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Original Article

Antibiotic Resistance Profiling and Efficacy Mapping of Clinically Relevant Bacteria in Benghazi: A 2025 Microbial Landscape

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Keywords

Antimicrobial resistance

Escherichia coli

Gentamicin

Levofloxacin

Antibiotic susceptibility.

ABSTRACT

Background: Antimicrobial resistance is an escalating global health threat, complicating the treatment of bacterial infections. The study aim to assess the in vitro antibiotic susceptibility of clinically significant bacterial isolates—*Pseudomonas aeruginosa*, *Escherichia coli*, and *Staphylococcus aureus*—to commonly used antibiotics in Benghazi, Libya, during 2025.

Methods: Standard disc diffusion techniques were employed to test seven antibiotics (Rifampicin, Clindamycin, Levofloxacin, Meropenem, Ampicillin, Gentamicin, and Tetracycline) against the three bacterial species. Sensitivity and resistance profiles were analyzed to determine the most effective therapeutic agents.

Results: Meropenem and Gentamicin exhibited the highest overall efficacy, each achieving a sensitivity rate of 90.9%, followed by Levofloxacin (81.8%). Ampicillin also demonstrated moderate sensitivity across isolates. Conversely, high resistance rates were observed for Rifampicin (72.7%), Tetracycline (72.7%), and Clindamycin, particularly among Gram-negative bacteria. Notably, *S. aureus* displayed greater overall susceptibility compared to *P. aeruginosa* and *E. coli*.

Conclusion: Meropenem, Gentamicin, and Levofloxacin were the most effective antibiotics against the studied isolates. However, the substantial resistance to several first-line agents emphasizes the urgent need for antimicrobial stewardship and continuous local resistance monitoring. Developing antibiotic policies tailored to regional susceptibility patterns is crucial to optimize treatment outcomes and mitigate the spread of multidrug-resistant organisms.

1. Introduction

The term "antibiotic" was originally defined as a substance produced by microorganisms capable of halting the growth or eliminating other microorganisms. Today, the definition has broadened to include compounds of both natural and synthetic origin that display a wide range of antibacterial activities. The primary mechanisms by which

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antibiotics act include: Inhibiting the synthesis of bacterial cell walls, Disrupting the integrity of cell membranes ,Blocking nucleic acid or protein synthesis and Interfering with various metabolic processes(Baran et al.2023)

The advent of antibiotics was among the greatest medical achievements, significantly reducing the mortality and morbidity caused by bacterial infections. During the so-called "Golden Age of Antibiotics," the discovery of new antibiotics peaked. However, the misuse and overuse of antimicrobial agents in subsequent decades accelerated the emergence of resistant bacterial strains, further worsened by excessive prescription practices by clinicians (Baran et al.2023)

Overall, antibiotic resistance is currently one of the most critical global public health concerns. Each year, antibiotic-resistant bacteria are responsible for approximately 700,000 deaths worldwide. Many existing antibiotics are ineffective against drug-resistant bacteri (Tarin-Pello et al.2022)

The World Health Organization (WHO) has compiled a global list of priority pathogens, classifying them into critical, high, and medium levels of antibiotic resistance. This classification aims to encourage research and the creation of innovative treatments(Karman et al.2022)

For example, Staphylococcus saprophyticus is recognized as the primary cause of uncomplicated urinary tract infections (UTIs). This bacterium has developed resistance to commonly used antibiotics for UTIs, including ampicillin and ciprofloxacin. Similarly, Streptococcus viridans, which is part of the upper respiratory tract flora, has acquired resistance to penicillin and other beta-lactam antibiotics due to changes in penicillin-binding proteins(Karman et al. 2022).

The aim of this study is to assess the in vitro antibiotic susceptibility of clinically significant bacterial isolates—Pseudomonas aeruginosa, Escherichia coli, and Staphylococcus aureus—to commonly used antibiotics in Benghazi, Libya, during 2025.

2. Materials and Methods

2.1. Antimicrobial Susceptibility Testing

Antimicrobial susceptibility profiles of clinically significant pathogens were systematically assessed using a selected panel of therapeutically relevant antimicrobial agents. The susceptibility testing was carried out following the standardized disk diffusion methodology in accordance with the Clinical and Laboratory Standards Institute (CLSI) guidelines (Haley et al., 2024).

Clinical isolates—comprising bacterial species—were obtained from diverse patient samples and initially cultured on appropriate selective and enriched media to ensure optimal growth and preliminary identification. The bacterial pathogens analyzed included *Escherichia coli, Klebsiella pneumoniae, Staphylococcus aureus, Streptococcus agalactiae , P.aeruginosa*

Definitive identification was achieved using the VITEK® 2 Compact system (BioMérieux, Marcy-l'Étoile, France), which enabled high-throughput, automated confirmation of the isolates. The antimicrobial agents tested—selected based on their clinical applicability and spectrum of activity—included Levofloxacin (LEV), gentamicin (CN), Clindamycine, Meropenem, Ampicillin, Tetracycline

Standardized inocula, adjusted to 0.5 McFarland turbidity, were inoculated onto Mueller-Hinton agar for bacterial isolates. After incubation, inhibition zone diameters were measured in millimetres and interpreted as Susceptible (S) or Resistant (R) according to the interpretive breakpoints outlined in CLSI guidelines.

2.2. Bacterial Strains and Culture Conditions

Clinical bacterial isolates were obtained from hospitalized patients diagnosed with confirmed bacterial infections. Samples were collected from a broad range of clinical sources, including stool, blood, cerebrospinal fluid (CSF), urine, and various swab specimens, encompassing patients of varying ages and both sexes. Ethical approval for the study was granted by the institutional review board, and informed consent was obtained from all participants to ensure adherence to ethical standards in clinical research.

The bacterial isolates represented both Gram-positive and Gram-negative pathogens. Gram-positive strains included Staphylococcus aureus, Streptococcus agalactiae, while the Gram-negative cohort comprised Escherichia coli, Pseudomonas aeruginosa, and Klebsiella pneumoniae. Initial identification and confirmation of isolates were performed using the VITEK® 2 Compact system (BioMérieux, Marcy-l'Étoile, France)

To maintain viability and purity, all isolates were routinely cultured on Mueller-Hinton agar (HIMEDIA, India) and subcultured on fresh nutrient agar plates as necessary throughout the experimental timeline. Antimicrobial susceptibility was evaluated using both the standardized disk diffusion and well-diffusion methods in accordance with CLSI guidelines.

2.3. Ethical approval

All clinical samples were anonymized prior to analysis to ensure patient confidentiality. The study was approved by the Institutional Ethics Review Board at Alnojoom Elsatea Collage and conducted in accordance with the ethical principles outlined in the Declaration of Helsinki

2.4. Statistical analysis

All data were processed and organized using Microsoft Excel 2023 and are presented as mean values ± standard deviation (SD). Statistical comparisons between groups were performed using the independent samples t-test to evaluate differences in mean values. A p-value of less than 0.05 ($p < 0.05$) was considered indicative of statistical significance. All analyses were conducted using SPSS software (SPSS Inc., Chicago, IL, USA)

3. Results

The variable (organism group) is distributed into gram-negative bacilli at a rate of 63.6% and gram-positive cocci at a rate of 36.4%. As The table shows the percentages of bacterial species as follows: *Pseudomonas aeruginosa, Escherichia coli*, (*E.coli*) and *Staphylococcus aureus* (*S.aureus*) at 18.8%, while the percentages of the species *Proteus*, *Klebsiella pneumoniae* (*K. pneumoniae*), *Streptococcus, Enterobacter cloacae* (*E.cloacae*) and *Bacillus* were at 9.1% (Table 1).

Table 1: The general characteristics of the study sample

Variables		Frequency	Percentage
specimen types	swab	11	100.0%
source	Others	8	72.7%
	Abscess	3	27.3%
Organism group	Gram negative bacilli	7	63.6%
	Gram positive cocci	4	36.4%
Bacteria	*Proteus*	1	9.1%
	P.aeruginosa	2	18.2%
	E.coli	2	18.2%
	K. pneumoniae	1	9.1%
	Streptococcus	1	9.1%
	S. aureus	2	18.2%
	E.cloacae	1	9.1%
	Bacillus	1	9.1%

3.1. Antibiotic Resistance Profiles

Sensitivity rates of 27.3% of the samples. The least sensitive types were Rifampicin and Ampicillin with a sensitivity rate of 18.2%, The table shows that the highest resistance rates were for the antibiotics Ampicillin, Tetracycline, and Rifampicin with rates of 81.8%, 72.7%, and 72.7% respectively. It is followed by Levofloxacin (5mg) with a resistance rate of 18.2%, and the lowest resistance rates were 9.1% for Meropenem and Gentamicin (Table 2).

The results presented in Figure 1 demonstrate that *Proteus spp.* exhibited complete susceptibility to all the antibiotics tested. These included Tetracycline, Gentamicin, Ampicillin, Meropenem, Levofloxacin, Clindamycin and Rifampicin. For each of these antibiotics, the sensitivity rate was 100%, with no resistance detected (0%).

The findings for *P.aeruginosa*, as illustrated in Figure 2, showed a mixed sensitivity profile. The bacteria were completely sensitive (100%) to Meropenem and Rifampicin, with no resistance observed. However, partial resistance was detected for several other antibiotics. Specifically, resistance rates of 18.2% were observed for Tetracycline, Gentamicin, Ampicillin, and Levofloxacin (5 mg), with corresponding sensitivity rates of 81.8%–82.0%. Clindamycin exhibited a slightly higher resistance rate of 20%, with 80% sensitivity.

Figure 3 shows that *E. coli* exhibited varied sensitivity to the antibiotics tested. The bacteria were completely sensitive (100%) to Meropenem and Rifampicin, with no resistance detected. However, partial resistance was noted for several antibiotics. Tetracycline, Gentamicin, and Ampicillin each showed a resistance rate of 18.2%, with corresponding sensitivity rates of 81.8%. Levofloxacin (5 mg) demonstrated slightly better sensitivity, with a resistance rate of 9.1% and sensitivity of 90.9%. Clindamycin exhibited the highest resistance among the tested antibiotics for *E. coli,* with a resistance rate of 20% and sensitivity of 80%. These findings indicate that Meropenem and Rifampicin remain highly effective against *E. coli,* while partial resistance has emerged against some other antibiotics.

In Figure 4, the antibiotic sensitivity and resistance profile of *K. pneumoniae* is illustrated. The bacteria displayed complete sensitivity (100%) to Meropenem and Rifampicin, with no resistance observed. Tetracycline, Gentamicin, and Ampicillin each showed a resistance rate of 9.1%, indicating high but not absolute sensitivity (90.9%). Levofloxacin (5 mg) demonstrated similar results, with a resistance rate of 9.1% and sensitivity of 90.9%. Clindamycin also showed complete sensitivity in this bacterial species, with no resistance detected. These results suggest that *K. pneumoniae* isolates are largely sensitive to the antibiotics tested, with only minor resistance observed against a few agents.

The antibiotic sensitivity profile of *Staphylococcus spp*, shown in Figure 5, demonstrated a generally high sensitivity to the antibiotics tested. The isolates exhibited complete sensitivity (100%) to Meropenem, Levofloxacin, Clindamycin, and Rifampicin, with no resistance detected. However, a resistance rate of 9.1% was recorded for Tetracycline, Gentamicin, and Ampicillin, resulting in a sensitivity rate of 90.9% for these antibiotics.

S. aureus results shown in Figure 6 indicate slightly higher resistance patterns. The isolates demonstrated complete sensitivity to Meropenem and Rifampicin (100%), but displayed a resistance rate of 18.2% for Tetracycline, Gentamicin, Ampicillin, and Levofloxacin, each showing a corresponding sensitivity of 81.8%. Clindamycin showed the highest resistance rate among the antibiotics tested, with 20% resistance and 80% sensitivity.

In Figure 7, *E.cloacae* isolates demonstrated a varied antibiotic response. Complete sensitivity (100%) was observed for Meropenem and Rifampicin, whereas Clindamycin showed the highest resistance rate at 20%, leaving an 80% sensitivity rate. Tetracycline, Gentamicin, Ampicillin, and Levofloxacin exhibited a resistance rate of 9.1%, with corresponding sensitivity rates of 90.9%–91.0%.

Table 5 shows the sensitivity and resistance of three types of bacteria *P. aeruginosa*, *E.coli, and S.aureus* to seven different antibiotics. For the antibiotic Rifampicin, all Isolates of *P. aeruginosa* and *E. coli* showed complete resistance (33.3%) and no sensitivity (0.0%). In contrast, Staphylococcus aureus exhibited partial sensitivity (33.3%) and no resistance (0.0%).

Regarding Clindamycin, *P. aeruginosa* and *E. coli* showed complete resistance (33.3%) with no sensitivity observed. *S. aureus* showed some sensitivity (33.3%) and no resistance. With Levofloxacin, all three bacterial strains, *P. aeruginosa, E. coli, and S. aureus*, demonstrated equal sensitivity (33.3%) and no resistance (0.0%), Indicating that levofloxacin was effective across all tested strains. For Meropenem, both *P. aeruginosa and E. coli* showed complete resistance (33.3%) with no sensitivity, whereas *S. aureus* demonstrated partial sensitivity (33.3%) and no resistance.

In the case of Ampicillin, all three bacterial strains were fully sensitive (33.3%) with no recorded resistance (0.0%), Indicating good effectiveness of the antibiotic. For Gentamicin, *P. aeruginosa and E. coli* exhibited higher sensitivity (18.2%) compared to S. aureus (9.1%), and no resistance was observed among any of the bacterial strains (0.0%). Lastly, *P. aeruginosa and E. coli showed* complete resistance to Tetracycline (33.3%) with no sensitivity, while S. aureus was sensitive (33.3%) and exhibited no resistance

Table 2: The distribution of antibiotic types according to the sensitivity and resistance variable.

Antibiotic name	Sensitive	Resistance
Rifampicin	2 (18.2%)	8 (72.7%)
Clindamycin	3 (27.3%)	7 (63.6%)
Levofloxacin	9 (81.8%)	2 (18.2%)
Meropenem	10 (90.9%)	1 (9.1%)
Ampicillin	2 (18.2%)	9 (81.8%)
Gentamicin	10 (90.9%)	1 (9.1%)
Tetracycline	3 (27.3%)	8 (72.7%)

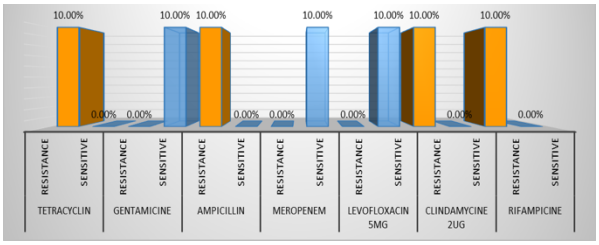


Figure 1: The antibiotic sensitivity and resistance profile of the bacteria *Proteus* against various antibiotics, including: Tetracycline Gentamicin Ampicillin Meropenem Levofloxacin Clindamycine Rifampicin. Data are expressed as percentages.

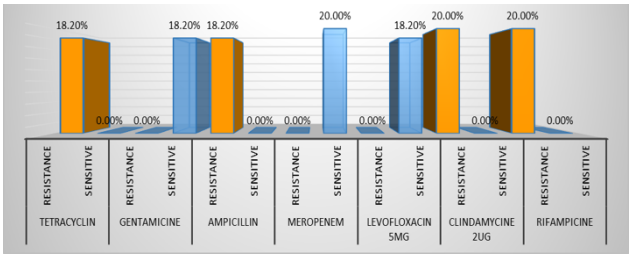


Figure 2: The antibiotic sensitivity and resistance profile of *P. aeruginosa* against various antibiotics, including: Tetracycline Gentamicin Ampicillin Meropenem Levofloxacin Clindamycine Rifampicin. Data are expressed as percentages.

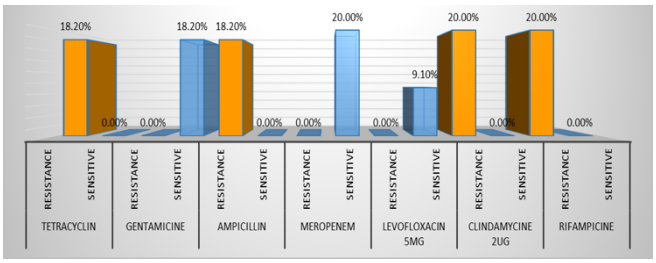
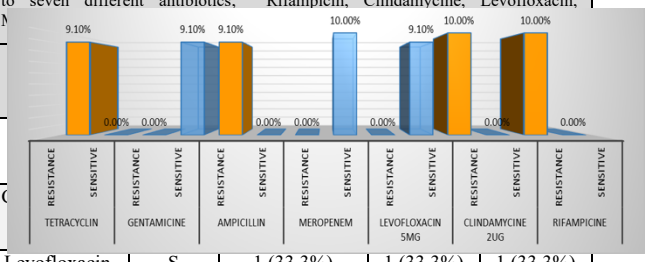


Figure 3: The antibiotic sensitivity and resistance profile of *E. coli* against various antibiotics, including: Tetracycline Gentamicin Ampicillin Meropenem Levofloxacin Clindamycine Rifampicin. Data are expressed as percentages.

Table 5: The sensitivity (S) and resistance (R) of *P. aeruginosa*, *E.coli, and S.aureus* to seven different antibiotics; Rifampicin, Clindamycine, Levofloxacin, M



Levofloxacin	S	1 (33.3%)	1 (33.3%)	1 (33.3%)
	R	0 (0.0%)	0 (0.0%)	0 (0.0%)
Meropenem	S	0 (0.0%)	0 (0.0%)	1 (33.3%)
	R	1 (33.3%)	1 (33.3%)	0 (0.0%)
Ampicillin	S	1 (33.3%)	1 (33.3%)	1 (33.3%)
	R	0 (0.0%)	0 (0.0%)	0 (0.0%)
Gentamicin	S	2 (18.2%)	2 (18.2%)	1 (9.1%)
	R	0 (0.0%)	0 (0.0%)	0 (0.0%)
Tetracycline	S	0 (0.0%)	0 (0.0%)	1 (33.3%)
	R	1 (33.3%)	1 (33.3%)	0 (0.0%)

Figure 4: The antibiotic sensitivity and resistance profile of *K. pneumoniae* against various antibiotics, including: Tetracycline Gentamicin Ampicillin Meropenem Levofloxacin Clindamycine Rifampicin. Data are expressed as percentages.

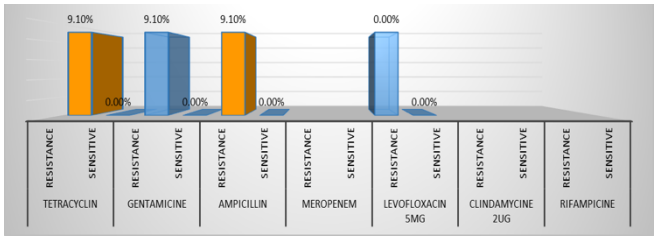


Figure 5: The antibiotic sensitivity and resistance profile of *Staphylococcus* against various antibiotics, including: Tetracycline Gentamicin Ampicillin Meropenem Levofloxacin Clindamycine Rifampicin. Data are expressed as percentages.

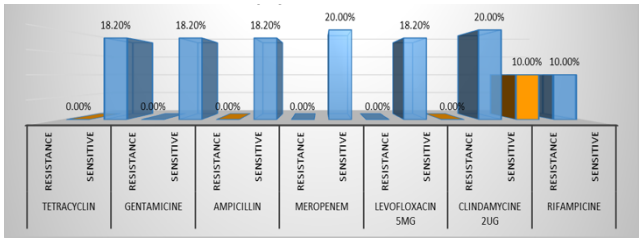


Figure 6: The antibiotic sensitivity and resistance profile of *S.aureus* against various antibiotics, including: Tetracycline Gentamicin Ampicillin Meropenem Levofloxacin Clindamycine Rifampicin. Data are expressed as percentages.

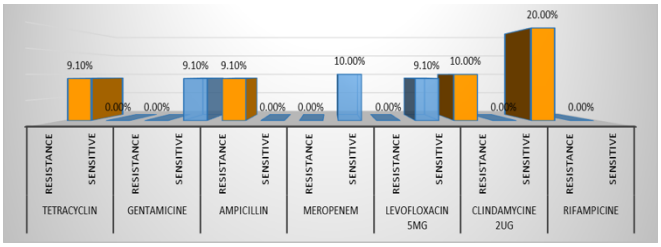


Figure 7: The antibiotic sensitivity and resistance profile of *E.cloacae* against various antibiotics, including: Tetracycline Gentamicin Ampicillin Meropenem Levofloxacin Clindamycine Rifampicin. Data are expressed as percentages.

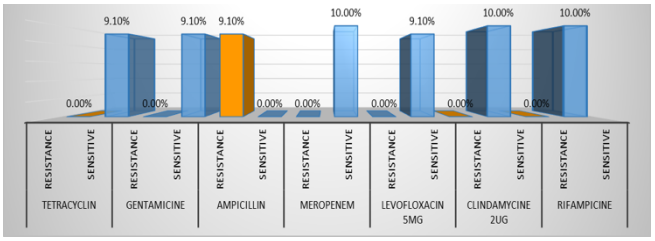


Figure 8: The antibiotic sensitivity and resistance profile of *Bacillus* against various antibiotics, including: Tetracycline Gentamicin Ampicillin Meropenem Levofloxacin Clindamycine Rifampicin. Data are expressed as percentages.

4. Discussion

This study assessed the antimicrobial susceptibility profiles of bacterial isolates in Benghazi and identified **Meropenem** and Gentamicin as the most effective antibiotics, both achieving sensitivity rates. Levofloxacin followed with a sensitivity rate of 81.8%. These findings align with previous research demonstrating the broad-spectrum efficacy of Meropenem against Gram-positive and Gram-negative bacteria, including multidrug-resistant strains (Caap-Ahlgren et al., 2001; Abbas et al., 2024).

The notable effectiveness of Meropenem can be attributed to its structural stability against β-lactamases and its high affinity for penicillin-binding proteins (PBPs), which disrupt bacterial cell wall synthesis. This is consistent with reports highlighting its clinical success in treating severe infections such as intra-abdominal sepsis and nosocomial pneumonia (Baran et al., 2023). Similarly, Gentamicin's bactericidal action, mediated through inhibition of protein synthesis by binding to the 30S ribosomal subunit, supports its broad efficacy against various pathogens (Parmanik et al., 2022).

In contrast, high resistance rates were observed for Ampicillin, Rifampicin, and Tetracycline reflecting global trends of increasing resistance to β-lactam and first-generation antibiotics. This resistance is largely driven by factors such as the widespread use of these agents and the dissemination of resistance genes like mecA and β-lactamase enzymes (Karaman et al., 2020; Qiu et al., 2020). The resistance of Gram-negative isolates, particularly *E. coli* and *P. aeruginosa*, to Rifampicin and Tetracycline further corroborates previous findings attributing this phenomenon to mechanisms such as altered membrane permeability and enhanced efflux pump activity (Tarín-Pelló et al., 2022).

Levofloxacin exhibited a moderate resistance rate of 18.2%, reinforcing its role as a reliable treatment

option. Nevertheless, the increasing global resistance to fluoroquinolones—primarily due to chromosomal mutations in **gyrA** and **parC** genes—warrants cautious use and ongoing monitoring (Sitovs et al., 2021).

Overall, the local resistance patterns identified in this study reflect global trends and emphasize the pressing need for antimicrobial stewardship**,** targeted antibiotic therapy**,** and the development of novel antimicrobial agents**.** Routine surveillance of antibiotic resistance patterns and the establishment of localized antibiograms are crucial for guiding empirical therapy and mitigating the spread of resistant pathogens (Abbas et al., 2024).

5. Conclusion

This study highlights an alarming resistance pattern among clinical bacterial isolates in Benghazi, particularly against commonly used antibiotics such as Ampicillin and Tetracycline. Despite this, Meropenem, Gentamicin, and Levofloxacin remain effective therapeutic options, demonstrating high sensitivity rates across various bacterial species. The findings underscore the urgent need to implement robust antimicrobial stewardship programs**,** regularly update local antibiograms**,** and conduct continuous surveillance of resistance patterns. These efforts are essential to inform empirical treatment strategies, preserve the efficacy of existing antibiotics, and curb the further spread of antimicrobial resistance within the community.

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