ- Ceftazidime, CPM- Cefepime, CRO- Ceftriaxone, AUG- Amoxicillin/Clavulanic acid, SAM- Ampicillin/Sulbactam, K- Kanamycin, TN- Tobramycin, LEV- Levofloxacin, IMI- Imipenem, of *K. pneumoniae* Isolates

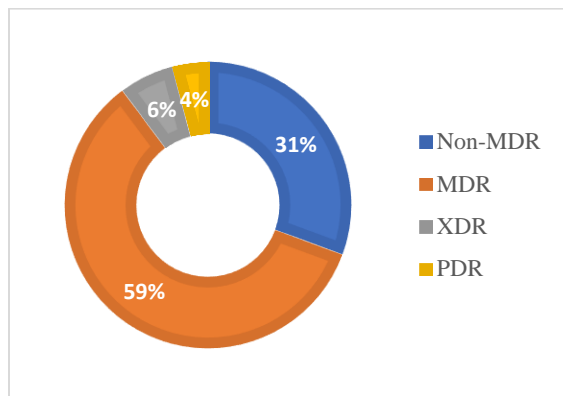


Figure 1: Classification of Levels of AMR of *Klebsiella pneumoniae* Isolates

4.0 DISCUSSION

Klebsiella pneumoniae has a high propensity to acquire antimicrobial resistance genes that limits its treatment options, it has the ability to acquire and transfer antimicrobial resistance genes through plasmids, transposons, integrons, and other mobile genetic elements (Han *et al.*, 2025). It causes a wide range of infections using different virulence factors to colonize and spread in the human body. The increasing antimicrobial resistance has caused hindrance to clinical treatment and Infection control, causing a menace in the health sector (Giubelan *et al.*, 2021). This study aims to provide information on the resistance pattern of *K. pneumoniae* isolated from selected hospitals within Ilorin.

The highest resistance was observed among the cephalosporin and penicillin class, thirty-six (36) isolates exhibited resistance to all the cephalosporins used while the remaining isolates were resistant to at least one cephalosporin, the highest was observed in cefotaxime (93.9%), ceftaxidime (85.7%) and ceftriaxone (79.6%), this is likely because of the widespread use of the antibiotics in the empirical treatment of several infections. High (61.2%) of the isolates were resistant to amoxicillin/clavulanic acid and ampicillin/sulbactam respectively, it was also observed that majority of the isolates that were resistant to more than one cephalosporins showed resistance to amoxicillin/clavulanic acid or ampicillin/sulbactam or both. Resistance to cephalosporins and co-resistance to cephalosporin and penicillin concurs with the findings of Santella *et al.*, (2024) and probably suggest the presence of Extended Spectrum Beta- Lactamases (ESBLs) such as blaSHV, blaNDM, blaTEM, blaKPC, or bla CTX-M (Awoke *et al.*, 2021) capable of hydrolyzing such antibiotics.

Moreso, 28.6% of the isolates showed resistance to Imipenem. It was observed that all isolates resistant to imipenem (28.6%) were also exhibited resistance to cephalosporins and penicillins used. This may be attributed to high level of abuse, misuse and overuse and possibly suggesting the presence of multiple resistance genes in the *K. pneumoniae* such as ESBLs and carbapenemases are able to hydrolyze carbapenems and most other beta-lactams. Some examples of carbapenemases are KPC (class A), NDM, VIM, IMP (class B), and OXA-48-like (class D) (Alvisi *et al.*, 2025). This co- resistance of Imipenem with cephalosporins and/or penicillins observed in this study is in concordance with Yang *et al.* (2020) which documented high resistance among carbapenem-resistant *Klebsiella pneumoniae* (CRKP) isolated from different clinical samples in China over the years which are of great clinical concern thus making the treatment difficult.

Furthermore, 18.4% isolates showed resistance all selected classes of antibiotics used in this study including levofloxacin. This exhibited multidrug resistance (MDR) probably suggest the emergence of ESBLs and carbapenem-resistant mediated by high level misuse of these antibiotics leading to selective pressure within the study area. This is in tandem with the finding of Okesanya *et al.* (2024) among different clinical isolates of *K. pneumoniae* in Asaba, Delta state – Nigeria, however with a higher percentage occurrence of 33.3%. Other notable resistance observed was resistance to tobramycin and kanamycin. Aminoglycoside resistance in *K. pneumoniae* is primarily due to Aminoglycoside Modyfying Enzymes (AMEs) which have three subclasses AACs, APHs and ANTs, uncommon genes include the 16S-RMTases such as ArmA and RMTases. One of the AMEs that have been characterized from *K. pneumoniae* isolates that exhibited resistance to tobramycin and kanamycin is aac (6') II enzyme (Vaez and Yazdanpour, 2024) posing serious threat to treatment.

K. pneumoniae isolates (38.8 %) in this study had multiple antibiotic resistance (MAR) index of ≥ 0.3 ranging from 0.3 to 1.0 for ten (10) selected antibiotics belonging to different classes. This might be due to high level selective pressure and environmental contamination with antibiotics thus increasing the circulation of resistant bacteria within the study area. This is comparative to the 31.57% reported in Nasarrawa state (Ashefo *et al.*, 2023). However, Oladipo *et al.* (2021) reported a higher MAR Index of 82.87% from clinical isolates of *K. pneumoniae* isolated from inpatients from selected health facilities in Oyo State, suggesting varying antimicrobial

resistance across different areas. The use of the MAR Index is therefore described as a cost-effective and valid method to track the source of bacteria (Mir *et al.*, 2022).

Thirty- three (33) different antibiotics resistance phenotypes was observed in this study, this differ with the report of Ashefo *et al.* (2023) who reported 19 different antibiotics resistance phenotypes. This may probably be due to a wide variety of resistant *K. pneumoniae* circulation within the the study area, posing serious health concern, prolong hospital stay thus increasing economic and social burden.

5.0 CONCLUSION

The prevalent types of *K. pneumoniae* resistance from isolates in Ilorin hospitals was determined to be in the Cephalosporins and Penicillin class, the highest resistance was observed in the cephalosporin class specifically Cefotaxime while the highest susceptibility was observed in Levofloxacin followed by Imipenem and Tobramycin. The incidence of carbapenem and aminoglycoside resistance in the area is of great health concern because they are considered as last resort and not easily available. Further research into molecular characterization of the resistant genes in the isolates is needed to better understand the mechanisms of resistance and to help in the surveillance and development of novel drugs that will bypass already established mechanisms of resistance.

6.0 ACKNOWLEDGMENTS

The authors sincerely wish to appreciate the State General Hospital and State Ministry of Health for their support during sample collection. The authors also like to appreciate all Laboratory staff of the Department of Pharmaceutical Microbiology for their assistance and support throughout the period of the Laboratory work.

REFERENCES

- Alvisi, G., Curtoni, A., Fonnesu, R., Piazza, A., Signoretto, C., Piccinini, G., Sasser, D., & Gaibani, P. (2025). Epidemiology and Genetic Traits of Carbapenemase-Producing Enterobacterales: A Global Threat to Human Health. *Antibiotics*, 14(2), 141. <https://doi.org/10.3390/antibiotics14020141>
- Ashefo, D. P., Ngwai, Y. B. and Ishaleku, D. (2023). Isolation and Antimicrobial Resistance Phenotype of klebsiella pneumonia from the urine. *FUDMA Journal of Sciences (FJS)*, 7(1), 119–125.
- Ashurst, J.V. and Dawson, A. (2023). *Klebsiella pneumoniae*. [Updated 2023 Jul 20]. In: StatPearls [Internet]. Treasure Island (FL): StatPearls Publishing; 2025 Ja

- n. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK519004/>
- Awoke, T., Teka, B., Seman, A., Sebre, S., Yeshitela, B., Aseffa, A., ... Abebe, T. (2021). High prevalence of multidrug-resistant klebsiella pneumoniae in a tertiary care hospital in Ethiopia. *Antibiotics*, 10(8), 1–9. <https://doi.org/10.3390/antibiotics10081007>
- Cheesbrough, M. (2006). *District Laboratory Practice in Tropical Countries*. Retrieved from www.cambridge.org
- Essalhi A, Nayme K, Maaloum F, Errami A, Zerouali K, Bousfiha AA, El Kettani A. (2024). Characterization of Aminoglycoside-Modifying Enzymes in Uropathogenic Enterobacterales of Community Origin in Casablanca, Morocco. *Acta Microbiologica Hellenica*. 69(4):311-321. <https://doi.org/10.3390/amh69040028>
- Giubelan, L., Dragonu, L., Stoian, A. C., & Dumitrescu, F. (2021). Antibiotic resistance profile of Klebsiella pneumoniae strains isolated in an infectious diseases clinic. *Romanian Journal of Infectious Diseases*, 24(1), 32–37. <https://doi.org/10.37897/RJID.2021.1.4>
- Han, B., Feng, C., Jiang, Y., Ye, C., Wei, Y., Liu, J., & Zeng, Z. (2025). Mobile genetic elements encoding antibiotic resistance genes and virulence genes in Klebsiella pneumoniae: important pathways for the acquisition of virulence and resistance. *Frontiers in Microbiology*, 16(February), 1–24. <https://doi.org/10.3389/fmicb.2025.1529157>
- Lynch, J. P., Clark, N. M., & Zhan, G. G. (2021). Escalating antimicrobial resistance among Enterobacteriaceae: focus on carbapenemases. *Expert Opinion on Pharmacotherapy*, 22(11), 1455–1474. <https://doi.org/10.1080/14656566.2021.1904891>
- Itani, R., Khojah, H.M.J., Kibrit, R. et al. (2024). Risk factors associated with multidrug-resistant Klebsiella pneumoniae infections: a multicenter observational study in Lebanese hospitals. *BMC Public Health* 24, 2958. <https://doi.org/10.1186/s12889-024-20474-0>
- Karampatakis, T., Tsergouli, K., & Behzadi, P. (2023). Carbapenem-Resistant Klebsiella pneumoniae: Virulence Factors, Molecular Epidemiology and Latest Updates in Treatment Options. *Antibiotics (Basel, Switzerland)*, 12(2), 234. <https://doi.org/10.3390/antibiotics12020234>
- Konaté, A., Dembélé, R., Guessennd, N. K., Kouadio, F. K., Kouadio, I. K., Ouattara, M. B., ... Barro, N. (2017). Epidemiology and antibiotic resistance phenotypes of diarrheagenic Escherichia coli responsible for infantile gastroenteritis in Ouagadougou, Burkina Faso . *European Journal of Microbiology and Immunology*, 7(3), 168–175. <https://doi.org/10.1556/1886.2017.00014>

- Li, Y., Kumar, S., Zhang, L., Wu, H., & Wu, H. (2023). Characteristics of antibiotic resistance mechanisms and genes of *Klebsiella pneumoniae*. *Open medicine* (Warsaw, Poland), 18(1), 20230707. <https://doi.org/10.1515/med-2023-0707>
- Magiorakos, A., Srinivasan, A., Carey, R. B., Carmeli, Y., Falagas, M. E., Giske, C. G., ... Hindler, J. F. (2011). *bacteria* : an international expert proposal for interim standard definitions for acquired resistance. *Clinical Microbiology and Infection*, 18(3), 268–281. <https://doi.org/10.1111/j.1469-0691.2011.03570.x>
- Mir, R., Salari, S., Najimi, M., & Rashki, A. (2022). Determination of frequency, multiple antibiotic resistance index and resistotype of *Salmonella* spp. in chicken meat collected from southeast of Iran. *Veterinary medicine and science*, 8(1), 229–236. <https://doi.org/10.1002/vms3.647>
- Munita, J. M., & Arias, C. A. (2016). Mechanisms of Antibiotic Resistance. *Microbiology spectrum*, 4(2), 10.1128/microbiolspec.VMBF-0016-2015. <https://doi.org/10.1128/microbiolspec.VMBF-0016-2015>
- Muteeb, G., Rehman, M. T., Shahwan, M., & Aatif, M. (2023). Origin of Antibiotics and Antibiotic Resistance, and Their Impacts on Drug Development: A Narrative Review. *Pharmaceuticals* (Basel, Switzerland), 16(11), 1615. <https://doi.org/10.3390/ph16111615>
- Ndzime, Y. M., Onanga, R., Michel, N., Pendy, L., Bignoumba, M., & Bisseye, C. (2023). Epidemiology of community origin of major multidrug - resistant ESKAPE uropathogens in a paediatric population in South - East Gabon. *Antimicrobial Resistance & Infection Control*, 12, 47–5. <https://doi.org/10.1186/s13756-023-01250-y>
- Okesanya, O., Udo, J., & Omosigho, P. (2024). Characterization of multidrug-resistant genes of *Klebsiella pneumoniae* from clinical isolates in Asaba, Delta State, Nigeria. *Microbes and Infectious Diseases*, 0(0), 0–0. <https://doi.org/10.21608/mid.2024.282748.1898>
- Oladipo, E. K., Awoyelu, E. H., Adeosun, I. J., & Ayandele, A. A. (2021). Antibacterial susceptibility of clinical isolates of *Klebsiella pneumoniae* in Nigeria to carbapenems. *Iraqi Journal of Science*, 62(2), 396–401. <https://doi.org/10.24996/ij.s.2021.62.2.5>
- Peterson, E., & Kaur, P. (2018). Antibiotic Resistance Mechanisms in Bacteria: Relationships Between Resistance Determinants of Antibiotic Producers , Environmental Bacteria , and Clinical Pathogens. *Frontiers in Microbiology*, 9(11), 1–21. <https://doi.org/10.3389/fmicb.2018.02928>
- Rong, F., Sun Y., Li X and Zhang, C. (2023). Retraction Retracted: Drug Resistance Mechanism of Enterobacteriaceae with Decreased Antibiotic Sensitivity. *Applied Bionics and Biomechanics*, 1–9.
- Salam, M. A., Al-Amin, M. Y., Salam, M. T., Pawar, J. S., Akhter, N., Rabaan, A. A., & Alqumber, M. A. A. (2023). Antimicrobial Resistance: A Growing Serious Threat for Global Public Health. *Healthcare* (Basel, Switzerland), 11(13), 1946. <https://doi.org/10.3390/healthcare11131946>
- Santella, B., Boccella, M., Folliero, V., Iervolino, D., Pagliano, P., Fortino, L., ... Franci, G. (2024). Antimicrobial Susceptibility Profiles of *Klebsiella pneumoniae* Strains Collected from Clinical Samples in a Hospital in Southern Italy. *Canadian Journal of Infectious Diseases and Medical Microbiology*, 2024. <https://doi.org/10.1155/2024/5548434>
- Shah, A. A., Alwashmi, A. S. S., Abalkhail, A. and Alkahtani, A. M. (2025). Emerging challenges in *Klebsiella pneumoniae*: Antimicrobial resistance and novel approach, *Microbial Pathogenesis*, Volume 202, 107399, <https://doi.org/10.1016/j.micpath.2025.107399>.
- Vaez, H., & Yazdanpour, Z. (2024). Distribution of Virulence-Associated and Aminoglycoside Resistance Genes Among Clinical Isolates of *Klebsiella pneumoniae* in the Southeast of Iran, During 2019–2023: A Cross-Sectional Study. *Health Science Reports*, 7(12). <https://doi.org/10.1002/hsr2.70309>
- Yang, P., Chen, Y., Jiang, S., Shen, P., Lu, X., & Xiao, Y. (2020). Association between the rate of fluoroquinolones-resistant gram-negative bacteria and antibiotic consumption from China based on 145 tertiary hospitals data in 2014. *BMC Infectious Diseases*, 20(1), 1–7. <https://doi.org/10.1186/s12879-020-04981-0>