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Original Article

Antibiotic resistance and bacterial profiles in an Iranian hospital (2018-2021)

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Abstract

Introduction: Antimicrobial resistance (AMR) poses a significant global health challenge, complicating the treatment of bacterial infections. This study investigated the prevalence of AMR among clinical isolates in an Iranian hospital from 2018 to 2021.

Methodology: This four-year retrospective study was conducted at Ganjavian Hospital in Dezful, Iran. A total of 4,522 clinical specimens were analyzed. Bacterial identification and antimicrobial susceptibility testing were performed using standard microbiological methods and the Kirby-Bauer disk diffusion method, and interpreted per the Clinical and Laboratory Standards Institute (CLSI) guidelines. Statistical analysis included descriptive statistics, Chisquare tests for trend, and 95% confidence intervals (CIs) for resistance proportions.

Results: A total of 4,282 bacterial isolates were recovered; of which 78% were Gram-negative, with Enterobacterales constituting the predominant group (51.4%). Among *Escherichia coli* isolates, 72.3% (95% CI: 69.9–74.6%) were non-susceptible to ceftriaxone. The prevalence of multidrug-resistant (MDR) Enterobacterales was 41.4% (95% CI: 39.2–43.6%), with significant annual variation observed during the study period ($\chi^2 = 5.48$, $p < 0.001$). *Acinetobacter* spp. exhibited high resistance to third-generation cephalosporins (94.1%; 95% CI: 91.1–96.2%). The prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA) was 29.7% (95% CI: 25.6–34.1%), and 40.0% of *Enterococcus* spp. were vancomycin-resistant.

Conclusions: The findings highlight the urgent need for enhanced infection-control and antimicrobial-stewardship programs. The high rates of resistance among common pathogens underscore the complexity of treating infections in critical care settings. This study emphasizes the necessity for surveillance and the development of targeted interventions to combat AMR, ensuring that effective treatment options remain available.

Key words: antimicrobial resistance; hospital; Enterobacterales; MRSA.

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Introduction

Antimicrobial resistance (AMR) is a calamitous health emergency and is reported to cause 1.27 million deaths every year. It has made the treatment of infections due to bacteria challenging, increased perioperative risks, and has also made the success of chemotherapy difficult in cancer patients [1]. A clear knowledge of the processes making antimicrobials resistant is necessary to ensure the continued effectiveness of antibiotics [2]. Bacterial infections such as bacteremia and pneumonia due to Enterobacteriaceae species can be dangerous and also cause healthcare-associated infections. However, the rates of resistance are also increasing; for example, carbapenem resistance rates of 54% have been reached in Egypt, making treatment difficult [3]. The rise in prevalence of extended-spectrum beta-lactamases (ESBLs) producing enteric pathogens and carbapenem-resistant Enterobacteriaceae (CRE) also poses new threats due to increased risks of colonization and then infection of new patients who have been exposed to prolonged healthcare and prior antibiotic treatment. The overgrowth of ESBL producers and CRE also poses significant risks to multiple patients due to increased risks of healthcare-associated infections [1,4].

Pseudomonas aeruginosa and *Acinetobacter baumannii* have been identified as serious opportunistic bacteria, with impressive resistance strategies aside from their biofilm formation and efflux pumps, in hospital environments in particular. They primarily target immunocompromised patients, making their treatment even more complicated. Environmental adaptation provides insight into potential strategies for combating problematic bacterial infections in hospital settings [5,6]. Additionally, *A. baumannii* is a significant potential threat to healthcare, which could have extensive implications for all patients. Rising resistance to first-line antibiotics, particularly in multi-drug resistant (MDR) strains, is making this problem even harder to control [7,8].

In recent years, the prevalence of both methicillin-resistant *Staphylococcus aureus* (MRSA) and

vancomycin-resistant enterococci (VRE) has kept healthcare institutions, including hospital-based or community health centers, on tenterhooks. The statistics indicate the emergence of MRSA at a rate of 1.42% among pus samples [9,10]. Recently, a study among Indian communities revealed the prevalence of VRE infection at 17.57%, mainly caused by the *Enterococcus faecium*, particularly among patients diagnosed with diabetes mellitus and neutropenia [11]. All the above observations demonstrate how Gram-positive bacteria resistant to antibiotics are developing at a rapid rate [12].

This study examined the prevalence of antibiotic resistance among clinical isolates (2018–2021) and analyzed resistance patterns across bacterial species. This study presents antibiotic resistance patterns and bacterial profiles from an Iranian hospital for regional AMR monitoring, focusing on surveillance data rather than resistance mechanisms.

Methodology

This retrospective descriptive study (2018–2021) was conducted at Ganjavian Hospital in Dezful, Iran, to analyze the prevalence and diversity of bacterial pathogens across 4,522 clinical specimens, including blood, urine, stool, bronchoalveolar lavage fluid (BALF), cerebrospinal fluid (CSF), pus, and pleural/ascitic fluid. Various culture media were employed based on the specimen type: MacConkey and blood agar for urine and wound samples; and chocolate agar was added for blood, BALF, CSF, and pleural/ascitic fluid to support capnophilic bacteria at 35 °C for 3 days in an atmosphere containing 10% CO_2. The culture media were obtained from Condalab (Madrid, Spain) and Merck (Darmstadt, Germany).

MacConkey agar, Hektoen enteric agar, and Gram-negative (GN) broth (as a selective enrichment medium) were used in stool cultures for enteric pathogen isolation. The GN broth was sub-cultured onto Hektoen enteric agar after 6 hours of incubation. All of the culture media were incubated at 35 °C for at least 24 hours under aerobic conditions [13].

Bacterial identification began with Gram staining for initial classification, followed by biochemical tests—including catalase, oxidase, coagulase, mannitol salt agar, DNase agar, bile esculin agar, 6.5% NaCl, Christie–Atkins–Munch-Petersen (CAMP) test, triple sugar iron (TSI), sulfide-indole-motility (SIM), methyl red–Voges-Proskauer (MR-VP), urease, phenylalanine deaminase, lysine, ornithine, and arginine decarboxylase—to characterize isolates based on their metabolic profiles. Additional tests were performed for non-fermenting bacteria, including hemolysis, glucose, and maltose oxidation-fermentation (OF), and growth at 42 °C. Stool isolates of enteropathogenic *Escherichia coli* (EPEC), *Salmonella*, and *Shigella* were initially identified using conventional biochemical tests, followed by confirmation with specific antisera and slide agglutination [13].

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method on Mueller-Hinton agar plates. Bacterial suspensions, adjusted to a 0.5 McFarland standard, were evenly spread across the plates. Antibiotic disks (MAST Group Ltd., Bootle, Merseyside, UK) were applied as follows: cefixime (30 µg), penicillin (10 units), ampicillin (10 µg), erythromycin (15 µg), clindamycin (2 µg), vancomycin (30 µg), trimethoprim-sulfamethoxazole (1.25/23.75 µg), amikacin (30 µg), gentamicin (10 µg), ciprofloxacin (5 µg), ceftriaxone (30 µg), ceftazidime (30 µg), cefotaxime (30 µg), imipenem (10 µg), meropenem (10 µg), piperacillin-tazobactam (100/10 µg), piperacillin (100 µg), nalidixic acid (30 µg), and nitrofurantoin (300 µg). The plates were incubated at 35 °C for 16–18 hours in ambient air. Incubation was extended to 24 hours for vancomycin and cefoxitin disks. The inhibition zone diameters were measured to the nearest millimeter using a ruler and interpreted according to the Clinical and Laboratory Standards Institute (CLSI) M100 guidelines [14].

Data were collected from the medical records of patients with positive cultures, and included the following: age, gender, diagnosis, site of infection, clinical isolates, culture positivity rates for each condition, and antibiotic sensitivity profiles for each isolate. Statistical analysis was performed using IBM SPSS to evaluate the prevalence and patterns of antibiotic resistance among the isolates. Descriptive statistics, including means and frequencies, were calculated to summarize the demographic data and isolate characteristics. Chi-square (χ^2) tests or Fisher's exact tests were employed, as appropriate, to assess trends and variations in resistance rates over the study period (2018–2021). Confidence intervals (95% CI) for key resistance proportions (e.g., MRSA, MDR Enterobacterales) were calculated. A p value of < 0.05 was considered statistically significant.

This study was conducted in accordance with the ethical principles of the Declaration of Helsinki and approved by the Ethics Committee of Dezful University of Medical Sciences (approval number: IR.DUMS.REC.1400.034).

Table 1. Frequency and percentage distribution of bacterial isolates by specimen type.

Bacterial species / group	Urine (N = 1963)	Feces (N = 299)	Wound (N = 496)	Blood (N = 813)	Respiratory secretions (N = 633)	Other (N = 78)	Total (N = 4282)
Staphylococcus aureus	83/1963 (4.2%)	0/299 (0%)	102/496 (20.6%)	180/813 (22.1%)	96/633 (15.2%)	17/78 (21.8%)	478/4282 (11.2%)
Enterococcus spp.	311/1963 (15.8%)	0/299 (0%)	40/496 (8.1%)	63/813 (7.7%)	18/633 (2.8%)	20/78 (25.6%)	452/4282 (10.6%)
Enterobacterales	1371/1963 (69.8%)	0/299 (0%)	233/496 (47.0%)	363/813 (44.6%)	214/633 (33.8%)	20/78 (25.6%)	2201/4282 (51.4%)
Non-fermenters	198/1963 (10.1%)	3/299 (1.0%)	121/496 (24.4%)	206/813 (25.3%)	304/633 (48.0%)	21/78 (26.9%)	853/4282 (19.9%)
Enteropathogens	0/1963 (0%)	296/299 (99.0%)	0/496 (0%)	0/813 (0%)	0/633 (0%)	0/78 (0%)	296/4282 (7.0%)

Results

Demographics and bacterial isolation

A total of 4,522 patients were enrolled in the study between 2018 and 2021. Of these, 49% (n = 2,224) were female, and 51% (n = 2,298) were male. The mean age of the participants was 48.7 ± 12.5 years (interquartile range: 18–71 years).

Analysis of infection distribution across hospital departments revealed that most bacterial isolates were obtained from intensive care units (ICUs), accounting for 1,270 cases (30%). This was followed by isolates from the emergency, medical, surgical, pediatric, neonatal, and coronary care unit (CCU) wards, in order of decreasing frequency.

Overall, 930 (22%) Gram-positive and 3,352 (78%) Gram-negative bacterial strains were recovered. Among pathogens, Enterobacterales were the most prevalent (2,201/4282 isolates; 51.4%), and non-fermentative bacteria, including *A. baumannii*, *P. aeruginosa*, and *Stenotrophomonas maltophilia*, collectively accounted for 19.9% of isolates (853/4282). *S. aureus* was the predominant Gram-positive species (478/4282 isolates;11.2%), followed by *Streptococcus* species (454/4282 isolates; 10.6%). The distribution of positive bacterial cultures from clinical samples collected during the 4 years is summarized in Table 1. Among the isolates obtained from stool cultures, enteropathogenic bacteria were predominantly *Shigella* species (263/298 isolates; 88.2%), followed by enteropathogenic *E. coli* (23/298 isolates; 7.7%) and *Salmonella* species (10/298 isolates; 3.3%). *P. aeruginosa* was identified in 1% of cases (3/298 isolates) (Table 1).

Antibiotic susceptibility testing

The antimicrobial resistance patterns of the Gram-positive isolates are summarized in Table 2. *Enterococcus* spp. showed the highest resistance to ciprofloxacin (73.9%), and 40% were identified as VRE (180/452 isolates). *S. aureus* isolates exhibited high resistance rates to penicillin (88.9%), erythromycin (70.5%), tetracycline (55.8%), and clindamycin (54%). Methicillin-resistant *S. aureus* (MRSA) accounted for 29.7% of isolates (n = 142; 95% CI: 25.6–34.1%), while MDR *S. aureus* strains represented 38% (n = 182; 95% CI: 33.7–42.5%).

High levels of non-susceptibility to third-generation cephalosporins were observed among Gram-negative pathogens, including *E. coli* isolates: 72.3% (95% CI: 69.6–74.6%) resistance to ceftriaxone and 72.0% (95% CI: 69.6–74.3%) resistance to cefotaxime. *Klebsiella* spp. also demonstrated substantial resistance to ceftriaxone and cefotaxime (60.2%; 95% CI: 56.4–63.9%), while resistance to tetracycline was observed in 57.4% of isolates (95% CI: 53.6–61.1%). In contrast, *Enterobacter* spp. showed preserved susceptibility to key agents, remaining fully susceptible to piperacillin–tazobactam (0% resistance), with comparatively lower resistance to amikacin (6.3%; 95% CI: 1.7–20.2%) and meropenem (17.9%; 95% CI: 7.8–34.8%). All *Proteus* spp. isolates were susceptible to imipenem, meropenem, and piperacillin–tazobactam, whereas resistance to nitrofurantoin was notably high (88.2%; 95% CI: 70.0–95.8%). High resistance rates were also observed among *Citrobacter* spp., particularly to tetracycline (75.0%; 95% CI: 64.1–83.7%) and nalidixic acid (57.1%; 95% CI: 39.4–73.7%). *Shigella* spp. exhibited marked resistance to trimethoprim–

Table 2. Antibiotic resistance patterns of Gram-positive pathogens.

Antibiotic	*S. aureus* (n/N, %)	*Enterococcus* spp. (n/N, %)
Penicillin	425/478 (88.9%)	–
Ampicillin	–	201/452 (44.5%)
Vancomycin	–	180/452 (40.0%)
Erythromycin	337/478 (70.5%)	–
Trimethoprim–Sulfamethoxazole	177/478 (37.0%)	–
Amikacin	33/478 (7.0%)	–
Gentamicin	83/478 (17.3%)	–
Ciprofloxacin	243/478 (50.8%)	334/452 (73.9%)
Nalidixic acid *	71/83 (85.5%)	–
Nitrofurantoin *	2/83 (2.4%)	27/311 (8.7%)
Tetracycline	267/478 (55.8%)	–
Clindamycin	258/478 (54.0%)	–

Resistance is reported as the number of resistant isolates divided by the total number of isolates tested for each organism (n/N, %). Denominators: *Staphylococcus aureus* (N = 478); *Enterococcus* spp. (N = 452). *Antibiotic susceptibility testing for nalidixic acid and nitrofurantoin was performed on urinary isolates.

sulfamethoxazole (90%; 95% CI: 85.6–93.2%) and third-generation cephalosporins, including ceftriaxone (86.0%; 95% CI: 81.1–89.8%) and cefotaxime (85.0%; 95% CI: 80.1–88.9%). Conversely, *Salmonella* spp. isolates remained fully susceptible to ceftriaxone and cefotaxime, with resistance observed only to trimethoprim-sulfamethoxazole (30.0%; 95% CI: 10.8–60.3%) (Table 3).

Among non-fermenting Gram-negative bacilli, *P. aeruginosa* isolates demonstrated the highest resistance rates to nalidixic acid (86.2%; 95% CI: 82.4–89.3%) and nitrofurantoin (81.7%; 95% CI: 77.7–85.2%), followed by ceftazidime (65.0%; 95% CI: 60.6–69.2%). Resistance to amikacin was observed in 25.4% of isolates (95% CI: 21.8–29.4%). *Acinetobacter* spp. exhibited near-universal resistance to third-generation cephalosporins, with 94.1% (95% CI: 91.2–96.1%) non-susceptibility to ceftriaxone, cefotaxime, and ceftazidime. In contrast, *S. maltophilia* demonstrated limited susceptibility to ceftazidime, with only 25.0% of isolates remaining susceptible (95% CI: 10.2–49.5%) (Table 3).

The overall prevalence of MDR among Enterobacterales recovered from clinical samples was 41.4% (95% CI: 39.2–43.6%), with *E. coli* accounting for the most significant proportion (61.5%). The annual trend showed significant fluctuation ($\chi^2 = 5.48$, $p < 0.001$), with the highest MDR rate observed in the first year (31.2%; 95% CI: 28.1–34.5%), followed by decreases in the second (22.5%; 95% CI: 19.8–25.4%) and third years (15.8%; 95% CI: 13.4–18.5%), and a subsequent rise in the fourth year (30.6%; 95% CI: 27.5–33.9%). Regarding specimen sources, most MDR isolates were recovered from urine samples (62.3%). Their prevalence was highest in ICUs (25.7%) and emergency departments (24.6%), whereas lower rates were observed in surgical (20.8%), pediatric (17.8%), and internal medicine wards (11.2%)

Discussion

The rise of AMR represents an ever-growing threat to worldwide public health, particularly for those regions where cases of treatment failure have been observed. This 4-year (2018–2021) study provides essential regional epidemiological data on antimicrobial resistance trends, offering a baseline for local therapeutic decision-making and public health strategies, even though it does not primarily focus on detailed mechanistic aspects.

Indeed, in this hospital, as in others, the emergence of antibiotic-resistant staphylococci has become a worrying concern. In this study, the frequencies of MRSA and MDR *S. aureus* were 29.7% and 38%, respectively, which is comparable to the

Table 3. Antibiotic resistance patterns of Gram-negative bacterial isolates.

Antibiotic	*E. coli* (N = 1398)	*Klebsiella* spp. (N = 663)	*Enterobacter* spp. (N = 37)	*Proteus* spp. (N = 26)	*Citrobacter* spp. (N = 76)	*P. aeruginosa* (N = 486)	*Acinetobacter* spp. (N = 354)	*Stenotrophomonas* spp. (N = 13)	*Shigella* spp. (N = 264)	*Salmonella* spp. (N = 10)
Ampicillin	–	–	–	–	–	–	–	–	195/264 (74.0%)	0/10 (0%)
Trimethoprim–Sulfamethoxazole	976/1398 (69.8%)	367/663 (55.3%)	17/37 (46.9%)	16/26 (60.0%)	31/76 (40.3%)	–	326/354 (92.0%)	7/13 (57.0%)	237/264 (90.0%)	3/10 (30.0%)
Amikacin	197/1398 (14.1%)	166/663 (25.0%)	2/37 (6.3%)	2/26 (8.3%)	14/76 (18.3%)	34/486 (25.4%)	318/354 (90.0%)	–	–	–
Gentamicin	428/1398 (30.6%)	237/663 (35.8%)	11/37 (30.3%)	5/26 (20.0%)	23/76 (31.0%)	–	318/354 (90.0%)	–	–	–
Ciprofloxacin	792/1398 (56.7%)	246/663 (37.1%)	14/37 (37.9%)	4/26 (16.0%)	20/76 (26.8%)	151/486 (31.0%)	322/354 (91.0%)	4/13 (33.0%)	29/264 (11.0%)	3/10 (30.0%)
Ceftriaxone	1011/1398 (72.3%)	399/663 (60.2%)	21/37 (57.6%)	4/26 (16.0%)	32/76 (42.5%)	–	333/354 (94.1%)	–	227/264 (86.0%)	0/10 (0%)
Cefotaxime	1006/1398 (72.0%)	399/663 (60.2%)	20/37 (56.3%)	4/26 (16.0%)	32/76 (42.5%)	–	333/354 (94.1%)	–	224/264 (85.0%)	0/10 (0%)
Ceftazidime	–	–	–	–	–	316/486 (65.0%)	333/354 (94.1%)	10/13 (75.0%)	–	–
Imipenem	94/1398 (6.7%)	160/663 (24.2%)	8/37 (21.4%)	0/26 (0%)	13/76 (16.8%)	170/486 (35.0%)	322/354 (91.0%)	–	–	–
Meropenem	92/1398 (6.6%)	156/663 (23.6%)	7/37 (17.9%)	0/26 (0%)	12/76 (15.3%)	170/486 (35.0%)	322/354 (91.0%)	–	–	–
Piperacillin–tazobactam	574/1398 (41.1%)	370/663 (55.9%)	0/37 (0%)	0/26 (0%)	38/76 (50.0%)	170/486 (35.0%)	326/354 (92.0%)	–	–	–
Nalidixic acid *	705/928 (76.0%)	123/239 (51.5%)	8/15 (53.3%)	7/18 (38.9%)	16/28 (57.1%)	106/123 (86.2%)	24/28 (85.7%)	–	–	–
Nitrofurantoin *	65/928 (7.0%)	88/232 (37.9%)	6/15 (40.0%)	15/17 (88.2%)	4/27 (14.8%)	98/120 (81.7%)	21/26 (80.8%)	–	–	–
Tetracycline	595/1398 (42.6%)	380/663 (57.4%)	21/37 (57.4%)	5/26 (20.0%)	57/76 (75.0%)	–	–	–	–	–

This resistance profile provides detailed insights into trends in antimicrobial susceptibility among clinically significant Gram-negative pathogens during the study period. Antimicrobial susceptibility testing and interpretation were performed in accordance with the Clinical and Laboratory Standards Institute (CLSI) 2021 M100 guidelines. N: number of resistant isolates; %: percentage of resistant isolates. *Antibiotic susceptibility testing for nalidixic acid and nitrofurantoin was performed on urinary isolates.

aforementioned global trends. MRSA is a major cause of Gram-positive antimicrobial resistance, posing new challenges for treating infections and limiting the spread of antibiotic resistance [15]. The high rates of resistance to penicillins, erythromycin, tetracyclines, and clindamycin illustrate the widespread distribution of the resistance determinants among *S. aureus* strains [16]. The rising levels of resistance, particularly to β-lactams and fluoroquinolones, underscore the clinical impact of these infections and highlight the need for stricter antibiotic stewardship and effective infection control programs [15]. The co-emergence of MDR and MRSA strains highlights the biological complexity of these pathogens and underscores the need for ongoing surveillance and robust management strategies to mitigate the risks associated with such virulent strains, as demonstrated in studies from Iran [17,18].

Isolates of enterococci in this study showed a VRE prevalence of 40%, together with a high ciprofloxacin resistance rate of 73.9%. These findings are in line with Iranian meta-analyses reporting VRE prevalence ranging from 14% to more than 40%, typically associated with prior hospitalization and antibiotic exposure [19,20]. Globally, VRE has become a major concern, particularly in ICUs and other acute-care units in both high- and low-resource settings [21,22]. The high level of ciprofloxacin resistance observed among different *Enterococcus* species in this study also mirrors current international trends.

The findings from this study demonstrated that Gram-negative bacteria comprised 78% of all isolates, with Enterobacterales being the predominant ones (51.4%). As has been noted globally, *E. coli* and *K. pneumoniae* were the predominant Gram-negative bacteria, particularly in regions where there are a large number of antibiotic-resistant strains [23]. The resistance pattern in the isolates identified in this study is rather alarming. Among the isolates, 72% of *E. coli* isolates demonstrated resistance to ceftriaxone; this is consistent with the reported high levels of ESBL-producing *E. coli* strains globally [23,24]. The overall resistance levels of *K. pneumoniae* isolates to ceftriaxone and ceftazidime were 60%, making it rather challenging to manage this pathogen's infection. Expectedly, there has been an increased emergence of carbapenem resistance in *K. pneumoniae* reported by European surveillance, rising from 19% in 2020 to 39% in 2021, emphasizing the need for new treatment agents [24].

The fluctuations in the prevalence of MDR Enterobacterales over these 4 years reflect the dynamic processes influenced by antimicrobial stewardship strategies as well as the coronavirus disease 2019 (COVID-19) pandemic. The first peak in the prevalence of MDR can be hypothesized as being caused by the predominance of resistance strains, coinciding with the overuse of antibiotics, followed by a successive fall as a result of improved infection control practices as well as antimicrobial stewardship strategies. The role of the pandemic in the third and fourth years, in which factors included having hospital wards dedicated solely to COVID-19 patients, reduced hospitalizations of patients with other infections, as well as growing reports of self-administration of broad-spectrum antibiotics, contributed to a successive fall in reported MDR cases in the third year. However, the successive rise in MDR in the fourth year can be associated with the renewed practice of all health and medical services and is also reflected in the community-level effects of unsupervised antimicrobial intake that contribute to the potential establishment and predominance of resistant bacterial strains. The dynamics of antimicrobial resistance, therefore, can be directly associated with the dynamics and extent of practice, and also the intake and use of healthcare and antimicrobials, respectively [16,25].

This study's findings align with regional and international data, highlighting a concerning rise in antimicrobial resistance (AMR). Similar research in Iran has noted comparable resistance patterns in Gram-negative bacteria, particularly in hospital ICUs where patients are vulnerable to multidrug-resistant (MDR) bacteria [26]. The 55.2% penicillin resistance among *S. aureus* isolates further stresses the need to address the high incidence of resistance, specifically in hospitals and in ICUs, which comprised 30% of the isolates.

The emerging dominance of non-fermentative Gram-negative bacilli such as *P. aeruginosa* and *A. baumannii* in this study also reflects the global scenario in other Asian regions. For instance, recent studies from India observed strong correlations between antibiotic resistance patterns among *P. aeruginosa* isolated from burn and surgical units, thereby reaffirming the importance of this organism as a nosocomial pathogen [27]. The study revealed high resistance rates in *Acinetobacter* spp. (94%) to ceftriaxone. The emergence of resistance among *Acinetobacter* spp. to third-generation cephalosporins and carbapenems also poses therapeutic hurdles to healthcare providers. MDR not only hinders treatment but also triggers morbidity and mortality among patients, thus underlining the need to resort to effective antimicrobial and novel therapeutic approaches [28].

The findings of this study align with earlier reports

on AMR in enteric pathogens, but reveal notable differences between species. *Shigella* showed high resistance to trimethoprim-sulfamethoxazole (90%), while *Salmonella* exhibited only moderate levels (30%), echoing patterns reported by Moghaddami *et al*. in northern Iran [29]. These contrasts likely arise from distinct resistance mechanisms and ecological pressures—prolonged antibiotic exposure in *Shigella* versus limited exposure to trimethoprim-sulfamethoxazole in *Salmonella*. Thus, trimethoprim-sulfamethoxazole may remain effective for susceptible *Salmonella* infections but should be avoided for *Shigella* in high-resistance regions [30]. In contrast, the variable resistance observed in *Salmonella*, including greater diversity among environmental isolates from Moroccan water, underscores the need for region-specific AMR surveillance and integrated clinical–environmental monitoring to refine treatment strategies [31].

Another critical consideration is the demographic composition of the region where the study was carried out, particularly because it is a region where there is a considerable inflow of people. As a referral point for individuals from other provinces, it is likely that the hospital affects the demographic composition of the patient base, which then affects trends related to antibiotic resistance. Individuals moving from different regions may have different bacterial strains and different levels of resistance, which may not be representative of the region's typical demographic composition. Evidence suggests that frequent patient movement is associated with increased microbial diversity, thus influencing the antibiotic resistance patterns of bacteria. [32,33]. It is recommended that global and regional health organizations should increase awareness regarding antimicrobial usage, particularly within regions where antimicrobial use is high, such as Iran, and in other settings worldwide. In these contexts, promoting appropriate use is essential to mitigate this public health threat [15,23]. Future studies should elucidate the molecular basis of resistance mechanisms among major pathogens and identify innovative ways to combat infections, such as combining antibiotics. Due to limited access to advanced technologies such as matrix-assisted laser desorption-ionization/time of flight mass spectrometer (MALDI-TOF MS) and 16S rRNA gene sequencing, incorporating these tools into future regional research would enhance species-level identification.

Conclusions

The key theme of this study is the alarming trend in bacterial antibiotic resistance, underscoring the urgent need to strengthen infection control practices and antimicrobial stewardship programs. A better understanding of the growing scenario of antibiotic resistance can be gained by comparing region-specific antibiotic resistance data with global data, leading to more targeted approaches. The results of this study paint a picture of the inadequacy of the present level of coordination between the medical, research, and regulatory communities in addressing the growing threat of antibiotic resistance. Therefore, more efforts should be made to develop techniques to address this threat and to develop surveillance training programs to ensure the effectiveness of antibiotics in the years to come.

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Authors' contributions

Conceptualization: BD, AK; methodology, formal analysis, and investigation: AK; data collection: HM, BD; writing—original draft preparation: BD, AK. All authors commented on the previous versions of the manuscript. All authors read and approved the final manuscript.

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Conflict of interest

No conflict of interest is declared.

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