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Prevalence and Antimicrobial Resistance Profiles of Bacterial Pathogens Isolated from Clinical Samples in Sabratha Region

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Abstract

Background: Antimicrobial resistance represents a major public health challenge, reducing the effectiveness of commonly used antibiotics and complicating the treatment of bacterial infections. Monitoring antimicrobial susceptibility patterns among clinically relevant bacterial species is essential for guiding appropriate antimicrobial therapy. **Objective:** This study aimed to evaluate and compare the antimicrobial susceptibility and resistance patterns of six bacterial species against different antimicrobial agents. **Methods:** Laboratory antimicrobial susceptibility data were analyzed for *Escherichia coli*, *Citrobacter* spp., *Klebsiella* spp., *Nitrobacteria* sp., *Pseudomonas* spp., and *Staphylococcus aureus*. Susceptibility and resistance frequencies and percentages were calculated for each species and antimicrobial agent. Overall differences in susceptibility and resistance patterns among bacterial species were assessed using the Pearson chi-square test. Pairwise comparisons were subsequently performed using Pearson chi-square tests, with Holm adjustment to account for multiple comparisons. Statistical significance was set at $p < 0.05$. **Results:** A total of 2,129 antimicrobial susceptibility test responses were analyzed, comprising 924 susceptible responses 43.4%) and 1,205 resistant responses (56.6%). The highest overall resistance rate was recorded for *Staphylococcus aureus* (68.2%), followed by *Citrobacter* spp. (59.1%), *E. coli* (58.1%), *Pseudomonas* spp. (56.2%), *Klebsiella* spp. (49.6%), and *Nitrobacteria* sp. (48.8%). Significant differences in the overall susceptibility–resistance distributions were observed among the six bacterial species ($\chi^2 = 31.11$, df = 5, $p < 0.001$). Holm-adjusted pairwise comparisons revealed significant differences between *E. coli* and *Nitrobacteria* sp. ($p = 0.0113$), *E. coli* and *S. aureus* ($p = 0.0346$), *Klebsiella* spp. and *S. aureus* ($p < 0.001$), *Nitrobacteria* sp. and *S. aureus* ($p < 0.001$), and *Pseudomonas* spp. and *S. aureus* ($p = 0.0412$). **Conclusion:** The findings demonstrate a considerable overall level of antimicrobial resistance, with marked variation among the investigated bacterial species. *Staphylococcus aureus* exhibited the highest resistance proportion, whereas *Nitrobacteria* sp. showed the lowest. These findings highlight the importance of continuous antimicrobial susceptibility surveillance and evidence-based antibiotic selection to support effective infection management and help limit the further emergence of antimicrobial resistance.

Keywords: Antimicrobial resistance; antibiotic susceptibility; bacterial pathogens; antimicrobial surveillance; Sabratha; Libya

Introduction

Escherichia coli is frequently isolated from clinical samples, particularly in urinary and bloodstream infections. It accounted for 69.44% of urinary infections and 48.12% of bloodstream infections in a study conducted at Hai Phong International Hospital (Trần et al., 2025). Similarly, it was the most common pathogen in a nationwide study in Bangladesh, comprising 32.48% of isolates (Rahman et al., 2025). *Staphylococcus aureus* is also prevalent, with a significant proportion being methicillin-resistant (MRSA). In Bangladesh, 95.7% of *S. aureus* isolates were MRSA (Hossain et al., 2024). In Ethiopia, *S. aureus* was the most common isolate from clinical samples (Abebe et al., 2019). Frequently isolated from sputum and urine samples, *K. pneumoniae* showed high prevalence in various studies, including 15.50% in Bangladesh (Rahman et al., 2025) and 18.08% in Saudi Arabia (Masoud & Mahdy, 2011). These bacteria, including *E. coli* and *K. pneumoniae*, often exhibit high resistance to cephalosporins and fluoroquinolones. In Bangladesh, resistance to third-generation cephalosporins was notably high, with *E. coli* showing 62.89% resistance to ceftriaxone (Rahman *et al*., 2025). In Ethiopia, resistance rates ranged from 60% to 100% against common antibiotics like ampicillin and tetracycline (Abebe et al., 2019). *S. aureus*, particularly MRSA, showed significant resistance to methicillin. However, linezolid and vancomycin remained effective against Gram-positive bacteria, with resistance rates as low as 1% and 2%, respectively, in Bangladesh (Hossain *et al*., 2024). Multidrug resistance (MDR) is a growing concern, with 69.6% of bacterial isolates in Bangladesh identified as multidrug-resistant (Hossain et al., 2024). In Saudi Arabia, the overall MDR rate among isolates was 28.72% (Masoud & Mahdy, 2011). A total of 709 cases of Extended Spectrum Beta-Lactamase (ESBL) production were found in *E. coli*, indicating significant multidrug resistance. Among *Staphylococcus aureus* isolates, 325 were classified as Methicillin-Resistant *Staphylococcus aureus* (MRSA), highlighting the threat of resistant strains. Carbapenems (ertapenem 94.50%, imipenem 91.40%, meropenem 91.00%) and linezolid (98.10%) showed high efficacy against resistant strains, while ciprofloxacin (48.60%) and levofloxacin (62.20%) demonstrated moderate effectiveness. (Trần *et al.,* 2025). Resistance patterns can vary significantly by region, necessitating localized studies to tailor antibiotic therapies effectively. For instance, carbapenems remained effective against resistant strains in Vietnam, while resistance to these drugs was lower in Bangladesh. (Rahman et al., 2025; Trần *et al.,* 2025).

While the studies highlight the critical issue of antimicrobial resistance, they also emphasize the importance of continuous surveillance and tailored interventions. The variability in resistance patterns across regions suggests that a one-size-fits-all approach may not be effective. Instead, localized data should guide the development of targeted strategies to combat the spread of resistant pathogens and improve patient care outcomes. Therefore, the present study aimed to evaluate and compare the prevalence and antimicrobial susceptibility profiles of major bacterial pathogens isolated from clinical samples in the Sabratha region, Libya.

Methods

Study Design and Study Area:

A retrospective descriptive study was conducted to investigate the prevalence and antimicrobial resistance patterns of bacterial pathogens isolated from clinical samples in the Sabratha region, northwestern Libya. Data were collected from different medical laboratories across the region.

Data Collection and Study Population:

The study included urine culture reports obtained from different medical laboratories in the Sabratha region. Six bacterial groups were identified: *Escherichia coli, Citrobacter spp., Klebsiella spp., Nitrobacteria sp., Pseudomonas spp.,* and *Staphylococcus aureus.* A total of 2,129 antimicrobial susceptibility test responses were recorded across the six bacterial groups. Among these, E. coli accounted for 744 test responses, comprising 312 susceptible responses (41.9%) and 432 resistant responses (58.1%). These data were used to evaluate and compare the antimicrobial susceptibility and resistance patterns of the identified bacterial groups.

Antimicrobial Susceptibility Testing:

Antimicrobial susceptibility data were obtained from routine laboratory records. The results were classified as susceptible (S) or resistant (R), according to the reports provided by the participating laboratories. Different antimicrobial agents were evaluated depending on bacterial species and laboratory records. No additional laboratory testing was performed during this study.

Statistical Analysis:

Data were entered, organized, and analyzed using Microsoft Excel. Frequencies and percentages were calculated to describe bacterial susceptibility and resistance patterns. The overall susceptibility and resistance rates were calculated from the total recorded antimicrobial test responses. Results were presented in tables to compare resistance patterns among bacterial groups and antimicrobial agents.

The Ethical Considerations:

The study was based on previously recorded laboratory data without direct patient involvement. Patient-identifying information was excluded, and permission to access laboratory records was obtained from the participating medical laboratories.

Results

The antimicrobial susceptibility profile of Staphylococcus aureus revealed an overall resistance rate of 68.2%, compared with a susceptibility rate of 31.8%, indicating a relatively high level of antimicrobial resistance among the tested isolates. The highest susceptibility was recorded for Augmentin (100%), followed by doxycycline (75%) and cefotaxime (60.0%). However, the number of observations differed between antibiotics, and these percentages should therefore be interpreted cautiously. In contrast, 100% resistance was observed against Bactrim, ceftazidime, erythromycin, imipenem, and penicillin. High resistance rates were also recorded for cephalexin and ofloxacin (90.9%), chloramphenicol (84.6%), and oxacillin (85.7%). These findings suggest reduced in-vitro activity of several tested antimicrobial agents against the examined isolates.

Data presented in table (1) revealed that, the overall comparison of antimicrobial susceptibility patterns revealed a higher resistance rate among Gram-positive bacteria (68.2%) than Gram-negative bacteria (51.2%). Conversely, Gram-negative bacteria exhibited a higher susceptibility rate (48.8%) compared with Gram-positive bacteria (31.8%). The overall antimicrobial resistance rate across both bacterial groups was 55.3%, indicating a considerable burden of resistance among the tested bacterial responses. Pearson's chi-square test demonstrated a highly significant association between Gram classification and antimicrobial susceptibility patterns ($\chi^2 = 25.32$, df = 1, $p < 0.001$). These findings suggest that Gram-positive bacteria exhibited a significantly higher proportion of antimicrobial resistance than Gram-negative bacteria, highlighting the importance of considering bacterial classification when evaluating antimicrobial susceptibility profiles.

Table (1). Overall Comparison of Antibiotic Susceptibility and Resistance Patterns Between Gram-negative and Gram-positive Bacterial Groups

Bacterial group	Susceptible, N (%)	Resistant, N (%)	Total
Gram-negative	442 (48.8)	464 (51.2)	906
Gram-positive	91 (31.8)	195 (68.2)	286
Total	533 (44.7)	659 (55.3)	1192

Statistical analysis: Pearson's $\chi^2 = 25.32$; df = 1; $p < 0.001$.

Table (2) presented the comparison of antimicrobial susceptibility and resistance patterns among the six bacterial species revealed considerable variations in their responses to the tested antimicrobial agents. Nitrobacteria sp. exhibited the highest susceptibility rate (51.2%), followed by Klebsiella spp. (50.4%), Pseudomonas spp. (43.8%), Escherichia coli (41.9%), and Citrobacter spp. (40.9%). In contrast, Staphylococcus aureus showed the lowest susceptibility rate (31.8%) and the highest resistance rate (68.2%). Citrobacter spp. and Escherichia coli also demonstrated relatively high resistance rates of 59.1% and 58.1%, respectively. Overall, antimicrobial resistance accounted for 56.6% of the 2,129 tested responses, compared with 43.4% susceptibility. Pearson's chi-square test demonstrated a highly significant difference in susceptibility and resistance distributions among the six bacterial species ($\chi^2 = 31.11$, df = 5, $p < 0.001$).

Table 2. Overall Comparison of Antimicrobial Susceptibility and Resistance Patterns Among the Six Bacterial Species

Bacterial species	S (N)	S (%)	R (N)	R (%)	Total
Escherichia coli	312	41.9	432	58.1	744
Citrobacter spp.	79	40.9	114	59.1	193
Klebsiella spp.	183	50.4	180	49.6	363
Nitrobacteria sp.	145	51.2	138	48.8	283
Pseudomonas spp.	114	43.8	146	56.2	260
Staphylococcus aureus	91	31.8	195	68.2	286
Total	924 (43.4%)	—	1205 (56.6%)	—	2129
Pearson χ^2	31.11				
Df	5				

Table (3) shows pairwise comparisons of antimicrobial resistance rates among the six bacterial species revealed statistically significant differences in four comparisons. Escherichia coli showed significantly different resistance rates compared with Nitrobacteria sp. (adjusted p = 0.0113) and Staphylococcus aureus (adjusted p = 0.0346). Similarly, Klebsiella spp. and Nitrobacteria sp. exhibited significantly different resistance rates compared with Staphylococcus aureus (adjusted p = 0.0000269 and p = 0.00000271, respectively). A significant difference was also observed between Pseudomonas spp. and Staphylococcus aureus (adjusted p = 0.0412). In contrast, the remaining pairwise comparisons did not reach statistical significance (p > 0.05). These findings indicate that antimicrobial resistance patterns varied significantly across selected bacterial species, particularly in comparisons involving Staphylococcus aureus.

Table (3). Pairwise Comparisons of Antimicrobial Resistance Rates Among the Six Bacterial Species

Pairwise comparison	Adjusted P-value	Significance
E. coli* vs. *Citrobacter spp.	1.0000	NS
E. coli* vs. *Klebsiella spp.	0.0696	NS
E. coli* vs. *Nitrobacteria sp.	0.0113	*
E. coli* vs. *Pseudomonas spp.	1.0000	NS
E. coli* vs. *S. aureus	0.0346	*
Citrobacter spp. vs. Klebsiella spp.	0.2311	NS
Citrobacter spp.* vs. *Nitrobacteria sp.	0.0670	NS
Citrobacter spp.* vs. *Pseudomonas spp.	1.0000	NS

Citrobacter spp.* vs. *S. aureus	0.2452	NS
Klebsiella spp.* vs. *Nitrobacteria sp.	0.4125	NS
Klebsiella spp.* vs. *Pseudomonas spp.	0.5280	NS
Klebsiella spp.* vs. *S. aureus	0.0000269	***
Nitrobacteria sp. vs. Pseudomonas spp.	0.1859	NS
Nitrobacteria sp.* vs. *S. aureus	0.00000271	***
Pseudomonas spp.* vs. *S. aureus	0.0412	*

NS: Not significant; *: $p < 0.05$; ***: $p < 0.001$. P-values were adjusted using the Holm method.

Table 4 illustrates the comparative antibiotic susceptibility and resistance profiles of Gram-negative and Gram-positive bacterial isolates against 25 antimicrobial agents. Overall, considerable variations in susceptibility patterns were observed between the two bacterial groups. Among Gram-negative bacteria, the highest susceptibility was recorded against penicillin (61.0%), followed by Augmentin (59.1%), amikacin (57.7%), and tetracycline (57.1%). In contrast, the highest resistance rates were observed against ofloxacin (66.7%), ampicillin (69.6%), and cefixime (65.7%). Regarding Gram-positive bacteria, complete susceptibility (100%) was observed against Augmentin, whereas complete resistance (100%) was recorded against Bactrim, ceftazidime, erythromycin, imipenem, and penicillin. Relatively high susceptibility was also observed against doxycycline (75.0%), cefotaxime (60.0%), and azithromycin (57.1%). Conversely, substantial resistance was detected against cephalexin (90.9%), ofloxacin (90.9%), chloramphenicol (84.6%), and oxacillin (85.7%). Notably, the comparative profiles revealed marked differences in antibiotic responses between the two bacterial groups. Augmentin demonstrated a particularly favorable activity against Gram-positive bacteria compared with Gram-negative bacteria (100.0% vs. 59.1%). Similarly, doxycycline showed greater activity against Gram-positive isolates (75.0% vs. 46.2%). Conversely, ceftazidime, imipenem, erythromycin, and penicillin exhibited considerably lower activity against Gram-positive bacteria. These findings highlight the variability of antimicrobial susceptibility between Gram-negative and Gram-positive bacteria and emphasize the importance of selecting antimicrobial agents based on bacterial identification and susceptibility testing rather than relying on generalized treatment assumptions.

Table (4). Comparative Antibiotic Susceptibility and Resistance Profiles of Gram-negative and Gram-positive Bacteria

Antimicrobial agent	Gram-negative S (%)	Gram-negative R (%)	Gram-positive S (%)	Gram-positive R (%)
Amikacin (AK)	57.7	42.3	44.0	56.0
Amoxicillin (AML)	54.3	45.7	45.0	55.0
Ampicillin (AMP)	30.4	69.6	36.4	63.6
Augmentin (AMC)	59.1	40.9	100.0	0.0
Azithromycin (AMZ)	51.5	48.5	57.1	42.9
Bactrim (SXT)	45.9	54.1	0.0	100.0
Cefixime (CFM)	34.3	65.7	58.8	41.2
Cefotaxime (CTX)	53.1	46.9	60.0	40.0
Ceftazidime (CAZ)	51.6	48.4	0.0	100.0
Ceftriaxone (CRO)	50.0	50.0	25.0	75.0
Cephalexin (CL)	51.1	48.9	9.1	90.9

Chloramphenicol (C)	39.5	60.5	15.4	84.6
Ciprofloxacin (CIP)	51.9	48.1	36.8	63.2
Oxacillin (OX)	54.0	46.0	14.3	85.7
Doxycycline (DO)	46.2	53.8	75.0	25.0
Erythromycin (E)	41.4	58.6	0.0	100.0
Gentamicin (CN)	40.0	60.0	30.0	70.0
Imipenem (IPM)	48.1	51.9	0.0	100.0
Nalidixic acid (NA)	47.1	52.9	33.3	66.7
Nitrofurantoin (F)	51.1	48.9	33.3	66.7
Ofloxacin (OFX)	33.3	66.7	9.1	90.9
Penicillin (P)	61.0	39.0	0.0	100.0
Tetracycline (TE)	57.1	42.9	22.2	77.8
Tobramycin (TOB)	52.4	47.6	22.2	77.8
Vancomycin (VA)	52.3	47.7	25.0	75.0

S = Susceptible; R = Resistant. Percentages for Gram-negative bacteria were recalculated using the combined counts of the three bacterial groups.

Table (5) clearing the overall analysis of antimicrobial susceptibility according to antibiotic classes revealed considerable variations in susceptibility and resistance patterns. The highest susceptibility rate was observed among β-lactam/β-lactamase inhibitor combinations (69.0%), followed by carbapenems (53.6%) and tetracyclines (50.0%). Conversely, phenicols exhibited the highest resistance rate (65.6%), followed by nitrofurans (62.3%), cephalosporins (60.4%), and fluoroquinolones (60.3%). Aminoglycosides and penicillinase-resistant penicillins showed resistance rates of 53.3% and 54.7%, respectively. Overall, resistance accounted for 56.6% of the 2,129 antimicrobial responses, compared with 43.4% susceptibility. Pearson's chi-square test demonstrated statistically significant differences in susceptibility and resistance distributions among the antibiotic classes (χ^2 = 33.46, df = 13, p = 0.00145). However, Cramér's V (0.125) indicated a relatively small effect size. These findings suggest that antimicrobial response patterns vary across drug classes, although the pooled results should be interpreted in consideration of the different bacterial species and individual antimicrobial agents included in each class.

Table 5. Overall Antimicrobial Susceptibility and Resistance Patterns According to Antibiotic Classes

Antibiotic class	Agents included	S (N)	S (%)	R (N)	R (%)	Total
Aminoglycosides	AK, CN, TOB	106	46.7	121	53.3	227
Penicillins	AML, AMP, P	100	41.2	143	58.8	243
β-lactam/β-lactamase inhibitors	AMC	40	69.0	18	31.0	58
Cephalosporins	CFM, CTX, CAZ, CRO, CL	179	39.6	273	60.4	452
Fluoroquinolones	CIP, OFX	62	39.7	94	60.3	156
Quinolones	NA	35	40.7	51	59.3	86
Macrolides	AMZ, E	59	40.7	86	59.3	145
Tetracyclines	DO, TE	79	50.0	79	50.0	158
Sulfonamides	SXT	51	45.5	61	54.5	112
Phenicols	C	32	34.4	61	65.6	93
Carbapenems	IPM	60	53.6	52	46.4	112
Nitrofurans	F	40	37.7	66	62.3	106
Glycopeptides	VA	42	44.2	53	55.8	95
Penicillinase-resistant penicillins	OX	39	45.3	47	54.7	86
Total	14 classes	924	43.4	1205	56.6	2129

Statistical analysis: Pearson $\chi^2 = 33.46$; df = 13; p = 0.00145; Cramér's V = 0.125.

The species-specific analysis demonstrated considerable heterogeneity in antimicrobial resistance profiles across antibiotic classes. E. coli exhibited particularly high resistance to penicillins (75.0%) and cephalosporins (71.2%), whereas Citrobacter spp. showed high resistance to macrolides (88.9%), quinolones (85.7%), and glycopeptides (83.3%). Klebsiella spp. displayed relatively high resistance to fluoroquinolones (67.7%) and carbapenems (60.0%). Nitrobacteria sp. showed complete resistance to phenicols (100.0%), while Pseudomonas spp. demonstrated high resistance to β-lactam inhibitor combinations (75.0%) and nitrofurans (77.8%). Staphylococcus aureus exhibited particularly high resistance to sulfonamides and carbapenems (100.0% in both groups), as well as phenicols (84.6%) and penicillinase-resistant penicillins (85.7%). These findings demonstrate that resistance profiles differ considerably according to both bacterial species and antibiotic class. Nevertheless, some percentages are based on small numbers of responses, particularly in classes containing only one or a few antimicrobial agents. Therefore, the observed percentages should be interpreted cautiously and should not be considered definitive evidence of resistance to an entire antibiotic class (Table 6).

Table 6. Comparative Antibiotic Class-Specific Resistance Profiles Among the Six Bacterial Species

Antibiotic class	*E. coli*	Citrobacter	Klebsiella	Nitrobacteria	Pseudomonas	Staphylococcus
Aminoglycosides	31/67 (46.3)	10/13 (76.9)	10/31 (32.3)	25/45 (55.6)	17/27 (63.0)	28/44 (63.6)
Penicillins	45/60 (75.0)	10/21 (47.6)	15/26 (57.7)	25/54 (46.3)	13/30 (43.3)	35/52 (67.3)
β-lactam inhibitors	3/18 (16.7)	6/13 (46.2)	0/9 (0.0)	6/9 (66.7)	3/4 (75.0)	0/5 (0.0)
Cephalosporins	141/198 (71.2)	6/23 (26.1)	48/91 (52.7)	18/39 (46.2)	26/47 (55.3)	34/54 (63.0)
Fluoroquinolones	29/53 (54.7)	4/7 (57.1)	21/31 (67.7)	6/11 (54.5)	12/24 (50.0)	22/30 (73.3)
Quinolones	19/33 (57.6)	6/7 (85.7)	9/14 (64.3)	4/12 (33.3)	5/8 (62.5)	8/12 (66.7)
Macrolides	33/58 (56.9)	8/9 (88.9)	9/25 (36.0)	9/14 (64.3)	15/23 (65.2)	12/16 (75.0)
Tetracyclines	27/56 (48.2)	14/24 (58.3)	13/26 (50.0)	5/16 (31.2)	11/19 (57.9)	9/17 (52.9)
Sulfonamides	28/59 (47.5)	7/10 (70.0)	9/15 (60.0)	6/11 (54.5)	5/11 (45.5)	6/6 (100.0)
Phenicols	22/34 (64.7)	2/3 (66.7)	5/17 (29.4)	9/9 (100.0)	12/17 (70.6)	11/13 (84.6)
Carbapenems	12/42 (28.6)	4/9 (44.4)	12/20 (60.0)	4/9 (44.4)	11/23 (47.8)	9/9 (100.0)
Nitrofurans	21/31 (67.7)	17/21 (81.0)	13/26 (50.0)	2/10 (20.0)	7/9 (77.8)	6/9 (66.7)
Glycopeptides	13/27 (48.1)	10/12 (83.3)	4/8 (50.0)	9/26 (34.6)	8/10 (80.0)	9/12 (75.0)

Penicillinase-resistant penicillins	8/8 (100.0)	10/21 (47.6)	12/24 (50.0)	10/18 (55.6)	1/8 (12.5)	6/7 (85.7)

Discussion

The present study revealed a considerable overall level of antimicrobial resistance among the investigated bacterial species, with 1,192 resistant responses (56.3%) compared with 924 susceptible responses (43.7%) out of 2,116 antimicrobial susceptibility test responses. Among the six bacterial groups, *Staphylococcus aureus* exhibited the highest overall resistance rate (68.2%), followed by *Citrobacter* spp. (59.1%), *Escherichia coli* (58.1%), *Pseudomonas* spp. (56.2%), *Klebsiella* spp. (49.6%), and *Nitrobacteria* sp. (46.3%). The observed differences in susceptibility and resistance distributions among bacterial species were statistically significant ($\chi^2 = 35.59$, df = 5, $p < 0.001$), indicating substantial variation in their antimicrobial response profiles. These findings emphasize that antimicrobial resistance is not uniform across bacterial species and highlight the importance of species-specific susceptibility testing when selecting appropriate antimicrobial therapy.

With respect to *E. coli*, the present study recorded an overall resistance rate of 58.1%, compared with 41.9% susceptibility across 744 antimicrobial test responses. The highest resistance rates were observed against ceftazidime (93.5%), amoxicillin (83.3%), and cephalexin (80.0%). The particularly high resistance to ceftazidime is concerning because third-generation cephalosporins are important therapeutic agents for infections caused by Gram-negative bacteria. This pattern may indicate the presence of beta-lactam resistance mechanisms, including the possible circulation of extended-spectrum beta-lactamase (ESBL)-producing *E. coli* strains. Nevertheless, resistance to ceftazidime alone cannot establish ESBL production, and confirmatory phenotypic or molecular testing is required. Similar concerns regarding the increasing resistance of *E. coli* to commonly used antimicrobial agents have been highlighted by Bonomo *et al*. (2018) and Bevan *et al*. (2017). Furthermore, Zorgani *et al.* (2017) documented the detection of the CTX-M-15 beta-lactamase among uropathogenic *E. coli* isolates from hospitals in Tripoli, providing molecular evidence of ESBL-associated resistance in Libya.

Comparisons with previous Libyan investigations reveal important differences in antimicrobial resistance patterns. Altayar *et al.* (2012) reported resistance rates of 30% to both ceftazidime and cefotaxime among clinical *E. coli* isolates in Benghazi, whereas the present study recorded substantially higher resistance to ceftazidime. Similarly, Shailabi et al. reported resistance rates of 62.5% to ceftriaxone and 47.11% to amoxicillin-clavulanic acid among urinary *E. coli* isolates in Al-Bayda. In contrast, Mohammed *et al*. (2016), in their investigation at Messalata Central Hospital, reported high effectiveness of amikacin and imipenem against urinary bacterial isolates. More recent Libyan evidence also supports the persistence of considerable beta-lactam resistance. A retrospective review of antimicrobial resistance studies from Arabian countries, including Libya, reported ceftazidime and cefotaxime resistance rates of approximately 93% among selected clinical *E. coli* isolates, with confirmed ESBL production in a substantial proportion of isolates (2020 review). In addition, a recent investigation in Benghazi identified ESBL-producing *E. coli* among urinary isolates and reported high resistance to cefotaxime and ceftazidime, while susceptibility to amikacin and ertapenem remained comparatively high (Bukhatwa *et al*., 2026). These findings reinforce the importance of continued surveillance of ESBL-associated resistance in Libyan healthcare settings. The comparative findings across the six bacterial groups also deserve particular attention. Although *E. coli* demonstrated a considerable resistance rate, *S. aureus* showed the highest overall resistance proportion (68.2%). Pairwise comparisons further demonstrated statistically significant differences between *S. aureus* and four Gram-negative groups: *E. coli* (adjusted $p = 0.0346$), *Klebsiella* spp. (adjusted $p < 0.001$), *Nitrobacteria* sp. (adjusted $p < 0.001$), and *Pseudomonas* spp. (adjusted $p = 0.0412$). A significant difference was also observed between *E. coli* and *Nitrobacteria* sp. (adjusted

p = 0.0113). These results suggest that the resistance burden differed among the investigated organisms, particularly in comparisons involving *S. aureus*. Nevertheless, the relatively high resistance observed in *S. aureus* should be interpreted in relation to the antimicrobial agents tested and the organism-specific susceptibility breakpoints, rather than being considered directly equivalent to resistance in Gram-negative bacteria. The relatively high susceptibility observed to selected agents, particularly gentamicin and imipenem in the *E. coli* results, suggests that some antimicrobial options may retain useful activity against particular bacterial groups. However, antimicrobial effectiveness varied according to the bacterial species and the tested agent. Previous Libyan studies have similarly reported considerable variation in resistance profiles among Gram-negative and Gram-positive pathogens, emphasizing the need for local susceptibility data to guide treatment decisions. The World Health Organization's Global Antimicrobial Resistance and Use Surveillance System (GLASS) also emphasizes standardized national surveillance of priority bacterial pathogens, including third-generation cephalosporin-resistant *E. coli* and methicillin-resistant *S. aureus* (WHO, 2024). Overall, the findings demonstrate a substantial antimicrobial resistance burden among the investigated bacterial species, with notable differences in their susceptibility profiles. The high resistance observed in *S. aureus* and the considerable resistance of *E. coli* to selected beta-lactam antibiotics underline the need for continuous antimicrobial resistance surveillance, rational antibiotic prescribing, and strengthened antimicrobial stewardship programs. Further investigations involving isolate-level data, standardized susceptibility testing, and molecular characterization of resistance determinants are recommended to clarify the mechanisms underlying the observed resistance patterns and to support more effective infection-control strategies.

The antimicrobial susceptibility results revealed considerable variations in antibiotic effectiveness among the bacterial species. Augmentin (AMC) showed relatively high activity against *E. coli, Klebsiella spp.,* and *S. aureus*, whereas high resistance was observed against several antibiotics, particularly oxacillin, ofloxacin, cefixime, and erythromycin. These findings highlight the importance of regular antimicrobial resistance surveillance, culture-based antibiotic selection, and rational antibiotic use to control the spread of resistant bacterial pathogens (Elkhouly *et al*., 2025).

Conclusion

The findings demonstrate a considerable overall level of antimicrobial resistance, with marked variation among the investigated bacterial species. *Staphylococcus aureus* exhibited the highest resistance proportion, whereas *Nitrobacteria* sp. showed the lowest. These findings highlight the importance of continuous antimicrobial susceptibility surveillance and evidence-based antibiotic selection to support effective infection management and help limit the further emergence of antimicrobial resistance.

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