

ORIGINAL ARTICLE

Surveillance of Antimicrobial Resistance Bacteria in a Healthcare Facility at an Industrial Site in Saudi Arabia

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SUMMARY

Background: This study aimed to perform surveillance and identify antimicrobial resistance (AMR) in the most common pathogenic bacteria in a healthcare facility in Rabigh City, Saudi Arabia.

Methods: A total of 1,933 samples were processed from patients during the study period from January 2022 to June 2022. Identification and antimicrobial susceptibility of the cultured isolates were performed using the Micro-Scan system.

Results: Out of the 1,933 tested samples, 11.1% (n = 214) were positive for bacterial growth. A relatively higher percentage of isolates was recovered from patients older than 50 years (55.9%). Gram-negative bacteria (67.3%) were significantly more prevalent than Gram-positive bacteria (32.7%). The Gram-negative pathogenic bacteria comprised mainly *Escherichia coli* and *Klebsiella pneumoniae*, followed by *Pseudomonas aeruginosa*. *Staphylococcus epidermidis* and coagulase-negative staphylococci were found at relatively high abundance in Gram-positive bacteria. Increased resistance to carbapenem antibiotics was observed in *K. pneumoniae*. In Gram-positive bacteria, > 50% of the isolates of *S. epidermidis* were resistant to 13 tested antimicrobial agents.

Conclusions: This study provided an overview of the distribution of pathogenic bacteria and antimicrobial susceptibility of the prevalent Gram-negative and Gram-positive pathogenic bacteria in a major healthcare facility in Saudi Arabia. It highlights the importance of continuously monitoring AMR bacteria in healthcare settings to ensure the effective use of antibiotics for treatment.

(Clin. Lab. 2024;70:xx-xx. DOI: 10.7754/Clin.Lab.2024.240433)

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KEYWORDS

surveillance, antimicrobial resistance, antibiotics, Gram-negative bacteria, Gram-positive bacteria

INTRODUCTION

Antimicrobial resistance (AMR) spread is a major healthcare concern [1]. Also, AMR's emergence and spread continue to pose serious threats resulting from the overuse of antibiotics in humans [2]. Antimicrobials impact financial sustainability, environmental forces, and social and economic change [3,4]. It leads to ad-

verse consequences, including severe illnesses, more prolonged hospital admissions, and increased healthcare costs [3-5]. The Global AMR rates from 78 countries were published in the World Health Organization (WHO)'s (GLASS) recent report: Early Implementation 2020 [6]. Critical topographical variety was seen in anti-microbial defenselessness. Reconnaissance and checking programs are supportive to creating experimental approaches for treating genuine diseases [7,8]. Multidrug-resistant Gram-negative bacteria are a major therapeutic challenge in hospitals [9,10] and got the attention of the scientific community to focus on antibiotic-resistant bacteria causing hospital- and community-acquired infection [11]. Species of the Enterobacteriaceae family commonly produce extended-spectrum β -lactamases (ESBLs), which confer resistance to advanced-generation cephalosporins and can lead to therapeutic dead ends. The plasmids regularly carry antimicrobial resistance genes for other antimicrobials, such as fluoroquinolones, aminoglycosides, and tetracyclines. Of specific concern are subsequent increments in healing center contaminations due to *Klebsiella spp.* and *Escherichia coli*, which are resistant to all first-line antibiotics [1,12]. These microorganisms were highlighted to monitor the resistance in the 5-year AMR strategy of the United Kingdom (2013 - 2018) [13]. *Pseudomonas aeruginosa* ranks among the top five organisms causing pulmonary, soft tissue, bloodstream, surgical site, and urinary tract infections, primarily in immune-compromised patients in hospitals [14,15]. In the United States, *P. aeruginosa* is the foremost common pathogen causing nosocomial pneumonia and is regularly involved in hospital-acquired urinary tract and circulation system diseases [16]. In Asia, nosocomial pneumonia caused by multidrug-resistant *P. aeruginosa* is commonly reported [17].

Monitoring Gram-positive bacteria is important, but the level of risk is less than that of Gram-negative bacteria. *Staphylococcus aureus* is one of the most frequently isolated pathogens in clinical specimens [18]. In the United States, approximately 60% of staphylococcal infections in the intensive care unit are now caused by methicillin-resistant *S. aureus* (MRSA) [19]. In this study, the surveillance of Gram-positive and Gram-negative bacterial pathogens and their antimicrobial susceptibility was performed at a healthcare facility in the industrial city of Rabiagh, Saudi Arabia, to help the appropriate antibiotic treatment selection and strengthen the country's effort to combat the AMR.

MATERIALS AND METHODS

Sample and data collection

This study was undertaken in a healthcare facility in Rabigh City, Makkah region, Saudi Arabia, for a period of 6 months. A total of 1,933 samples were processed from patients during the study period. Clinical specimens were comprised of blood, urine, wound swabs,

sputum, and other body sites and fluids, irrespective of whether they came from in- or outpatients. Demographic data (age, gender, nationality, type of infection, and date of specimen collection) was collected from the medical record. If available, laboratory results of the clinical specimens of those patients (type of microorganisms and antimicrobial susceptibilities) were collected from the medical and laboratory records for each patient on a standardized collection form.

Isolation and identification of bacteria

The samples were spread on different bacterial culture media agar plates based on sample types, such as sheep blood agar, chocolate agar, Columbia agar, MacConkey agar, and mannitol salt agar [20], to grow Gram-negative and Gram-positive bacteria. All the inoculated culture media plates were incubated at 35 to 37°C for 24 hours. Additionally, chocolate agar plates were incubated in a 5% CO₂ atmosphere. All culture plates were initially examined for growth after 24 hours, and cultures with no growth were incubated for 48 hours. Bacterial identification was obtained via MicroScan (Beckman Coulter, USA) by adding 115 μ L of broth suspension to each well in the panel, which provide the identification of the species based on metabolic traits.

Antimicrobial susceptibility testing and data analysis

Antimicrobial susceptibility testing was performed by using the MicroScan WalkAway (Beckman Coulter, USA) system. Basic principles of MicroScan in brief: it is an automated bacterial identification and susceptibility testing system, using MicroScan rapid fluorescent panels to determine the identity and antibiotic susceptibilities of Gram-negative and Gram-positive organisms. The Gram-negative isolates from this study were tested against the following antibiotics: amikacin, amoxicillin/clavulanate, ampicillin/sulbactam, ampicillin, aztreonam, ceftazidime, cefepime, cefotaxime, cefotaxime/clavulanate, ceftazidime, cefuroxime, ciprofloxacin, colistin, ertapenem, gentamicin, imipenem, levofloxacin, meropenem, moxifloxacin, nitrofurantoin, norfloxacin, piperacillin/tazobactam, tigecycline, tobramycin, and trimethoprim/sulfamethoxazole. The Gram-positive isolates from this study were tested against amoxicillin/clavulanate, ampicillin, azithromycin, ceftazidime, ciprofloxacin, clindamycin, daptomycin, erythromycin, fosfomycin, fusidic acid, gentamicin, imipenem, levofloxacin, linezolid, moxifloxacin, mupirocin, nitrofurantoin, oxacillin, penicillin, rifampin, synergid, teicoplanin, tetracycline, trimethoprim/sulfamethoxazole, and vancomycin. The isolates were classified as sensitive, intermediate, and resistant to the tested drugs following the Clinical and Laboratory Standards Institute (CLSI) guidelines for 2022. Data from this study were recorded in an Excel sheet and analyzed using IBM SPSS software (version 22.0; IBM Corp., Armonk, NY, USA) [21,22] by using appropriate statistical methods.

Table 1. Distribution of Gram-negative and Gram-positive bacterial pathogens according to demographic and clinical data of a healthcare facility in Saudi Arabia.

Source		Total number		Gram-positive		Gram-negative	
		No.	%	No.	%	No.	%
Gender	Male	113	52.8	43	38.1	70	61.9
	Female	96	44.9	25	26	71	74
Age	Infants (< 5 years)	22	10.3	12	54.5	10	45.5
	Children (6 - 17 years)	2	0.9	1	50	1	50
	Adults (18 - 50 years)	71	33.2	21	29.6	50	70.4
	Elderly (> 50 years)	118	55.1	37	31.4	81	68.6
Nationality	Saudi Arabia	149	69.6	57	38.3	92	61.7
	Bangladesh	13	6.1	2	15.4	11	84.6
	Yemen	15	7	1	6.7	14	93.3
	Somalia	8	3.7	0	0	8	100
	Sudan	8	3.7	4	50	4	50
	Myanmar	4	1.9	0	0	4	100
	Others	11	5.1	4	36.4	7	63.6
Specimen type	Urine	72	33.6	15	20.8	57	79.2
	Wound	48	22.4	19	39.6	29	60.4
	Blood	42	19.6	32	76.2	10	23.8
	Sputum	14	6.5	0	0	14	100
	Throat swab	13	6.1	0	0	13	100
	Genital swab	12	5.6	0	0	12	100
	Tracheal swab	7	3.3	0	0	7	100
	Foot swab	3	1.4	2	66.7	1	33.3
	Eye swab	2	0.9	1	50	1	50

RESULTS

Demographic and clinical data analysis

In the 1,933 screened samples, 11% (n = 214) were positive for bacterial culture. Demographic data analysis indicated a similar gender distribution among bacterial culture-positive cases, 52.8% male (n = 113) and 44.9% female (n = 96), and the difference was statistically non-significant ($p > 0.05$) (Table 1). The isolates purified from positive culture were identified by MicroScan and comprised of 67.3% Gram-negative bacteria (n = 144) and 32.7% Gram-positive bacteria (n = 70). In both genders, more Gram-negative bacteria were isolated, 74.0% in females (n = 71) and 61.9% in males (n = 70), and compared to Gram-positive bacteria, it was 26.0% (n = 25) and 38.1% (n = 43), respectively (Table 1).

The average age of the patients was 53 years, ranging from 0.1 to 107 years, with a median age of 55 years. A relatively higher percentage of pathogenic isolates was obtained from the elderly patients group older than 50 years (54.9%, n = 118), followed by the adult group aged between 18 - 50 years (33.0%, n = 71). The least

number of bacterial pathogens were recovered from children between 6 and 17 years of age (0.9%, n = 2). Gram-negative pathogenic bacteria were mainly identified in the adult age group (70.4%, n = 50) and elderly patients' group (68.6%, n = 81). In the infant age group, Gram-positive bacteria (54.5%, n = 12) recovered relatively more than Gram-negative bacteria (45.5%, n = 10). The pathogenic bacteria were mainly isolated from Saudi patients (71.6%), followed by Yemeni (7.0%, n = 15), Bangladesh (6.0%, n = 13), Sudanese (3.7%, n = 8), Somalia (3.7%, n = 7), Myanmar (1.9%, n = 4), and 5.1% (n = 11) isolates recovered from patients of 8 other nationalities (Table 1). The isolates were cultured from heterogeneous clinical specimens, mostly from urine (33.5%, n = 72), followed by wound swabs (22.3%, n = 48), blood samples (19.5%, n = 42), and sputum (6.5%, n = 14) (Table 1).

Gram-negative pathogens and antimicrobial susceptibility analysis

The Gram-negative isolates were classified into 12 bacterial species (Figure 1), and mainly comprised *Escherichia coli* (n = 44), followed by *Klebsiella pneumoniae*

Table 2. Antimicrobial susceptibility analysis of the common Gram-negative bacterial pathogens recovered from the clinical specimens.

Antibiotics	<i>E. coli</i>		<i>K. pneumoniae</i>		<i>P. aeruginosa</i>	
	No.	%	No.	%	No.	%
Amikacin	11	25	22	52.4	5	23.8
Amox/clavulanate	16	36.4	22	52.4	-	-
Amp/sulbactam	21	47.7	21	50	-	-
Ampicillin	41	93.2	40	95.2	-	-
Aztreonam	13	29.5	23	54.8	17	81
Cefazolin	16	36.4	7	16.7	1	4.8
Cefepime	20	45.5	27	64.3	12	57.1
Cefotaxime	8	18.2	26	61.9	-	-
Cefoxitin	11	25	33	78.6	-	-
Ceftazidime	8	18.2	21	50	15	71.4
Cefuroxime	24	54.5	34	81	-	-
Ciprofloxacin	22	50	25	59.5	9	42.9
Colistin	-	-	-	-	11	52.4
Ertapenem	7	15.9	21	50	9	42.9
Gentamicin	12	27.3	20	47.6	6	28.6
Imipenem	9	20.5	22	52.4	11	52.4
Levofloxacin	19	43.2	20	47.6	6	28.6
Meropenem	6	13.6	18	42.9	5	23.8
Moxifloxacin	25	56.8	17	40.5	-	-
Piperacillin/tazobactam	12	27.3	15	35.7	16	76.2
Tigecycline	5	11.4	9	21.4	-	-
Tobramycin	12	27.3	15	35.7	6	28.6
Trimethoprim/sulfamethoxazole	23	52.3	15	35.7	-	-

(n= 42), *Pseudomonas aeruginosa* (n = 21), and *Proteus mirabilis* (n = 16) (Figure 1). Patients older than 50 years were infected with a total of 81 Gram-negative pathogens, in which *K. pneumoniae* was the most common isolated microorganism (n = 24), followed by *E. coli* (n = 23) and *P. aeruginosa* (n = 10). Patients with age groups ranging from 18 - 50 years were most commonly infected with *E. coli* (n = 19), followed by *K. pneumoniae* (n = 14) and *P. aeruginosa* (n = 8) (Figure 1). *K. pneumoniae* infection was relatively high in the male patients (n = 23), and *E. coli* infection was more common in the female patients (n = 31).

Antimicrobial susceptibility for selected antimicrobial agents against the Gram-negative pathogens that were found at relatively high abundance is mentioned in Table 2. Among *E. coli*, more than 50% of the isolates were resistant against ampicillin (n = 41), moxifloxacin (n = 25), cefuroxime (n = 24), and trimethoprim/sulfamethoxazole (n = 23). Low resistance levels were observed in *E. coli* isolates against tigecycline (n = 5) and

meropenem (n = 6). The *K. pneumoniae* isolates showed high resistance to ampicillin (n = 40), cefuroxime (n = 34), cefoxitin (n = 33), and cefotaxime (n = 26). Compared to *E. coli*, relatively high resistance was observed against carbapenem antibiotics in *K. pneumoniae* isolates (Table 2). In *P. aeruginosa* isolates, resistance was observed mainly against aztreonam (n = 17), piperacillin/tazobactam (n = 16), and ceftazidime (n = 15) (Table 2).

Gram-positive pathogens and antimicrobial susceptibility analysis

The Gram-positive isolates were classified into 13 species (Figure 1). The prevalent Gram-positive pathogens in this study were *Staphylococcus epidermidis* (n = 16) and coagulase-negative staphylococci (n = 16), followed by *Staphylococcus hyicus* (n = 7) and *Staphylococcus simulans* (n = 7) (Figure 1). Patients over 50 years of age were infected with 37 Gram-positive pathogens, in which *S. epidermidis* was the most common

Table 3. Antimicrobial susceptibility analysis of the common Gram-positive bacterial pathogens recovered from the clinical specimens.

Antibiotics	CoNS		<i>S. epidermidis</i>		<i>S. hyicus</i>	
	No.	%	No.	%	No.	%
Amoxicillin/clavulanate	7	43.8	13	81.3	3	42.9
Ampicillin	7	43.8	13	81.3	3	42.9
Azithromycin	6	37.5	10	62.5	2	28.6
Ciprofloxacin	4	25	10	62.5	-	-
Clindamycin	10	62.5	12	75	2	28.6
Daptomycin	-	-	-	-	-	-
Erythromycin	7	43.8	13	81.3	2	28.6
Fosfomycin	3	18.8	8	50	3	42.9
Fusidic Acid	3	18.8	7	43.8	-	-
Gentamicin	2	12.5	6	37.5	1	14.3
Imipenem	10	62.5	13	81.3	3	42.9
Levofloxacin	5	31.3	11	68.8	-	-
Linezolid	1	6.3	9	56.3	-	-
Moxifloxacin	7	43.8	11	68.8	-	-
Mupirocin	4	25	7	43.8	3	42.9
Oxacillin	7	43.8	13	81.3	3	42.9
Penicillin	7	43.8	13	81.3	3	42.9
Rifampin	3	18.8	6	37.5	-	-
Synercid	5	31.3	4	25	-	-
Teicoplanin	6	37.5	8	50	2	28.6
Tetracycline	6	37.5	5	31.3	5	71.4
Trimethoprim/sulfamethoxazole	3	18.8	9	56.3	-	-
Vancomycin	1	6.3	4	25	-	-

CoNS - coagulase-negative staphylococci.

isolated microorganism. Antimicrobial susceptibility for selected antimicrobial agents against prevalent Gram-positive pathogens is shown in Table 3.

Relatively increased resistance was observed in *S. epidermidis* isolates. More than 50% of the tested isolates were resistant to 13 tested antimicrobial agents, including ampicillin, penicillin, oxacillin, amoxicillin/clavulanate, erythromycin, clindamycin, imipenem, and levofloxacin. The tested isolates of *S. epidermidis* were susceptible to daptomycin. In coagulase-negative staphylococci isolates, 62.5% were resistant to each clindamycin and imipenem, followed by 43.8% of tested isolates, which were resistant to each penicillin, amoxicillin/clavulanate, ampicillin, oxacillin, moxifloxacin, and erythromycin. Relatively high resistance to tetracycline was observed in *S. hyicus* isolates (71.4%). Other tested antimicrobial agents showed resistance to < 50% of the tested *S. hyicus* isolates.

DISCUSSION

AMR manifests as a catastrophic risk to human health. Mainly, escalation in the transmission of hospital-acquired infection, especially with antimicrobial-resistant bacteria, is a major health challenge around the globe, including in the Middle East. Surveillance studies for AMR are obligatory to detect newly emerging resistances, provide appropriate management support to infection control in healthcare-providing facilities, and improve antimicrobial stewardship programs. In this first study from the Rabigh Industrial City of Saudi Arabia, we studied the prevalence of Gram-negative and Gram-positive pathogenic and opportunistic bacteria and provided comprehensive antimicrobial resistance from a healthcare facility at the selected site. The results demonstrated that a total of 144 Gram-negative bacteria and 70 Gram-positive bacteria were identified during the six months of study.

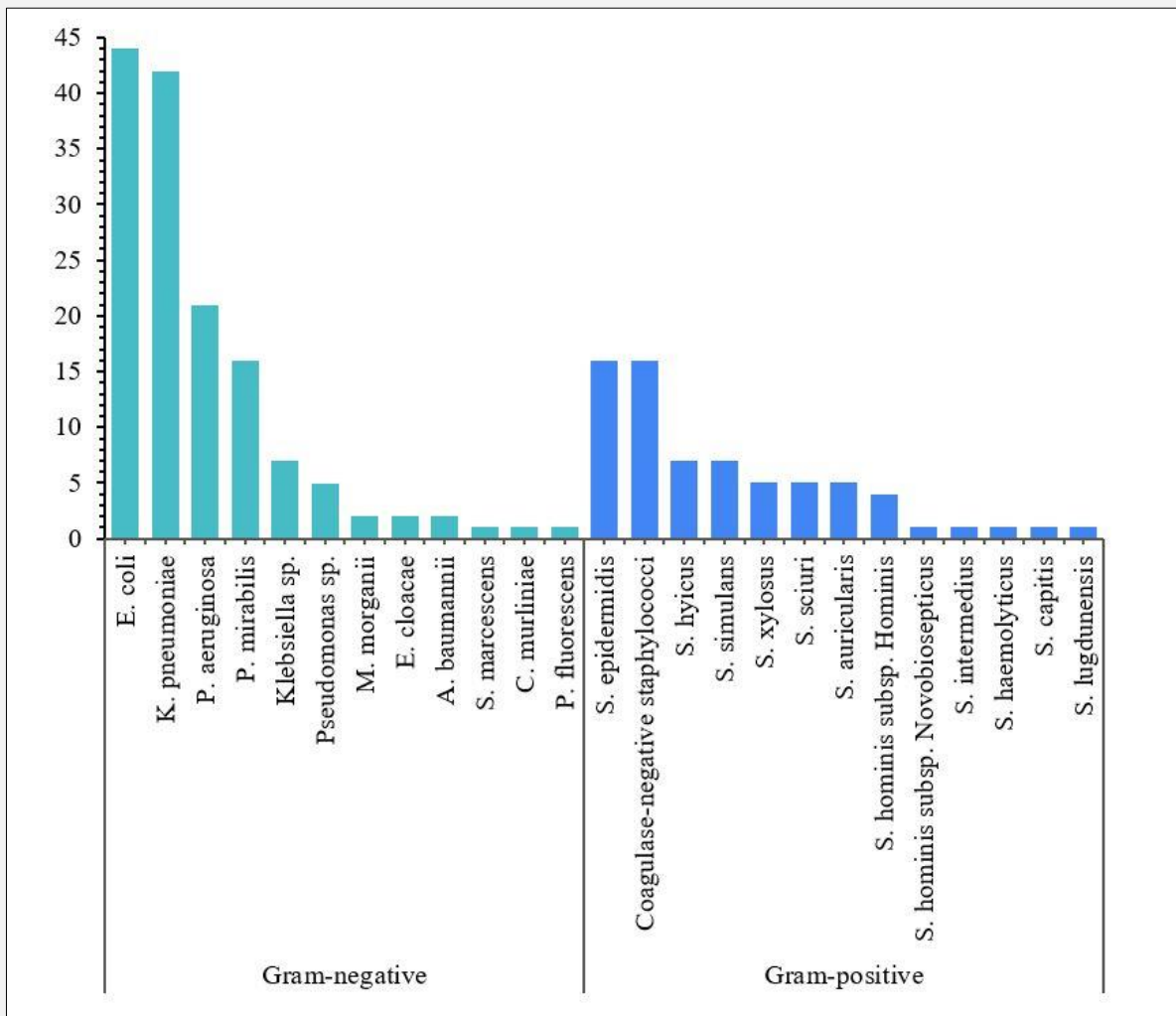


Figure 1. The number of isolates of Gram-negative and Gram-positive bacterial species recovered from the clinical specimens of a healthcare facility in Saudi Arabia.

Out of the 1,933 clinical specimens tested in the study period, 11% were positive for pathogenic and opportunistic bacteria, while 89% were negative. A relatively higher percentage of isolates was obtained from patients older than 50 years of age. Importantly, Gram-negative bacteria were more prevalent than Gram-positive bacteria. The strains were primarily isolated from Saudi patients. Previously, a study in 2 main tertiary care hospitals in Makkah city of Saudi Arabia reported 1,137 Gram-negative bacteria from various body site infections. The most prevalent Gram-negative bacteria were *E. coli* (31.6%) and *P. aeruginosa* (31.2%), followed by *A. baumannii* and *Klebsiella pneumoniae*. Study data showed a high resistance rate among Gram-negative pathogens compared to other countries [23]. A cross-

sectional study conducted between January and December 2009 inspected 8,908 clinical bacteria from 24 healthcare centers across Saudi Arabia. Out of the 8,908 isolates, the foremost predominant were *P. aeruginosa* (72.9%), followed by *A. baumannii* (25.3%) and *Stenotrophomonas maltophilia* (1.8%). Resistance rates among non-fermenters were high in Saudi Arabia and were variable among regions [24]. Bacterial pathogens were recovered from 24.9% of the samples in a study from the Aseer region of Saudi Arabia and mainly comprised of *E. coli*, *K. pneumoniae*, *Enterococcus* spp., and *S. aureus* [19]. The most clinical specimens were from urine and wound swabs, followed by blood samples. *E. coli* (30.6%), *K. pneumoniae* (29.2%), and *P. aeruginosa* (14.6%) were the main Gram-negative path-

ogens isolated in the hospitals under this study. Many international studies reported that *E. coli* and *K. pneumoniae* were the most frequently isolated Gram-negative bacteria and other bacterial isolates [1,12], followed by *P. aeruginosa* [25], whereas the main Gram-positive pathogens isolated were *S. epidermidis* (22.9%) and coagulase-negative staphylococci (22.9%), followed by *S. hyicus* (10.0%). A previous study reported *Staphylococcus aureus* as one of the most frequently isolated pathogens from clinical specimens [18]. This difference in the frequency of the type of bacterial isolates between hospitals is most probably due to the variation in patient populations, departments in each hospital, and subsequently, the type of specimens sent to laboratories. Similarly, *S. aureus* was identified as the main etiological agents at Aseer Central Hospital and Abha General Hospital in Saudi Arabia [19]. WHO reported Methicillin-resistant *S. aureus*, along with vancomycin-resistant *Enterococcus faecium* and drug-resistant *Streptococcus pneumoniae*, to be causing serious healthcare and community-associated infections and resistant to current treatments; it requires the development of new antibiotics for combating the resistance [26].

Overall, susceptibility rates for *E. coli* strains were high in this study for most tested antimicrobial agents. High resistance rates were observed against ampicillin, moxifloxacin, and cefuroxime. *E. coli* isolates showed a very low resistance rate to tigecycline and meropenem. Another study reported the same pattern of resistance in *E. Coli* against ampicillin and cephalosporin antibiotics (except ceftazidime), followed by fluoroquinolone [27]. The *K. pneumoniae* isolates showed the same resistance as *E. coli* to most antibiotics. Relatively high resistance was noticed in *K. pneumoniae* isolates, which showed resistance to ampicillin, aztreonam, cefuroxime, and ceftazidime and sensitivity to ceftazidime, piperacillin/tazobactam, levofloxacin, tigecycline, and tobramycin. The lowest resistance was observed in *P. aeruginosa* isolates. A longitudinal study of over six years (2013 - 2018) in a healthcare facility from Saudi Arabia did not observe changes in the pattern of AMR in Gram-negative bacteria that were mainly comprised of *E. coli*, *K. pneumoniae*, and *P. aeruginosa* [28]. The prevalence of ESBL isolates among *K. pneumoniae* and *E. coli* was approximately 26% and 20%, respectively [28]. Among ESBL *E. coli* strains, the least effective antibiotics were ciprofloxacin and trimethoprim-sulfamethoxazole [28]. Al-Zalabani et al. observed unprecedented emergence of resistance to carbapenems (38.4%, n = 436) and imipenem (46.1%, n = 371) among *K. pneumoniae* isolates in the period between 2014 to 2018 in a healthcare facility of Medina [29].

The antibiotic resistance observed in this study of Gram-positive pathogens was *S. epidermidis* and coagulase-negative staphylococci, followed by *S. hyicus*. Antimicrobial resistance rates for *S. epidermidis* strains were high in this study for most tested antimicrobial agents. High resistance rates were observed in amoxicillin/clavulanate, ampicillin, clindamycin, erythromycin,

imipenem, oxacillin, and penicillin, but most sensitivity was to synergicid, tetracycline, rifampin, mupirocin, and fosfomycin. The coagulase-negative staphylococci isolates showed moderate resistance to most antibiotics, while *S. hyicus* showed the lowest resistance observed. *S. hyicus* was mainly resistant to tetracycline, oxacillin, penicillin, mupirocin, fosfomycin, imipenem, amoxicillin/clavulanate, and ampicillin and most sensitive to trimethoprim/sulfamethoxazole, rifampin, synergicid, linezolid, and daptomycin. Methicillin-resistant *Staphylococcus aureus* (MRSA) and *E. coli* were resistant to third generation cephalosporins [30]. Similarly, in a study about coagulase-negative staphylococci from Makkah, *S. epidermidis* was the most common species found in neonatal septicemia. Consistent with our findings, the highest antibiotic resistance was observed against penicillin, ampicillin, oxacillin, and augmentin among the species [31]. In the national surveillance of antimicrobial resistance among Gram-positive bacteria in Saudi Arabia, *Staphylococcus aureus* was most commonly reported, followed by non-group A beta-hemolytic streptococci, group A beta-hemolytic streptococci, coagulase-negative staphylococci, pneumococci, and enterococci [32]. Resistance rates were high among *S. aureus* (methicillin-resistant *S. aureus*, coagulase-negative staphylococci (oxacillin: 63%), and pneumococci (penicillin G: 33%)) [32].

CONCLUSION

In conclusion, a relatively high abundance of Gram-negative pathogens was recovered from the clinical specimens, mainly from the elderly patients. The Gram-negative pathogens were mainly comprised of *E. coli*, *K. pneumoniae*, and *P. aeruginosa*. The Gram-positive isolates were primarily comprised of *S. epidermidis* and coagulase-negative staphylococci. Relatively high resistance was observed against several antibiotics from penicillin and cephalosporin groups in isolates from both Gram-negative and Gram-positive bacteria. Relatively high resistance to carbapenem antibiotics was noticed in *K. pneumoniae* isolates. This study highlights the importance of multicenter continuous monitoring of antimicrobial resistance bacteria in the region to ensure the effective use of antibiotics for treatment and combating antimicrobial resistance.

Acknowledgment:

The authors acknowledge the Ministry of Health for giving them the opportunity to conduct research in one of their hospitals. The authors are extremely thankful to Rabigh General Hospital.

Source of Funds:

This research received no external funding.

Ethical Approval:

This research project was approved by the Institutional Research Board of the Ministry of Health in Jeddah (IRB A01631).

Declaration of Interest:

The authors have no conflicts of interest to declare.

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