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# ANTIBIOTIC RESISTANCE PATTERNS OF COMMON UROPATHOGENS ISOLATED FROM FEMALES AT ZAKHO CITY, KURDISTAN REGION, IRAQ.

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**ABSTRACT:**

Background: Urinary tract infection (UTI) is an infection in any part of the urinary system, including kidneys, ureters, bladder, and urethra. Uropathogenic bacterial-antibiotic resistance has become a severe challenge among UTI-causative agents. Objective: This work attempted to screen the activity of a wide range of antibiotics routinely used for UTI-derived infection management to assess the impact of antibiotics on some common UTI pathogens isolated from females. Method: This retrospective study was performed at Zakho Emergency Hospital, Kurdistan region of Iraq, from January 2016 to December 2019. Conventional bacteriological tests were used to identify the most common isolated uropathogens in females. The antibiotic sensitivity test was performed according to the Clinical and Laboratory Standards Institute (CLSI). The bacterial-antibiotics assay was determined using the disk diffusion (Kirby-Bauer) method, which depended on the microbiology laboratory records. Results: Out of 1730 urine samples, 1040 (60.4%) were found to be pathogens-positive samples. The most common uropathogens isolated were *Staphylococcus* spp 44% (*n*=460), *Escherichia coli* strains 25.35% (*n*=265), *Klebsiella* spp 15.78% (*n*=65), and *Streptococcus* spp 14.83 (*n*=155). Regarding the microbial-antibiotic resistance, ≤ 25% of the UTI investigated cases, except *Streptococcus* spp, meropenem, imipenem, and amikacin, showed a remarkable effect against all addressed pathogens. Vancomycin was the first choice against gram-positive bacteria in addition to rifampicin and doxycycline for *Streptococcus* spp. Gentamycin was found to be the most effective antimicrobial against *Klebsiella* spp. Concerning bacterial-antibiotic resistance ≥75% and excluding Streptococcus spp, amoxicillin, ampicillin/cloxacillin, erythromycin, clindamycin, cloxacillin, and metronidazole were completely non-functional against all bacteria. Azithromycin, norfloxacin, oxacillin, cefixime, nalidixic acid, and ceftazidime showed relatively weak activity against gram-positive bacteria in addition to cephalexin, ceftriaxone, and cloxacillin for *Streptococcus* spp. Ampicillin, augmentin, penicillin, and cephalexin were comparatively non-functional against gram-negative pathogens in addition to vancomycin, rifampicin, cephalothin, oxacillin, and trimethoprim for *Klebsiella* spp. All remaining antibiotics produced an activity ranging between ≥25% to ≤75% of examined cases. The results of this work may help clinicians to accurate their antibiotic-bacterial infection empirical treatment. **Conclusion**: All subjected bacteria exhibited a strong resistance to a broad spectrum of antibiotics. Therefore, except for imipenem, meropenem, or amikacin, an antibiotic sensitivity test should be conducted prior to prescribing any antibiotic.

**KEYWORDS***: antibiotic sensitivity, antibiotic resistance, bacteria, infectious disease, urinary tract infection, uropathogens.*

## 1. INTRODUCTION

Antibiotic resistance is a globally continuously increasing threat to patient management (Paul, 2018). Urinary tract infections (UTIs) are recorded to be the most common infections leading to clinical intervention all over the world (Flores-Mireles *et al*., 2015). UTIs may lead to a high rate of mortality and morbidity in a number of infected groups, such as immunocompromised patients (Eliakim-Raz *et al*., 2019), women, older patients, diabetes, obesity, and people who have frequent intercourse (Sabih & Leslie, 2023) as well as those with long-term catheters (Nagaraj, 2023) and frequent sexual activity (Seid *et al*., 2023).

A wide range of Gram-negative and ----positive pathogens was isolated from patients with UTI. Based on the epidemiology of UTIs, uropathogenic *E. coli* is the most common causative agent (Naqid *et al*., 2020a), followed by *Klebsiella pneumoniae*, *Staphylococcus saprophyticus*, *Enterococcus faecalis*, group B *Streptococcus* (GBS), *Proteus mirabilis*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, in addition to other bacteria cause opportunistic UTIs (Flores-Mireles *et al*., 2015) as well as fungi (Nyirjesy *et al*., 2022).

All UTI patients face serious problems associated with bacterial-antibiotic resistance (Nickel, 2007). According to Guclu *et al*., the initial bacterial antibiotic resistance was detected in patients with diabetes or renal reflux (2021). Resistance later broadened to include other nosocomial pathogens. However, nowadays, a large number of community-acquired infections with resistance to antimicrobials are noticed (Mares *et al*., 2024). Bacterial antibiotic resistance is not limited to any particular country, but it is a global phenomenon.

Antibiotics are the mainstay of treatment for any bacterial infection, and UTIs are no exception. Nevertheless, the relentless and misused use of antibiotics for human and veterinary or agro-industrial purposes (Tiseo *et al*., 2020) in the last decades has given rise to a severe public health issue: the drastic rise in the antibiotic-resistance of bacteria (Wiedemann *et al*., 2014; Alhazmi *et al*., 2023). The occurrence of antibiotic-resistant bacteria in UTIs exceeds the garden homogeneity of the European Union, with over half a million cases (WHO and ECDC report, 2023). The European Center for Disease Prevention and Control (ECDC) and WHO report occasional emergence of antibiotic resistance blazing across these strains for quick and effective action.

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Unfortunately, Iraq, including the Kurdistan region, has one of the highest rates of antibiotic consumption in the Middle East, with low knowledge of the appropriate use of antibiotics by the public. As a consequence, recent data bring to light the burden of antimicrobial resistance in this country and the necessity of monitoring the prudent use of these categories of drugs (Qurbani *et al*., 2024). Bacterial-antibiotics resistance studies in the local setting also showed increased resistance of bacteria to ampicillin, aztreonam, and nitrofurantoin. In contrast, the integrity of amikacin, ciprofloxacin, imipenem, and nitrofurantoin sensitivity is still preserved (Osman, 2019).

Current research evaluates the recent evolution of antimicrobial resistance in female patients. It updates the knowledge regarding the resistance and sensitivity of uropathogens to antimicrobials in Kurdistan of Iraq, associated with the presentation of relevant clinical data of patients that may constitute risk factors in the context of antibiotic-resistance UTIs. This work aimed to assess the activity of a wide range of antibiotics against several common UTI causative agents and to discuss the susceptibility pattern of antimicrobials based on urine-culture sensitivity assay. By studying bacterial sensitivity patterns to antibiotics in indicated pathogens, a new review could be proposed for treatment protocol in such patients.

## 2. MATERIALS AND METHODS

**Study design and sample collection:**

This retrospective study was carried out among females for a period of four years (Jan 2016 to Dec 2019), including 1730 urine samples at the Microbiology Laboratories in Zakho Emergency Hospital, located in the Kurdistan region of Iraq. To prevent contamination, first, midstream morning urine samples were collected from female patients of all ages in sterile containers. All participants exhibited one or more symptoms indicative of UTI, including pain or a burning sensation during urination (dysuria), increased frequency of urination during both the day and night (nocturia), urgent or sudden urges to urinate, and the presence of cloudy or bloody urine.

**Bacterial identification:**

Bacteria isolates were initially identified by their morphological characteristics post-culturing on blood agar, mannitol salt agar, and MacConkey agar based on standard microbiological culture as per the Clinical and Laboratory Standards Institute (CLSI, 2020) guidelines. Each sample was cultured immediately on an appropriate agar and then incubated in aerobic conditions at 37 °C for 24 to 48 hours with aeration (Giuliano *et al*., 2019).

**Antimicrobial susceptibility test:**

Antibiotic susceptibility was assessed using the disk diffusion (Kirby-Bauer) method. Upon collection, samples were promptly analyzed microbiologically. Initially, samples were incubated overnight at 37 °C on blood agar. In samples yielding uniform bacterial growth, microorganisms were transferred and spread on Mueller-Hinton agar plates using a sterile cotton swab. Antibiotic discs were applied on plates seeded with bacterial lawn and incubated at 37 °C for 24-48 h. The results were interpreted based on the size of the inhibition zone around the antibiotic disc according to the guidelines that are provided by (CLSI, 2020). Vaginal yeast infection agents were excluded from this research. The data analysis concentrated on four prevalent uropathogens: *Staphylococcus* spp., *Streptococcus* spp., strains of *E. coli*, and *Klebsiella* spp. Antibiotic types, abbreviations, and concentrations are shown below.

**Ethical approval:**

The study design and procedure were approved by the College of Medicine, University of Zakho, Kurdistan region, Iraq. Ethics considerations, including the privacy of personal data, were considered during all steps of the study. Written informed consent was acquired from each subject before sampling.

## 3. RESULTS

Out of 1,730 urine samples, they were collected from females for bacterial identification and antibiotic resistance profiling. Of those, 1,045 (60.4%) exhibited bacterial growth on various microbiological media. This study specifically examined different strains of *Staphylococcus* spp and *Streptococcus* spp as representatives of gram-positive bacteria, as well as *E. coli* and *Klebsiella* spp as examples of gram-negative bacteria (see Table 1). The bacterial isolates were tested against a comprehensive array of Bioanalyse® ATS antibiotic discs (manufactured in Turkey), each containing the same concentration of their respective antibiotics.

The most significant number of isolates was observed for *Staphylococcus* spp (460 samples, 44.01%), followed by *E. coli* strains (265 samples, 25.35%), *Klebsiella* spp (165 samples, 15.78%), and then *Streptococcus* spp, in that order (Table 1). The identification of *Klebsiella* and *Streptococcus* species (155 samples, 14.83%), along with *E. coli* strains and *Staphylococcus* spp, was excluded from the bacterial-antibiotic analysis unless specifically requested by physicians. Based on years, the total number of bacteria isolated was highest in 2016 (n=493), followed by 2019 (n=461), 2018 (n=409), and then 2017 (n=367).

Table 1: Number of the Pathogen Isolates and Their Antibiotics Resistance Percentages for 2016-19.

| Year | Total Urine Samples | Bacterial Urine Samples | Bacterial Numbers and Percentages | | | |
|---|---|---|---|---|---|---|
| | | | *Staph*. spp. | *Strept*. spp. | *E. coli* | *Klebsiella* spp. |
| 2016 | 493 | 344 (69.77%) | 128 (37.20%) | 55 (15.98%) | 113 (32.84%) | 48 (13.95%) |
| 2017 | 367 | 238 (64.85%) | 110 (46.21%) | 48 (20.16%) | 49 (20.58%) | 31 (13.02%) |
| 2018 | 409 | 259 (63.32%) | 155 (59.84%) | 29 (11.19%) | 43 (16.60%) | 32 (12.35%) |
| 2019 | 461 | 204 (44.25%) | 067 (32.84%) | 23 (11.27%) | 60 (29.41%) | 54 (26.47%) |
| Total | 1730 | 1045 (60.40%) | 460 (44.01%) | 155 (14.83%) | 265 (25.35%) | 165 (15.78%) |

Over the indicated period, Staphylococcus aureus, S. albus, S. saprophyticus, and S. epidermidis species were isolated from 460 (~44.0 %) bacterial-positive samples. *Staphylococcus* spp illustrated an antibacterial resistance rate of ~ 66% of cases (20 out of 31). The highest rate (75-100%) of *Staph*-antibiotic resistance was found with MTZ (100%), CTZ (97.5%), CFX (95.8%), NA (95.1%), E (92.2), DA (92.0%), CX (91.7%), APX (89.1%), AZM (88.6%), OX (87.1%), AX (80.5%), and NOR (76.6%) respectively (Table 2, Fig 1). Another eight antibiotics did not show any lethal effect in 50-74% of cases, such as in AMP, AUG, CL, CRO, CTX, P, TE, and TMP. Relatively, KF, CIP, DX, GN, NIT, and RF produced better antimicrobial activity compared to the previous group of antibiotics, as Staphylococcus spp demonstrated resistance in (25-49%) of test cases (not shown in Fig 1). Only four antibiotics, MEM (15.5%), AK (10.8%), VA (7.2%), and IMP (2.6%), were found to be effective antimicrobials as pathogens produced resistance only in ≤24% of the tested cases (Table 2, and Fig 1). *Staphylococcus* spp was grown in 100% of cases when challenged against metronidazole (MTZ), which is considered to be the most ineffective antibiotic.

On the other side, imipenem (IMP) was the first choice for Staphylococcus-related infections, where Staphylococcus spp grew in only 2 out of 76 cases (2.6%) (Table 2 and Fig. 1).

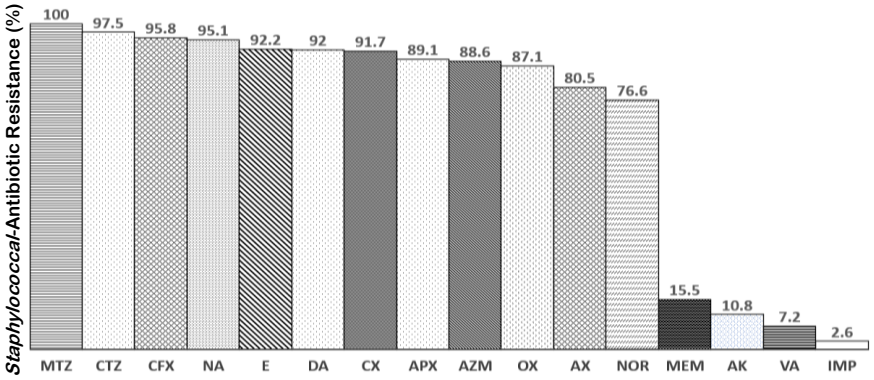


Figure 1: *Staphylococcus*-antibiotic resistance profile. Cases per antibiotic; MTZ (11), CTZ (83), CFX (288), NA (164), E (123), DA (75), CX (157), APX (138), AZM (185), OX (70), AX (103), NOR (30), MEM (126), AK (322), VA (236), IMP (76). Percentages represent the total number of each bacterial-antibiotic analysis for the period of 2016-2019. Only antibiotics with activity of ≥ 75% or ≤ 25% of investigated cases are shown. All the other antibiotics with active rates between 25-74% are not included.

*Escherichia coli* was isolated from 265 (25.35%) cases of those bacterial-positive samples over the period mentioned above. Isolated *E. coli* strains produced antibiotic resistance (>50%) in 21 out of 29 applied antibiotics. *E. coli* showed antimicrobial confrontation at (75-100%) of investigated samples when challenged against ten antibiotics, including MTZ (100%), P (96.0%), E (95.3%), CX (95.2%), AX (93.3%), APX (92.0%), DA (86.5%), AMP (84.7%), AUG (82.5%), and CL (76.9%) respectively. Additional 11 antibiotics were not effective in a range of 50-74% of analyzed cases, such as CFX, CRO, CTX, CTZ, DX, KF, NA, RF, TE, TMP, and VA. Fife antibiotics like; AZM, CIP, GN, NIT, and NOR were relatively functional as they killed or inhibited the *E. coli* strains growth in 50-74% of the investigated cases (not shown in Fig. 2). Only three antibiotics, AK (8.9%), MEM (7.5%), and IMP (0.0%) were considerably effective against *E. coli* strains as they produced lethal phenomena in 75-100% of the addressed cases (Table 2, and Fig. 2). *E. coli* strains were grown in 100% (49 cases) when tested against the combination of ampicillin and cloxacillin (APX) which should not be prescribed for the controlling of *E. coli* infections. In contrast, *E. coli* strains were produced in only 8.9% and 7.5% of cases when countered against AK and MEM, respectively. Furthermore, IMP was the most effective antibiotic as it prevented the E. coli strains from growing in 100% of tested cases (Table 2, Fig. 2).

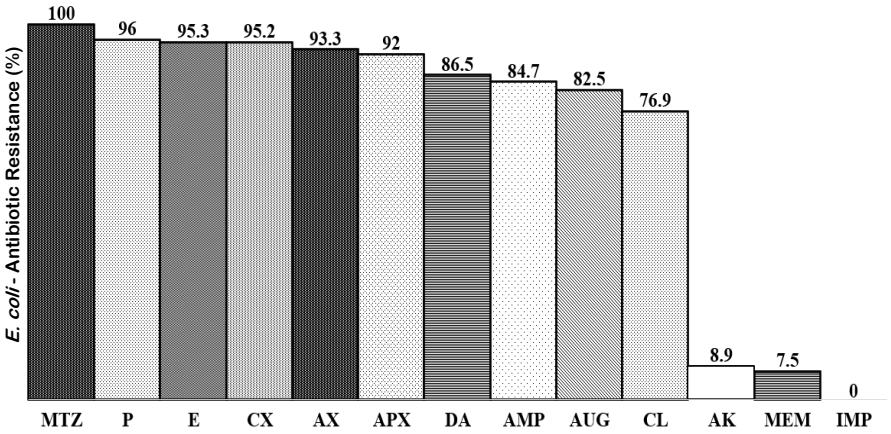


Figure 2: Activity of Antibiotics against *Escherichia coli*. Cases per antibiotic: MTZ (100), P (25), E (85), CX (21), AX (45), APX (75), DA (88), AMP (118), AUG (189), CL (52), AK (223), MEM (71), IMP (59). Other details are in Fig. 1.

In spite of a comparatively low number of Streptococcus-positive samples, *Streptococcus* spp showed a different pattern of antimicrobial-resistance phenomena compared to other species of indicated bacteria. Only 155 cases (14.83%) out of 1045 bacterial-positive cultivations were found to be *Streptococcus* spp. All *Streptococcus* spp samples showed different levels of bacterial-antibiotic tolerance. As expected, 20 out of 29 antibiotics were relatively non-functional as *Streptococcus* spp displayed resistance to antibiotics from 50-100% of analyzed cases. Non-functional antibiotics (from high to low resistance) included NOR (100.0%), CTZ (94.4%), OX (94.1%), CFX (84.1%), AZM (82.2%), NA (81.0%), CL (77.2%), COR (76.4%), and CX (75.0%) as bacteria were respectively resistant in 75 to 100% of the investigated cases. AMP, APX, CFX, DA, E, AX, KF, GN, TMP, IMP, and TE were non-lethal in 50 to 74% of bacterial-positive cases. P, CIP, AK, AUG, and NIT were also partially non-working but better than above antimicrobial as the bacterial resistance was found only in 25-49% of the cases (not shown in Fig. 3). The range of the active antibiotics was restricted

in DX (19.0%), RF (18.1%), MEM (15.3%), and VA (14.8%) as they killed or prevented bacterial growth in 0-24% of the tests (Fig 3 and Table 2).

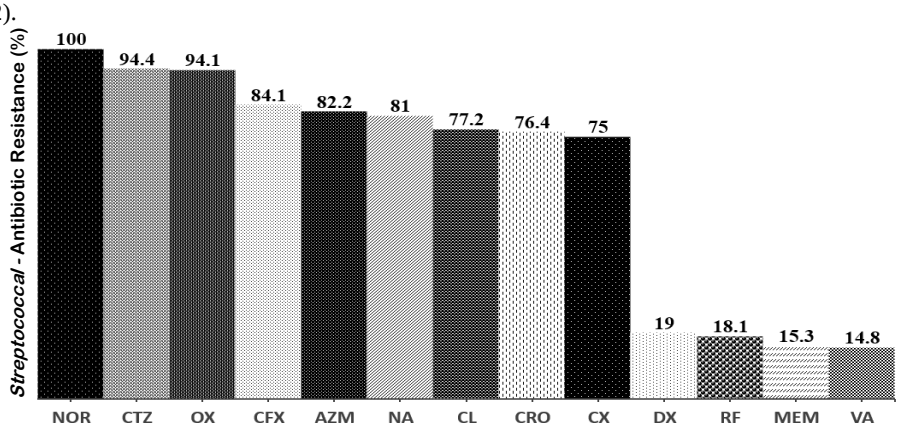


Figure 3: Analysis of *Streptococcus*-antibiotic interactions. Cases per antibiotic: NOR (5), CTZ (18), OX (17), CFX (63), AZM (62), NA (37), CL (22), CRO (68), CX (36), DX (27), RF (44), MEM (30), VA (54). Other details are in Fig. 1.

Through all the bacterial-positive samples, *Klebsiella* spp were isolated only from 165 (15.78%) samples during the same period. *Klebsiella* spp demonstrated resistance to a broader range of antibiotics compared to other bacteria. *Klebsiella* spp were resistance to 15 antimicrobials; MTZ, OX, and APX (100.0%), P (96.2%), E (92.6%), DA (92.1%), AX (91.0%), AMP (88.0%), CL (85.0%), KF (83.3%), VA (80.9%), AUG and TMP (80.0%), RF (75.8%), and CTX (75.2%) for ≥ 75% of analyzed cases and also another eight antibiotics (CFX, CTZ, CRO, NA, NOR, CX, TMP, and TE) did not show any ability to kill or prevent bacterial growth for 50-74% of the tested cases (not shown in Fig .4). Therefore, such 23 out of 33 antibiotics were non-functional in at least ≥ 50% of investigated samples. However, AZM, CIP, DX, and NIT were found to be more functional than those mentioned above by preventing the *Klebsiella* spp to grow in 25-49% of cases via their positive action against *Klebsiella* spp. Finally, GN (18.2%), AK (7.0%), MEM (3.4%), and IMP (2.95) were the first choices in *Klebsiella*-related infections where they were fatal in 75-100% of tested samples (Table 2, Fig. 4). Antimicrobials like; APX, MTZ, OX were entirely non-functional (100%) against *Klebsiella* spp in addition to P (96.2%) of analyzed samples. On the other side, IMP was the most functional (97.1%) antibiotic against *Klebsiella* spp in addition to MEM (96.6%), AK (93.0%), and GN (82.8%).

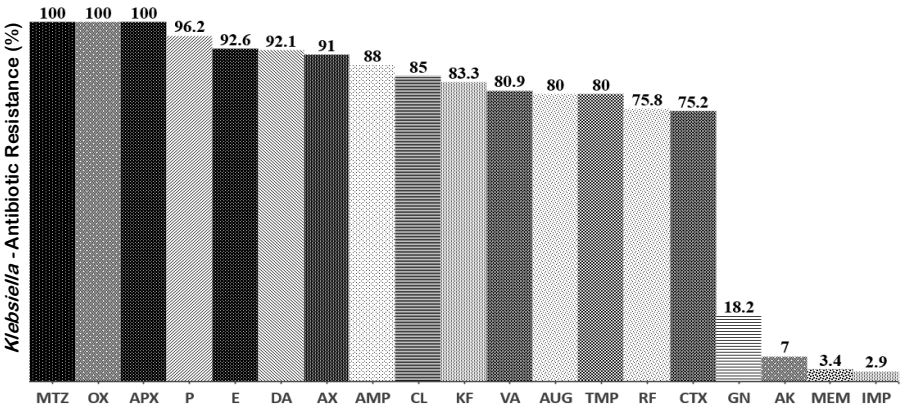


Figure 4: *Klebsiella*-Antibiotics Sensitivity Analysis. Cases per antibiotic: MTZ (22), OX (4), APX (49), P (27), E (41), DA (51), AX (6), AMP (67), CL (34), KF (12), VA (21), AUG (115), TMP (15), RA (58), CTX (101), GN (126), AK (26), MEM (29), IMP (34). Other details are in Fig. 1.

Table 2: Distribution of antibiotics according to their activity against indicated bacteria.

| | Bacterial-Antibiotic Resistance (%) | | | |
|---|---|---|---|---|
| **Bacteria** | **75-100** | **50-74** | **25-49** | **0-24** |
| ***Staphylococcus* spp** | AX, APX, E, DA, CX, MTZ, CFX, NA, CTZ, AZM, NOR, OX. | AMP, CL, AUG, TE, CTX, P, CRO, TMP. | KF, CIP, DX, GN, NIT, RF. | AK, IMP, MEM, VA. |
| ***Escherichia coli*** | AX, APX, E, DA, CX, MTZ, AMP, AUG, P, CL. | KF, CFX, CTX, CTZ, CRO, DX, NA, RF, TMP, VA, TE. | AZM, CIP, GN, NIT, NOR. | AK, IMP, MEM. |
| ***Streptococcus* spp** | NOR, CTZ, OX, CFX, AZM, NA, CL, CRO, CX. | AMP, APX, CFX, DA, E, AX, KF, GN, TMP, IMP, TE. | P, CIP, AK, AUG, NIT. | DX, RF, MEM, VA. |
| ***Klebsiella* spp** | AX, APX, E, DA, CTX, MTZ, AMP, AUG, P, CL, VA, RF, KF, OX, TMP. | CFX, CTZ, CRO, NA, NOR, TE, TMP, CX. | AZM, CIP, DX, NIT. | AK, IMP, MEM, GN. |

## 4. DISCUSSION

All tested bacterial strains demonstrated significant resistance to a broad spectrum of antibiotics, with each genus showing resistance to at least ten different antibiotics. This resistance presents a severe challenge in combating bacterial infections. Most antibiotics were ineffective, failing to kill or inhibit bacterial growth in at least 75% of the cases tested. Conversely, only a few antibiotics, such as AK, IMP, MEM, VA, DX, RF, and GN, showed lethal effects in ≥75% of the tested cases, with no more than four effective antibiotics per genus. Unfortunately, these findings highlight the alarming rate of antibiotic resistance among uropathogenic bacteria.

*Staphylococcus*, especially *S. aureus*, has become adept at resisting antibiotics through a variety of mechanisms. This resistance is especially concerning with strains like MRSA (Methicillin-Resistant *S. aureus*), which can cause serious infections that are hard to treat (Nandhini *et al*., 2022). In line with our results, *Staphylococcus* species previously obtained from the upper respiratory tract exhibited susceptibility to MEM, IMP, and AK (Ullah *et al*., 2022), as well as to VA (Ali *et al*., 2022). Nonetheless, as suggested in various earlier studies, *Staphylococcus* species were also identified as resistant to a broad spectrum of antibiotics (Van *et al*., 2024). These findings align with a previous study conducted in Kurdistan-Iraq, where *Staphylococcus* spp were observed to be resistant to VA (Abdulrahman & Taher, 2018) NIT and P but yet remained susceptible to AK (Mohamed, 2023). However, research by Abduljabar and Naqid (2022) indicates that *Staphylococcus* spp found in the nasal passages of athletes are highly susceptible to RF, GN, and fusidic acid.

Moreover, and consistent with current work presented findings, strains of *E. coli* isolated from hospitalized patients with various infections demonstrated susceptibility to AK, MEM, and IMP (Esfahani *et al*., 2024). Conversely, some *E. coli* strains derived from children were identified as resistant to these antibiotics (Luo *et al*., 2023). This variation in antibiotic response could be linked to several factors, including bacterial population density, genetic variation, or prior exposure to pathogens. Similar to the current study's findings, *E. coli* strains in research conducted in the Kurdistan region were found to be resistant to P and E but showed sensitivity to IMP and MEM (Assafi & Ali, 2022).

The present antibiotic susceptibility profile of *Streptococcus* species aligns with findings from a previous study by Alhamadani and Oudah (2022). Their research indicated that *Streptococcus* spp showed complete resistance to NOR, marking it as the least effective antibiotic against this pathogen. On the other hand, among the antibiotics evaluated in this study, VA showed the most excellent effectiveness against *Streptococcus* spp., consistent with the results of a study by Chiorescu *et al*. (2024). Furthermore, the current findings of Klebsiella spp are parallel with those of other research conducted in the Kurdistan region, where *K. pneumoniae* was found to be resistant to a broad range of antimicrobials, especially AMP. At the same time, IMP showed complete lethality against the isolates (Naqid *et al*., 2020b). In another study by Mhawesh *et al*., 2021, *Klebsiella* strains were observed to be resistant to VA and RF but sensitive to AK and MEM. However, the pattern of antibiotic resistance in *Klebsiella* spp appears to vary between studies due to differences in pathogen strains, antibiotic concentrations, and the bacteria's resistance capabilities. *Klebsiella-mediated* biofilms contribute to the failure of antibiotic treatments by obstructing access to the cells in the deeper layers of the biofilm matrix and creating drug resistance (Sharma *et al*., 2023). *Klebsiella* strains were also found to be resistant to multiple antimicrobials due to plasmid-mediated properties (Li *et al*., 2023).

Bacteria have developed multiple methods to resist antibiotics, including breaking down antibiotic molecules through enzymes (Pathak et al., 2023) and altering their internal targets. Hence, the drugs are ineffective (Varela *et al*., 2021), using broad-spectrum efflux pumps to remove antibiotics from their cells (Gaurav *et al*., 2023) and reducing their cell membrane permeability, which limits the number of antibiotics that can enter (Maher & Hassan, 2023). The bacteria studied in this work might employ one or more of the previously mentioned antibiotic resistance mechanisms to survive in environments heavily saturated with antimicrobial agents.

Several risk factors contribute to the emergence of an antibiotic-resistance problem. However, the primary reasons for the rise in bacterial-antibiotic resistance in the Kurdistan region include the overuse of antibiotics, a common practice among the public (Ghazala *et al*., 2023), incomplete treatment courses (Borek *et al*., 2023), and poor infection control in some healthcare settings (Abalkhail & Alslamah, 2022). Other contributing factors are global travel and trade, environmental contamination (Coque *et al*., 2023), molecular reasons such as horizontal gene transfer (Michaelis & Grohmann, 2023), and chromosomal point mutations (Simone *et al*., 2023). The differences between presented results and findings from other studies may be due to several reasons: genetic variability from one strain to another, environmental conditions, antibiotic concentrations, bacterial population density, pathogens' previous exposure, susceptibility measurement methods, and the presence of resistance mechanisms which differ from species to another. By combining responsible antibiotic use, improved hygiene practices, international collaboration, and continuous research, substantial progress can be achieved in addressing the challenge of bacterial antibiotic resistance.

## CONCLUSION

Meropenem (MEM) and amikacin (AK) are recommended as the primary treatment options for urinary tract infections (UTIs) caused by the pathogens discussed above. Among the antibiotics tested, imipenem (IMP) and vancomycin (VA) demonstrated the highest effectiveness against *Staphylococcus* species, with fatal activity rates of 97.8% and 92.4%, respectively. Additionally, IMP is considered the first-line treatment for infections caused by *E. coli* strains and *Klebsiella* spp, with lethal activity levels reaching 100% and 97.1%, respectively. For treating infections derived from *Streptococcus*, vancomycin (85.2%) and meropenem (84.3%) were identified as the most potent antimicrobials.

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### Abbreviations and concentrations of antibiotics/µg

**AK** Amikacin (10), **AMP** Ampicillin (10), **APX** Ampicillin/Cloxacillin (25/5), **AUG** Amoxicillin/Clavulanic acid (Augmentin) (20/10), **AX** Amoxicillin (10), **AZM** Azithromycin (15), **C** Chloramphenicol (10), **CFX** Cefixime (30), **CIP** Ciprofloxacin 10), **CL** Cephalexin (30), **CRO** Ceftriaxone (10), **CTX** Cefotaxime (10), **CTZ** Ceftazidime (10), **CX** Cloxacillin (10), **DA** Clindamycin (10), **DX** Doxycycline (10), **E** Erythromycin (100), **GN** Gentamycin (10), **IMP** Imipenem (10), **KF** Cephalothin (30), **LEV** Levofloxacin (5), **ME** methicillin, **MEM** Meropenem (10), **MTZ** Metronidazole (30), **NA** Naldixic acid (30), **NIT** Nitrofurantoin (100), **NOR** Norfloxacin (30), **OX** Oxacillin (10), **P** Penicillin (10), **RF** Rifampicin (5), **TE** Tetracycline (25), **TMP** Trimethoprim (10), **VA** Vancomycin (10).

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