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Antibiotic Susceptibility of Klebsiella pneumoniae Isolates Recovered from Liver Transplant Recipients: A Comparative Analysis Before and After the Surgery

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ABSTRACT

Liver transplantation (LT) has developed as a well-established therapeutic option for end-stage liver disease, specific primary and a few secondary hepatic malignancies, and a few uncommon metabolic liver disorders. The rate of rejection in the transplant population has significantly decreased because the use of immunosuppressive medications, immunosuppressive has increased patient sensitivity to opportunistic infections. For patients with LT, infections continue to be a significant source of morbidity and mortality. 180 urine and stool samples from 30 LT patients at Mansoura University's Gastroenterology Surgical Center (GEC), Egypt, were included in this investigation from March 2021 to March 2023. Fourteen commercial antibiotics belonging to different families with different modes of action were used. 16S rRNA was done to confirm the identification of *Klebsiella pneumoniae* (*K. pneumoniae*) by detecting the 16S rRNA gene. This study's findings demonstrated that *K. pneumoniae* strains are entirely resistant to seven different kinds of antibiotics Nitrofurantoin, Ceftazidime, Amoxicillin, Vancomycin, Tobramycin, Erythromycin, and Gentamicin, and the most effective type of antibiotic was Amikacin (50%). This study focuses on the surveillance of *K. pneumoniae* in liver transplant patients before and after the surgery. It also demonstrates the resistance levels of the isolated *K. pneumoniae* against different antibiotics. Among various antibiotics used, Amikacin remains the most effective antibiotic (with 50% effectiveness). Therefore, this study underscores Amikacin's potential role in managing infections in LT patients. These results are crucial for developing targeted therapeutic strategies and improving patient outcomes in liver transplantation.

Keywords: *Klebsiella pneumoniae,* Liver transplantation, Immunocompromised patients, Antibiotic resistance, Opportunistic infections.

1. Introduction

Liver transplantation is a life-extending procedure for individuals suffering from end-stage liver disorder (ESLD). Opportunistic infections become prevalent within the first year after the surgery due to suppressed individual immune systems (Lin et al., 2018). Among Liver transplant patients, bacterial infections are the most prevalent, constituting up to 70% of all infections, followed by fungal and viral infections. The risk of infection fluctuates depending on the postoperative duration; this timing aspect plays a significant role in determining the susceptibility to microbial infections (Fishman, 2011). The three most common infections among postoperative patients are

pneumonia, bacteremia, and urinary tract infections (UTIs) (Kim, 2014).

Patients undergoing liver transplantation are at risk for pneumonia due to several factors, including immune suppression before surgery, prolonged use of a ventilator following liver transplantation, preoperative malnourishment, and compromised immunity. Pneumonia was found to have a morbidity rate ranging from 13% to 51% in LT patients, making it the second most common infectious complication and potential cause of mortality. Pneumonia-related mortality among LT patients ranged from 4 to 53%. According to reports, bacteria were the cause of almost 60% of pneumonia cases in LT recipients, and one of the most frequent sites of bacteremia in LT patients was the lung (Ma et al., 2005). Gram-negative *K. pneumoniae* is an encapsulated, non-spore-forming, facultatively anaerobic bacteria. It has a rod-like form. On MacConkey agar, it manifests as a mucoid lactose fermenter with a colony that is 2 μm by 0.5 μm in size (Cortés et al., 2002). It exists as a normal flora of the intestines, mouth and skin, and intestines. If breathed, it can cause harmful alterations to the lungs of humans and animals, especially to the alveoli, where bloody sputum is produced (Ryan and Ray, 2004). *K. pneumoniae* was the most critical member of the Enterobacteriaceae in hospital infections. Recently, *Klebsiella* species have emerged as significant pathogens in nosocomial infections (Li et al., 2014).

Most cases of *Klebsiella* infections occur in those with compromised immune systems. Men with incapacitating illnesses who are middle-aged or older are most affected by illness. Individuals in this patient population with diabetes, alcoholism, malignancy, liver disease, renal failure, and occupational exposures are believed to have affected the host's respiratory defenses. Many diseases are acquired during hospital stays for other conditions, like nosocomial infections. Feces are the most common source of patient infection, followed by touching contaminated objects. Pneumonia is the most frequent infection carried on by *Klebsiella* bacteria outside hospitals (Jagessar & Alleyne, 2011). In immunocompromised people, *K. pneumoniae* the common strains cause a variety of serious infections, whether acquired in the community or through medical care, such as pneumonia, sepsis, bacteremia, meningitis and urinary tract infections (UTIs) (Tsay et al., 2002 and Paczosa & Mecsas, 2016). Antibiotic overuse raises the alarming probability that *K. pneumoniae* will be a multidrug resistant (MDR) in nosocomial infections instead of infections acquired in the community. Antibiotic-resistant flora is thus present in many patients. *K. pneumoniae* infections are common in both industrialized and developing nations, with a high death rate, a poor prognosis, and significant financial consequences. The misuse of antibiotics increases the likelihood that *K. pneumoniae* will develop multidrug resistance in nosocomial infections compared to community-acquired infections, as most patients already harbor antibiotic-resistant flora (Kawai et al. 2004; Ricklin et al. 2016, Shaaban et al. 2021a, and Shaaban et al. 2021b).

Individuals with compromised immune systems are primarily affected by infections carried on by microorganisms. The persistence and virulence of *K. pneumoniae* may be affected by some virulence factors. Studies suggest that *K. pneumoniae* phenotypes and genomes are vulnerable to quick changes. The global rate of *K. pneumonia* resistant to drugs increased to 70%, and the mortality rate from infection-related causes has also reached 40%–70% (Iredell et al., 2016). The characterization of antimicrobial resistance of *K. pneumonia*e can create biofilm and virulence factors. To understand the pathogenicity of this bacterium in the clinical environment and achieve more effective antimicrobial therapy, it is crucial to study the emergence of the resistant strain *K. pneumonia*e (Shaaban et al. 2024). This strain is responsible for increased morbidity and mortality, particularly in severely ill patients, making the investigation of its resistance pattern essential.

2. Material and methods

2.1 SAMPLES COLLECTIONS

Urine and stool samples were collected from thirty liver transplantation (LT) patients in Mansoura University's Gastroenterology Surgical Center (GEC), Egypt, during the period from March 2021 to March 2023. The samples have been divided into the following three groups:

Group I: One week before liver transplant surgery (1 WBLTS), this group constituted thirty participants.

Group II: This group constituted thirty participants one week after liver transplant surgery (1 WALTS).

Group III: This group constituted thirty participants two weeks after liver transplantation surgery (2 WALTS).

The total number of samples collected from all patients was 180, divided between urine (n=90) and stool (n=90).

2.2 BACTERIAL ISOLATION AND CULTURE CONDITIONS

All samples collected were processed according to The Clinical and Laboratory Standards Institute (CLSI) for every type of specimen. Urine samples were inoculated with MacConkey's and blood agar and incubated for 24 h at 37°C. Samples of stool were inoculated in MacConkey's agar and Xylose Lysine Deoxycholate (XLD) media (Qaiser et al., 2011).

2.3 BACTERIAL IDENTIFICATION

The isolated colonies were evaluated for gram staining reaction and colony morphology and then examined for biochemical and molecular evaluation. For biochemical identification, *K. pneumoniae* was identified using the Analytical Profile Index (API 20E, BioMérieux, France), which screened for catalase (Reiner, 2010), oxidase (Tarrand & Gröschel, 1982), indole (MacWilliams, 2012), motility, H_2S production, and triple sugar iron (Lehman, 2005). The colonies were also further confirmed by using the API system (Irfan et al., 2023).

2.4 ANTIBIOTIC SUSCEPTIBILITY TEST (AST)

The isolated colonies from different culture media were examined for an antimicrobial sensitivity test (AST) using the Kirby Bauer technique (Hudzicki, 2009) per the recommendations and interpretations of the CLSI guidelines (Mojica Medina et al., 2020). For AST analysis, we examined the following antibiotics, including meropenem (MEM 10 µg), ciprofloxacin (CIP 5 µg), nitrofurantoin (F 300 µg), imipenem (IPM 10 µg), piperacillin (PRL 100 µg), norfloxacin (NOR 10 µg), ceftazidime (CAZ 10 µg), gentamicin (CN 10 µg), amikacin (AK 30 µg), amoxicillin (AX 30 µg), vancomycin (V 30 µg), tobramycin (TOB 10 µg), ofloxacin (OFX 5 µg) and erythromycin (E 15 µg).

2.5 MOLECULAR IDENTIFICATION

Bacterial DNA was isolated using a DNeasy Blood & Tissue Kit (Qiagen company, Germany). The quality of extracted DNA was evaluated by Agarose gel electrophoresis, and the concentration was estimated by nanodrop. The targeted region (16S rRNA) was amplified using two sets of universal primers: 27F: AGAGTTTGATCMTGGCTCAG, and 1492R: ACGGYTACCTTGTTACGACTT (Saif & Khan, 2018). Every amplification was carried out in 20 µL containing 10 µL Master Mix 1x GoTaqGreen (Promega, USA), 2 µL of DNA, 6 µL of sterilized water, and 1 µL of each of forward and reverse primer. The amplification was done at 95°C for 5 min and 35 cycles of 94°C for 40 s, 50 °C for 30 s, and 72 °C for 1 min, and final extension 72°C for 10 min. The temperature was then set at 4 °C for infinite time as a final step. 2 µL of amplification DNA was established using 1.2% agarose gel electrophoresis inTris acetate EDTA (TAE) buffer. A DNA ladder of 100 bp (Promega, USA) was used as a marker. Products of PCR (1500 bp) approximately were sequenced. Sanger sequencing used in South Korea, Macrogen, using the universal primers; 785F GGATTAGATACCCTGGTA and 907R CCGTCAATTCMTTTRAGTTT (Shaaban et al., 2024). The obtained consensus sequences and the sequencing data were analyzed using BioEdit v 7.0 software (Russell et al., 2006).

The sequences from the sequencing machine were aligned, and the contig was submitted to the NCBI GenBank (NCBI Resource Coordinators, 2013). The deposited sequence can be retrieved via the accession number OQ096687. This sequence was used as a query against the 16S rRNA bacterial-type strains (Zayed & Badawi, 2020). The retrieved sequences were aligned using MAFFT version 7 (Katoh et al., 2019). Then, the phylogenetic tree was built using the maximum likelihood method with the HKY+F model (Hoang et al., 2018; Kalyaanamoorthy et al., 2017; Nguyen et al., 2014). Finally, the tree was visualized using the Interactive Tree of Life web server (Letunic & Bork, 2016).

3. Results

3.1 BACTERIAL ISOLATION

A total of 30 liver transplant patients were recruited in this study. 30 Urine and 30 stool samples of these patients were examined one week before the LT operations, one week postoperative, and two weeks after the LT surgery using standard laboratory procedures. The total samples collected for all patients were 180, divided between urine (n=90) and stool (n=90). A total of 12 cultures (6.66 %) were found positive for *K. pneumonia*. These positive cultures constitute four cultures (4.44 %) from urine specimens and eight cultures (8.88 %) from the stool samples (Table 1).

3.2 BACTERIAL IDENTIFICATION

Thirty liver transplant patients were recruited in this study, a total of 90 urine samples; 30 before one week of operation, 30 after one week of a liver transplant, and the same number after two weeks of operation were analyzed, and *K. pneumonia*e was detected in one urine patient samples before surgery and two stool patient sample. The *K. pneumonia*e was detected in one stool patient sample collected after one week, three urine, and five stool samples after two weeks of liver transplant. Gram staining result showed *K. pneumonia*e as a Gram-negative rod.

Table 1. Positive and Negative Culture Counts of *K. pneumoniae* in Urine and Stool Samples across Various Patients at Different Time Points Before and Following Liver Transplantation Surgery.

		Pathogenicity			
Samples	**Sampling Times**	**+ve**	**%**	**-ve**	**%**
Urine n=90	**1 WBLTS n=30**	1	3.33	29	96.66
	1 WALTS n=30	0	0	30	100.00
	2 WALTS n=30	3	10	27	90.00
Stool n=90	**1 WBLTS n=30**	2	6.66	28	93.33
	1 WALTS n=30	1	3.33	29	96.66
	2 WALTS n=30	5	16.66	25	83.33
Total (n=180)		12	6.66	168	93.33

Where, 1 WBLTS = One week before liver transplant surgery, 1 WALTS = One week after liver transplant surgery, and 2 WALTS = Two weeks after liver transplantation surgery. Additionally, "+ve" denotes samples that positive for *K. pneumoniae*, whereas "-ve" indicates samples that tested negative for *K. pneumoniae.*

The isolated bacterial colonies tested positive against urease, citrate catalase, Vogas, and Proskauer. However, they tested negative for oxidase, indole, and coagulase tests. Further, the colonies were identified as *K. pneumonia*e based on the Analytical Profile Index (API). The API results indicate that the *K. pneumonia*e showed a positive reaction to citrate, a negative reaction with arginine dihydrolase (ADH bydecarboxylation of the amino acid arginine), non-hydrolyzing the gelatine (indicating the absence of gelatinase), and nitrate reduction (Figure 1).

ANTIBIOTIC SUSCEPTIBILITY TEST (AST

All twelve *K. pneumonia*e strains, four isolated from urine and eight identified from stool, were tested for drug sensitivity and resistance. The tested result indicated that all twelve strains exhibit resistance to nitrofurantoin, ceftazidime, amoxicillin, Vancomycin, tobramycin, erythromycin, and gentamicin, followed by piperacillin and norfloxacin**,** and only two strains exhibit resistance to ciprofloxacin, meropenem and imipenem. The details of all 14 antibiotics tested among all 12 strains of *K. pneumoniae* isolated from liver transplant patients' urine and stool samples are shown in (Table 2). The consistency of XDR and MDR of *K. pneumonia* isolates was higher in all samples (Table 3 and Table 4).

Figure 1. Standard *K. pneumoniae* identification (A) as grown on MacConkey agar, and (B) via the Analytical Profile Index (API) system.

Table 2. Antibiotic sensitivity tests for the 12 *K. pneumoniae* positive cultures using disk diffusion method according to the Clinical and Laboratory Standards Institute (CLSI), 2018.

Antibiotics					***Zones of Inhibition (mm)***											
					Urine samples (KU 01: KU 04)				**Stool samples (KS 05: KS 12)**							
					01	**02**	**03**	**04**	**05**	**06**	**07**	**08**	**09**	**10**	**11**	**12**
	Conc.	***R***	***I***	***S***												
Ciprofloxacin^{CIP}	5	≤ 15	16-20	≥ 21	R	R	S	S	S	S	S	S	S	S	S	S
Norfloxacin^{NOR}	10	≤ 12	13-16	≥ 17	R	S	I	S	R	S	R	S	R	R	S	S
Ofloxacin^{OFX}	5	≤ 14	15-21	≥ 22	I	I	R	S	S	I	S	I	S	I	I	S
Nitrofurantoin^{F}	300	≤ 14	15-16	≥ 17	R	R	R	R	R	R	R	R	R	R	R	R
Meropenem^{MEM}	10	≤ 13	14-15	≥ 16	S	S	S	S	S	S	R	S	S	S	S	R
Imipenem^{IPM}	10	≤ 13	14-15	≥ 16	S	S	S	S	S	S	R	S	S	S	S	R
Ceftazidime^{CAZ}	10	≤ 14	15-17	≥ 18	R	R	R	R	R	R	R	R	R	R	R	R
Amoxicillin^{AX}	25	≤ 13	14-17	≥ 18	R	R	R	R	R	R	R	R	R	R	R	R
Vancomycin^{V}	30	≤ 9	10-11	≥ 12	R	R	R	R	R	R	R	R	R	R	R	R
Amikacin^{AK}	30	≤ 14	15-16	≥ 17	I	I	I	I	I	S	I	S	S	S	S	S
Tobramycin^{TOB}	10	≤ 12	13-14	≥ 15	R	R	R	R	R	R	R	R	R	R	R	R
Erythromycin^{E}	15	≤ 13	14-17	≥ 18	R	R	R	R	R	R	R	R	R	R	R	R
Gentamicin^{GN}	10	≤ 12	13-14	≥ 15	R	R	R	R	R	R	R	R	R	R	R	R
Piperacillin^{PRL}	100	≤ 14	15-17	≥ 18	R	I	R	S	S	S	S	S	R	R	S	R

Where KU= *Klebsiella pneumoniae* isolated from Urine samples, KS= *Klebsiella pneumoniae* isolated from Stool samples, R = Resistant, I = Intermediate, and S = Susceptible.

Table 3. Prevalence of the Multi drug resistant (MDR) and extensively drug resistant (XDR) of *K. pneumonia* isolates.

Specimen Code	Resistance profile	MDR	XDR	Number of Tested classes	Number of Non-susceptible classes	CIP	NOR	OFX	NIT	MEM	IPM	CAZ	AMOX
KU 01	CIP NOR OFX NIT CAZ AMOX	MDR	Possible XDR	4	3	R	R	I	R	S	S	R	R
KU 02	CIP OFX NIT CAZ AMOX	MDR	Possible XDR	4	3	R	S	I	R	S	S	R	R
KU 03	NOR OFX NIT CAZ AMOX	MDR	Possible XDR	4	3	S	I	R	R	S	S	R	R
KU 04	NIT CAZ AMOX			4	2	S	S	S	R	S	S	R	R
KS 05	NOR NIT CAZ AMOX	MDR	Possible XDR	4	3	S	R	S	R	S	S	R	R
KS 06	OFX NIT CAZ AMOX			4	3	S	S	I	R	S	S	R	R
KS 07	NOR NIT MEM IPM CAZ AMOX	MDR	Possible XDR	4	4	S	R	S	R	R	R	R	R
KS 08	OFX NIT CAZ AMOX			4	3	S	S	I	R	S	S	R	R
KS 09	NOR NIT CAZ AMOX	MDR	Possible XDR	4	3	S	R	S	R	S	S	R	R
KS 10	NOR OFX NIT CAZ AMOX	MDR	Possible XDR	4	3	S	R	I	R	S	S	R	R
KS 11	OFX NIT CAZ AMOX			4	3	S	S	I	R	S	S	R	R
KS 12	NIT MEM IPM CAZ AMOX	MDR	Possible XDR	4	3	S	S	S	R	R	R	R	R

Where KU= *Klebsiella pneumoniae* isolated from Urine samples, KS= *Klebsiella pneumoniae* isolated from Stool samples, R = Resistant, I = Intermediate, and S = Susceptible.

Table 4. Percentages of resistant samples and sensitive ones to the total isolates.

ANTIBIOTIC NAME	ANTIBIOTIC CODE	%R	%I	%S
AMOXICILLIN	AMOX_ND25	100	0	0
PIPERACILLIN	PIP_ND100	41.7	8.3	50
CEFTAZIDIME	CAZ_ND10	100	0	0
IMIPENEM	IPM_ND10	16.7	0	83.3
MEROPENEM	MEM_ND10	16.7	0	83.3
AMIKACIN	AMK_ND30	0	50	50
GENTAMICIN	GEN_ND10	100	0	0
TOBRAMYCIN	TOB_ND10	100	0	0
CIPROFLOXACIN	CIP_ND5	16.7	0	83.3
NORFLOXACIN	NOR_ND10	41.7	8.3	50
OFLOXACIN	OFX_ND5	8.3	50	41.7
ERYTHROMYCIN	ERY_ND15	100	0	0
NITROFURANTOIN	NIT_ND300	100	0	0
VANCOMYCIN	VAN_ND30	100	0	0

R = Resistance, I= Intermediated, S = Susceptible

3.4 MOLECULAR IDENTIFICATION

Identifying isolates at the molecular level through 16S rRNA has been ensured through the amplified products, as shown in the gel image (Figure 2). These were then processed for Sanger sequencing using both targeted regions. The consensus sequences were processed for BLAST analysis, and it is noted that the bacteria strain exhibits high nucleotide similarity to *K. pneumoniae* species. Maximum likelihood phylogenetic tree based on data set for 16S rRNA gene *K. pneumoniae* homologous sequences (Figure 3). The sequenced data with read length 1244 nucleotides of 16S rRNA gene (accession No. OQ096687) exhibit the closest similarity to *K. pneumoniae* various strains.

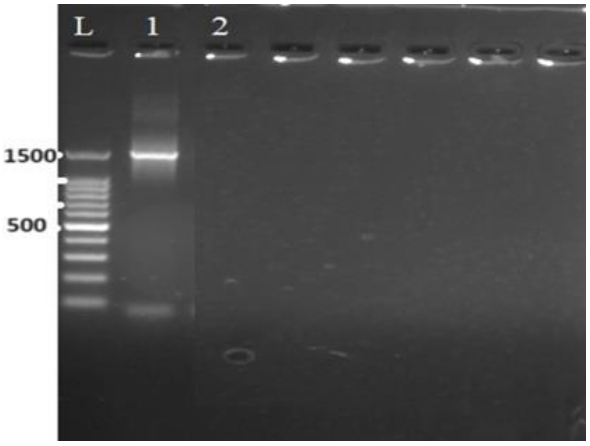

Figure 2. Gel electrophoresis of 16S rRNA of *K. pneumonia*. L: ladder, 1: *K. pneumoniae*, 2: negative control.

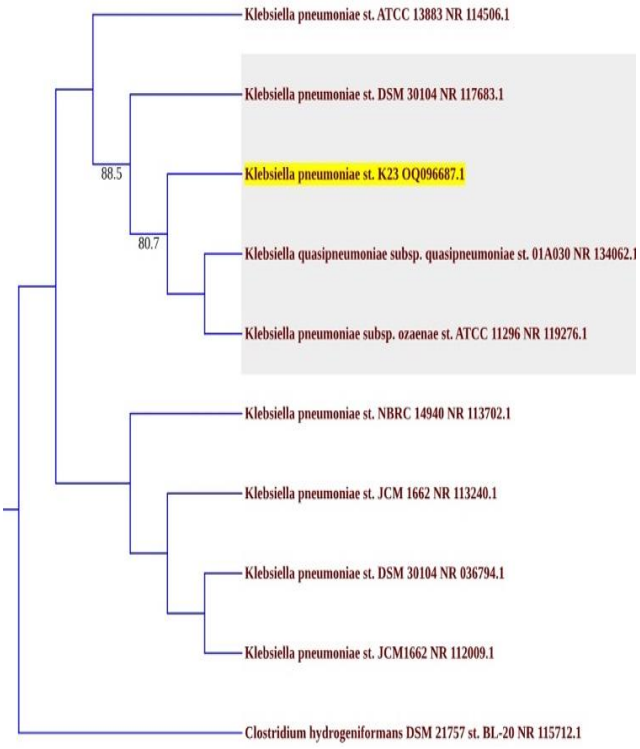

Figure 3. A maximum likelihood phylogenetic tree based on a data set of 16S rRNA gene homologous sequences from *K. pneumonia.* Our *K. pneumonia* isolate is highlighted in yellow.

4. Discussion

First, this work aimed to identify *K. pneumoniae* isolates related to LT patients and estimate their antibiotic sensitivity in urine and stool

samples. Our result showed that 90 urine samples were collected from LT patients divided into 3 Groups: Group I: one week before LT (n=30); Group II: one week after LT (n=30); and Group III: two weeks after LT (n=30). For the first Group, one positive case appeared with a percentage of 3.33%; the second Group did not show any positive case with a percentage of 0%; for the third Group, three positive cases appeared with a percentage of 10%. On the other hand, 90 stool samples were collected from liver transplant patients, who were also divided into 3 Groups: Group I: one week before LT (n=30); Group II: one week after LT (n=30); and Group III: two weeks after LT (n=30). The first Group showed two positive cases with a percentage of 6.66%, the second Group showed one positive case with a percentage of 3.33%, while the third Group showed five positive cases with a percentage of 16.66 %. Twelve (6.66 %) samples were found positive for *K. pneumoniae* in all urine and stool samples, 4 (4.44 %) from urine specimens, and 8 (8.88%) samples for stool samples.

The urinary tract infections with gram-negative bacteria were the most isolated (80%) (Shaaban et al., 2020). *K. pneumoniae* has been the most common bacterial infection associated with surgical wounds (Custovic et al., 2014). Additionally, more than 60% of nosocomial pneumonia infections are caused by gram-negative bacteria (Denys & Relich, 2014). *Klebsiella* sp. was responsible for only 5.2 % of all UTIs (Shaikh et al., 2008). The highest prevalence rate of nosocomial infection was detected in (40%) of *K. pneumoniae* (Abdel-Raouf et al., 2019).

In the present study, the results of susceptibility tests showed an apparent variation in the response of bacterial isolates understudy to the antibiotics used. Antibacterial susceptibility testing revealed 100 % *K. pneumoniae* resistance to Nitrofurantoin, Ceftazidime, Amoxicillin, Vancomycin, Tobramycin, Erythromycin, and Gentamicin. The isolates showed a resistance rate of 41.66% against Norfloxacin and Piperacillin, while they exhibited 16.66 % resistance rate towards Imipenem, Meropenem, and Ciprofloxacin. Finally, Ofloxacin, showed a resistant rate of 8.33%. Most *K. pneumoniae* strains were susceptible to Ciprofloxacin (94.5%), Penicillin, Aminoglycosides, Macrolides, and Quinolones (Naqvi et al., 2013). On the other hand, most *K. pneumoniae* strains were susceptible to Ciprofloxacin and Ampicillin (Marchisio et al., 2015). *Klebsiella* species resist Carbapenems, other β-lactams, Quinolones, and Tetracycline while sensitive to Colistin and Amikacin (Singh et al., 2018). In Turkey, in community-acquired infections, the empirical treatment of the most common antibiotic, Amoxicillin-clavulanic acid shows that employing this antibiotic against *K. pneumoniae* was still partially active. Addressing the issue of antibiotic resistance requires proper scientific research and the allocation of adequate resources and personnel. Despite this necessity, certain corporations have reduced their budgets for antibiotic research. Conversely, countries like the United States have implemented recent antibiotic management policies proactively (Ibrahim et al., 2020; Özgen & Eyüpoğlu, 2020; Shaaban et al., 2015).

Klebsiella pneumoniae exhibited intermediate sensitivity to antibiotics NOR, OFX, AK, and PPL due to the presence of Extended Spectrum Beta-Lactamase (ESBL) in urine and blood samples. *Klebsiella pneumoniae* were resistant to Ampicillin, even when protected and used third generation Cephalosporins. These isolates were susceptible to Meropenem, Amikacin, and Ciprofloxacin (Paterson et al., 2004). Multi drug resistant Gram-negative rods are reported in all countries because of the widespread and unnecessary use of antibiotics. In recent years, treating hypervirulent strains by producing Oxacillinase, high-level Carbapenemase, and AmpC β-lactamase become a significant problem because of the discovery in intensive care patients multiple-resistance strains (BALIKÇI et al., 2014).

5. Conclusion

The clinical presentation of infection before and after liver transplant may be unusual, and the use of antibiotics should be carefully considered in terms of immunity and other routine therapies. The bacterium *Klebsiella pneumoniae* causes serious bacterial infections, affecting various areas such as urine, stool, sputum, and blood. The increasing prevalence of drug-resistant *K. pneumoniae* infections is concerning. In liver transplant patients receiving immunosuppression, which weakens the immune response, *K. pneumoniae* can overcome the body's defenses. Following liver transplantation, infection is the leading cause of death and morbidity in patients, particularly when *K. pneumoniae* is resistant to numerous antibiotics, resulting in longer recovery times, increased expenses, and higher mortality risk. The likelihood of recovery improves with appropriate treatments and adherence to health precautions. Therefore, this research article reports the prevalence of antibiotic-resistant *K. pneumoniae* strains in liver transplant patients at Mansoura University's Gastroenterology Surgical Center, Egypt, from March 2012 to March 2023 and identifies the most effective antibiotics against these strains.

ETHICS APPROVAL AND CONSENT TO PARTICIPATION

The study follows the principles of the Declaration of Helsinki. Approval (MDP.23.08.129) was obtained from

the Ethical Committee in the Faculty of Medicine, Mansoura University, Egypt.

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AUTHORS' CONTRIBUTIONS
Mohamed T. Shaaban: Experiments design and interpretation of data. **Mohamed Abdel-Raouf**: Experimental design and collecting sample. **Muhammad Zayed**: Conceptualization, formal analysis, and writing. **Mahmoud A. Emara**: Experimental work and writing the manuscript.

CONFLICT AND INTEREST
The authors have no relevant conflicts of interest to declare.

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