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RESEARCH ARTICLE

DISTRIBUTION AND ANTIBACTERIAL RESISTANCE OF WOUND PATHOGENIC BACTERIA IN PATIENTS OF SANA'A HOSPITALS, YEMEN

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Abstract

Background and objectives: Cutaneous wounds are a common symptom in human medical practice. Understanding the physiology of the wound healing process and using the right therapeutic intervention are necessary for managing the existing healing in wound patients. Infection can cause wounds to take longer to heal, cosmetic surgery outcomes to be less satisfactory, and medical expenses to rise. So, general care hospitals in Sana'a, Yemen, undertook a study to identify the different types, locations, and prevalence of wound contamination caused by various bacteria, as well as to examine the antibiotic susceptibility pattern of wound-isolated bacteria.

Subjects and methods: This cross-sectional study was carried out among 699 wound patients with clinically diagnosed wound infections at NCPHL during the years 2021-2022. Pus and wound swab samples were processed using standard microbiological procedures at NCPHL. A modified Kirby Bauer disc diffusion technique was used to investigate the susceptibility of bacteria to various antibiotics. From pre-questionnaire and laboratory records of the NCPHL, clinical information about patients was gathered, including the types and locations of wounds.

Results: Out of 699 samples, 580 (82.98%) were positive for bacterial cultures. The most common wound was postoperative (30.8%), followed by diabetic foot ulcer (24.5%), traumatic wound (18.7%) and bullet wound (16.9%), while it was less frequent for caesarean section (5.7%) and sharp cut (2%). The present study revealed that Gram-negative bacteria were less frequent than Gram-positive bacteria (43.3% vs. 56.7%). Also gram-positive bacteria show a very high percentage (92.1%) of multidrug resistant (MDR) in compared to gram-negative bacteria (37.8%).

Conclusion: In the current study's wound bacteriological profile, *Staphylococcus aureus* was shown to be highly prevalent, followed by *Escherichia coli*, *S. epidermidis* (CoNS), *Acinobacter* spp., and *Pseudomonas aeruginosa*. Their sensitivity to widely used antibiotics showed a pattern of decline. It is crucial to be informed of the current bacterial profile trend and to adjust the antibiotic schedule in accordance with sensitivity.

Keywords: Antibiotic sensitivity, bacteriological profile, multidrug resistant (MDR), wound infections.

INTRODUCTION

A wound is a sudden onset of injury characterized by torn or punctured skin (an open wound), or bruising (a closed wound) from pressure or blunt trauma. In pathology, a wound is an acute injury that damages the epidermis of the skin[1,2]. A bacterial infection of a wound can impede healing and result in potentially fatal consequences[1,3]. Wounds that do not heal should be examined for their causes; several factors, including microbiological ones, may be responsible. A baseline work-up comprises an assessment of the wound, its degree and severity[1]. Cultures are normally acquired from blood circulation or from the wound site[1]. One or more resistance mechanisms to each of the major classes of antimicrobial drugs have been detected in bacteria species isolated from a variety of body samples[2,3]. However, a wound offers a moist, warm, and nourishing environment that is complimentary for microbial colonization, growth, and infection[4,5]. An imbalanced cellular defense mechanism, prolonged inflammation, and a high bacterial burden are the hallmarks of infected wounds[6]. *E. coli*, *P. aeruginosa*, *S. aureus*, *K. pneumoniae*, *Proteus* species, *Streptococcus* species, *S. pyogenes*, and *Enterococcus* species are the normal bacterial pathogens connected to wound infection[7]. Wound infections are a major cause of mortality in underdeveloped nations like Yemen; these infections are both preventable and treatable[8].

It has been discovered that the spectrum of bacteria that cause diseases and their susceptibility pattern differ depending on the environment[8-14]. Despite the fact that overusing antibiotics in both humans and animals has significantly sped up the emergence of resistance. Inhibiting particular antimicrobial processes, such as cell wall construction, nucleic acid synthesis, ribosome activity, protein synthesis, foliate metabolism, and cell membrane function, frequently results in the development of antibiotic resistance[15,16]. Access to and abuse of antimicrobials is further influenced by the lack of stringent laws governing their sales. Antimicrobials can normally be obtained without a prescription in underdeveloped nations[17]. Additionally, it is typical in Yemen to purchase antibiotics without a prescription from a licensed physician; this encourages public antibiotic overuse and aids in the formation and growth of antimicrobial resistance[8]. There have been a few studies done in Yemen to determine the antimicrobial resistance pattern of various samples[18,19,20]. Studies focusing on the types and locations of wounds as well as the resistance of bacterial isolates to antibiotics are extremely uncommon. Determining the types and locations of wounds, the prevalence of various bacteria in wound contamination, and studying the antibiotic suscepti-bility pattern of isolated bacteria were the goals of this study, which was conducted at public hospitals in Sana'a, Yemen.

SUBJECTS AND METHODS

Study population: This cross sectional study was carried out at National Center for Public Health Laboratories (NCPHL) belonged to Ministry of Public Health and Population. Patients were selected from both public and private hospitals in Sana'a, Yemen, over a two-year period and transferred to the department of microbiology at the National Center for Public Health Laboratories (NCPHL). Over the course of two years, from January 2021 to December 2022, 699 wound patients were gathered.

Clinical data: A thorough clinical history was gathered, including information on the patient's age, gender, length of discharge, type of wound, and prior antibiotic usage. While attending the NCPHL, data were gathered.

Wound specimens: Under sterile conditions, a sample of the wound fluids was taken from the wound using a cotton swab, or pus was drawn from the site using a sterile 21 G syringe. Following collection, the samples were immediately cultured directly in the proper medium.

Microbiological procedure: Three loops were inoculated: one to McConkey agar, one to chocolate agar, and one to blood agar. MacConkey agar and blood agar were incubated for 24 hours in an aerobic environment at 37°C. The inoculated chocolate agar was incubated for 24 hours at 37°C in a carbon dioxide-rich environment. Standard bacteriological techniques were then used to identify the growth[20].

Antibiotic sensitivity: In Mueller-Hinton agar, the modified Kirby-Bauer disc diffusion technique was used to test the antibiotic sensitivity of bacterial isolates. The 2022 Clinical Laboratory Standards Institute recommendation was used to interpret the inhibitory zone diameter[22,23].

Ethical consideration: All participants gave their consent after being informed that participation was optional and that they might decline at any time without providing a justification.

Statistical analysis: The Epi Info statistical tool version 6 (CDC, Atlanta, USA) was used to analyze the data. Quantitative information, such as mean values and standard deviation (SD), should be communicated because the data were regularly distributed. Percentages were used to express the qualitative data.

RESULTS

The study included 699 wounded patients, 53.2% of whom were males and 46.8% were females. Among them, 580 (82.98%) positive cultures were isolated. Patients were distributed among all age groups with the highest rates in the age groups 16-25 years (24.7%), 26-35 years (27.2%) and ≥46 years (24.9%) (Table 1).

Table 1: Age and gender distribution of wound patients attending public hospitals in Sana'a city, N=699.

Characters	Number (%)
Sex Ratio	
Male	372 (53.2)
Female	327 (46.8)
Age groups	
≤15 years	89 (12.7)
16-25 years	173 (24.7)
26-35 years	190 (27.2)
36-45 years	73 (10.4)
≥46 years	174 (24.9)
Total	**699 (100)**
Mean	34.4 years
SD	17.2 years
Min	1 years
Max	75 years
Median	30 years
Mode	24 years

The ages ranged from 1 to 75 years, with a mean of 34.4 ± 17.2 years. The most common type of wound was postoperative (30.8%), followed by diabetic foot ulcer (24.5%), traumatic wound (18.7%) and bullet wounds with 16.9% while it was less frequent for caesarean section (5.7%) and sharp cut (2%). Also, the most common body site of the wounds was foot (33.8%), abdominal part (27.3%), legs (15.6%), and hands (11.4%). While backside, breast, chest, and head and neck region were less frequent (Table 2).

Table 2: Types of wounds among wound patients.

Type of wounds	Number (%)
Post Surgical	215 (30.8)
Diabetic foot ulcer	171 (24.5)
Traumatic (Road Traffic Accidents)	131 (18.7)
Gun shoot	118 (16.9)
Caesarean section	40 (5.7)
Sharp cut	14 (2)
Others	10 (1.4)
Total	699 (100)

Gram-negative bacteria were less frequent than Gram positive bacteria (43.3% vs 56.7%). About 14 different bacterial species were isolated and identified. *S. aureus* (41.6%) was the most common isolate followed by *E. coli* (12.2%), *S. epidermidis* (CoNS) (10.5%), *P. aeruginosa* (5.2%), *Citrobacter freundii* (5.3%). *Proteus mirabilis* (2.6%), *K. pneumoniae* (1.4%), and *P. vulgaris* (1.2%) (Table 3). *S. aureus* showed a high rate of resistant to penicillin G (85.5%), azithromycin (77.2%) and cefixime (99.2%). CoNS showed a high rate of resistance to penicillin G (73.8%), azithromycin (45.9%) and cefixime (95.1%). *S. pyogen* showed a high rate of resistance to trimethoprim/sulfamethoxazole (68.4%), rifampin (42.1%), ciprofloxacin (63.2%) and azithromycin (63.2%).

Table 3: Sits of wounds among wound patients who attended public hospitals in Sana'a city (n=699).

Site of wounds	Number (%)
Foot	236 (33.8)
Abdominal part	191 (27.3)
legs	109 (15.6)
Hand	80 (11.4)
Backside	34 (4.9)
Chest	22 (3.1)
Head and neck	16 (2.3)
Breast	11 (1.6)
Total	699 (100)

S. pneumoniae showed a high rate of resistance to trimethoprim/sulfamethoxazole (50%), clindamycin (50%), penicillin g (50%) and azithromycin (50%) (Table 5). *E. coli* showed a high rate of resistance more than 50% for co-trimoxazole (50.7%), amoxicillin-clavulanic acid (52.1%), ceftriaxone (54%), cefuroxime (56.3%), cefotaxime (66.2%), ciprofloxacin (54.9%) and ampicillin (88.7%). Citrobacter spp showed a high rate of resistance to co-trimoxazole (65.3%), amoxicillin-clavulanic acid (88%), ceftriaxone (78.7%), cefuroxime (89.3%), ceftazidime (74.7%), ciprofloxacin (64%) and ampicillin (94.7%). *Acinetobacter* spp showed a high rate of resistance to ampicillin (87.1%), amoxicillin-clavulanic acid (77.4%), ceftriaxone (80.6%), cefuroxime (90.3%), ceftazidime (64.5%), ciprofloxacin (64.5%) and cefixime (90.3%). *P. aeruginosa* showed a high rate of resistance to ceftazidime (40%), cefixime (46.7%), cefotaxime (40%), and gentamicin (73.3%). *Proteus* spp showed a high rate of resistance to amoxillin clavulanate (40.9%), ampicillin (81.8%), trimethoprim/sulfame-thazole (77.3%), and colistin (86.3%).

Table 4: Bacterial etiology isolated from wounds in selected hospitals in Sana'a city (n=580 isolates).

Name of isolated pathogens	Frequency (%)
Gram positive bacteria	
S. aureus	241 (41.6)
S. epidermidis	61 (10.5)
S. pyogens	19 (3.3)
S. pneumoniae	8 (1.4)
Total Gram positive	329 (56.7)
Gram negative bacteria	
E. coli	71 (12.2)
C. freundii	44 (7.6)
Acinatobcter spp	31 (5.3)
Citrobacter	31 (5.3)
P. aeruginosa	30 (5.2)
P. mirabilis	15 (2.6)
Enterobacter spp	10 (1.7)
K. pneumoniae	8 (1.4)
P. vulgaris	7 (1.2)
M.organi	4 (0.7)
Total Gram Negative	251 (43.3)
Total bacterial isolates	580 (100)
Poly-microbial specimen	20 (2.9)
Mono-microbial specimen	539 (77.1)
Mixed growth specimen	21 (3)
No growth specimen	119 (17)
Total specimens	699 (100)

Enterobacter spp showed a high rate of resistance to cefuroxime (60%), amoxillin clavulanate (80%), ampicillin (80%), and trimethoprim/sulfamethazole (70%) (Table 6). All isolated organisms from the wound specimens displayed varying degrees of multi-drug resistance (MDR), Gram-positive bacteria exhibit a very high percentage of MDR (92.1%) in comparison to gram-negative bacteria (37.8%). Among the gram-positive bacteria isolated, *S. aureus* (98%), followed by CoNS (91.8%), Showed the highest percentage of MDR (Table 7). Among the gram-negative bacteria isolated, *E. coli* (57.7%), followed by *Citrobacter* spp (48%), showed the highest percentage of MDR (Table 8).

DISCUSSION

In the current study, 539 (77.1%) of the positive cultured samples showed mono- microbial growth, and 17% were negative for aerobic bacterial growth. This result is higher than that reported in Nepal[24] who reported that 60% of wounds had positive growth of aerobic bacteria. The study included 699 patients, 53.2% of whom were males and 46.8% were females.

In this study, male patients differentially outnumbered female patients from Rajput *et al.*, study where female patients were predominant[25] but other studies showed that wound infection was higher in males than in females as was our findings[26,27]. Patients were distributed among all age groups and the highest rates were in the age groups 16-25 years (24.7%), 26-35 years (27.2%) and 46 years (24.9%) and the ages of the patients ranged from 1 to 75 years, with a mean of 34.4±17.2 years. This differs with the study of Alam *et al.*, where a higher prevalence of wound incidence has been reported among patients aged 60-80 years[28]. Also, our result was different from the study in Ethiopia, where 87.5% of wound infection was in patients ≥ 60 years of age[29].

Table 5: Antibiotic sensitivity pattern of gram-positive microorganisms isolated from wounds.

Antibiotics Resistance (%)	*S. aureus* n=241 No (R %)	CoNS *n=61* No (R %)	*S. pyogens*, n=19 No (R %)	*S. pneumoniae* n=8, No (R%)
Trimethoprim/sulfamethoxazole	78 (32.4)	17 (27.9)	13 (68.4)	4 (50)
Clindamycin	67 (27.8)	14 (23)	3 (15.8)	4 (50)
Erythromycin	110 (45.6)	21 (34.4)	00 (00)	0 (0.0)
Fusidic acid	27 (11.2)	7 (11.5)	-	-
Penicillin G	205 (85.5)	45 (73.8)	00 (00)	4 (50)
Gentamicin	49 (20.3)	5 (8.2)	-	1 (25)
Rifampin	0 (00)	(00)	8 (42.1)	0 (0.0)
Cefoxitin	66 (27.4)	10 (16.4)	-	-
Ciprofloxacin	147 (61)	31 (50.8)	12 (63.2)	-
Cephalexin	-	-	00 (00)	0 (0.0)
Amoxiclav;	59 (24.5)	21 (34.5)	00 (0.0)	2 (25)
Azithromycin	186 (77.2)	28 (45.9)	12 (63.2)	4 (50)
Cefixime	239 (99.2)	58 (95.1)	1 (5.3)	1 (12.5)
Ceftriaxone	123 (51)	4 (6.6)	00 (0.0)	1 (12.5)
Cefuroxime;	47 (19.5)	3 (4.9)	00 (0.0)	0 (0.0)
Vancomycin;	2 (0.83)	00 (0.0)	00 (0.0)	0 (0.0)
Linezolid	3 (1.2)	(00) 0.0	00 (0.0)	0 (0.0)

Gram-negative bacteria were marginally less common than Gram-positive bacteria, according to the current study (43.3% vs. 56.7%). These results differ from those observed in earlier studies, which showed 71.6% for Gram-negative and 28.4% for Gram-positive bacteria[23]. Another distinction is that a prior study found that Gram-negative bacilli (70%) are more common than Gram-positive bacteria (30%), which is another difference. In addition, Gram-negative rods were the prevalent and main source of wound infection in a different study, and these results diverge from those of earlier investigations conducted in Asia and Africa[30-32]. Other studies, however, revealed about comparable frequencies of both Gram-positive and negative bacteria[33]. *S. aureus* in our study was one of the dominant bacteria in wound infections (41.6%) followed by *E. coli* (12.2%), and *S. epidermidis* (CoNS) (10.5%) and this result is consistent with some previous studies[22]. *S. aureus* may have a dominant cause since it is a typical component of human skin flora and is very easily spread through wounds.

Table 6: Antibiotic sensitivity pattern of gram-negative microorganisms isolated from wound patients.

Antibiotics Resistance Percentage (%)	*E. coli* n=71	Citrobacter spp n=75	*Acinetobacter* spp. n=31	*P. aeruginosa* n=30	*Klebsiella* spp. n=8	*Proteus* spp. n=22	*Enterobacter* spp. n=10
Amikacin	5 (7.04)	15 (20)	12 (38.7)	3 (10)	2 (25)	3 (13.6)	2 (20)
Ceftriaxone	39 (54.9)	59 (78.7)	25 (80.6)	-	2 (25)	4 (18.2)	2 (20)
Cefuroxime 2nd	40 (56.3)	67 (89.3)	23 (74.2)	-	1 (12.5)	4 (18.2)	6 (60)
Ceftazidime 3rd	29 (40.8)	56 (74.7)	20 (64.5)	12 (40)	2 (25)	1 (4.5)	4 (4 0)
Cefixime 4^{th}	45 (63.4)	73 (97.3)	28 (90.3)	14 (46.7)	2 (25)	6 (27.3)	3 (30)
Cefotaxime 3^{rd}	47 (66.2)	24 (32)	28 (90.3)	12 (40)	2 (25)	6 (27.3)	3 (30)
Imipenem	5 (7.04)	9 (12)	7 (22.6)	4 (13.3)	1 (12.5)	6 (27.3)	4 (40)
Meropenem	4 (5.6)	12 (16)	12 (38.7)	3 (10)	1 (12.5)	1 (4.5)	1 (10)
Ciprofloxacin	39 (54.9)	48 (64)	20 (64.5)	7 (23.3)	4 (50)	1 (4.5)	5 (5 0)
Piperacillin-tazobactam	15 (21.1)	32 (42.7)	12 (38.7)	4 (13.3)	1 (12.5)	1 (4.5)	3 (30)
Cefepime 4^{th}	32 (45.1)	-	14 (45.2)	4 (13.3)	1 (12.5)	1 (4.5)	1 (10)
Gentamicin	23 (32.4)	42 (56)	12 (38.7)	22 (73.3)	4 (50)	6 (27.3)	3 (30)
Amoxillin clavulanate	37 (52.1)	66 (88)	24 (77.4)	-	4 (50)	9 (40.9)	8 (80)
Ampicillin	63 (88.7)	71 (94.7)	27 (87.1)	-	6 (75)	18 (81.8)	8 (80)
Trimethoprim/ sulfamethazole	36 (50.7)	49 (65.3)	15 (4.8)	-	6 (75)	17 (77.3)	7 (70)
Colistin	2 (2.8)	00 (0.0)	1 (3.2)	1 (3.3)	1 (12.5)	19 (86.3)	1 (10)

Table 7: MDR pattern of selected Gram-positive bacteria isolated from infected wounds.

Antimicrobial class used to define MDR	Degree	*S. aureus* n=241 No (%)	CoNS n=61 No (%)	*S. pyogen* n=19 No (%)	*S. pneumoniae* n=8 No (%)
1-Glycopeptide (Vancomycin)	R0	1 (0.41)	2 (3.3)	6 (31.6)	4 (50)
2-Aminoglycosides (Gentamycin)	R1	2 (0.82)	3 (4.9)	1 (5.3)	1 (12.5)
3-Cephalosporin (Cefixime)	R2	1 (0.41)	27 (44.3)	0 (0)	2 (25)
4-Quinolone (Ciprofloxacin)	R3	47 (19.5)	3 (4.9)	4 (21)	0 (0)
5-Sulfonamides (Cotrimoxazole)	R4	29 (12)	11 (18)	7 (36.8)	1 (12.5
6-Oxazolidinones (Linezolid)	R5	69 (28.6)	12 (19.7)	1(5.3)	0 (0)
7-Macrolides (Azithromycin)	R6	53 (22)	0 (0)	00 (0)	0 (0)
Total MDR=303 (92.1%)	R7	39 (16.2)	0 (0)	0 (0)	0 (0)
	MDR	237 (98)	56 (91.8)	12 (63.2)	3 (37.5)

R0: Sensitive against all selected antibiotic class; R1: Resistant to at least one antibiotic class; R2: Resistant to two antibiotic class; R3: Resistant to three antibiotic class; R4: Resistant to four antibiotic class; R5: Resistant to five antibiotic class; R6: Resistant to six antibiotic class; R7: Resistant to all seven antibiotic class; MDR: Resistant to at least three antibiotic class.

According to Upreti *et al.*,[34] 13 distinct bacteria were recovered from pus samples, accounting for 82.5% of the bacterial growth, with *S. aureus* predominating (57.7%), followed by *E. coli* (11%), and CoNS (3%). Other microorganisms from pus samples that were discovered included *P. aeruginosa* (5.2%), *C. freundii* (5.3%). *P. mirabilis* (2.6%), *K. pneumoniae* (1.4%), and *P. vulgaris* (1.2%) (Table 5) is roughly similar to that reported in Iran[28] in which *S. aureus* was the most common bacteria (49%) found in wound infections followed by *E. coli* (25.9%), *Klebsiella* spp. (9.5%), *P. aeruginosa* (8.6%), and *Proteus* spp. (4%).

Table 8: MDR pattern of Gram-negative bacteria isolated from infected wounds.

Antimicrobial class used to define MDR	Degree	*E. coli* n=71	Citrobacter spp n=75	*Acinetobacter* spp. n=31	*P. aeruginosa* n=30	*Klebsiella* spp. n=8	*Proteus* spp. n=22	*Enterobacter* spp. n=10
1-Penicillin	R0	26(36.6)	14 (18.7)	3 (9.7)	16 (53.3)	2 (25)	3 (13.6)	3 (30)
2-Aminoglycosides	R1	2 (2.8)	24 (32)	8 (25.8)	7 (23.3)	2 (25)	2 (9.1)	3 (30)
3-Cephalosporin	R2	2 (2.8)	1 (1.3)	8 (25.8)	3 (10)	2 (25)	11 (50)	2 (20)
4-Quinolone	R3	1 (1.4)	16 (21.3)	0 (0.0)	1 (3.3)	0 (0.0)	3 (13.6)	0 (0.0)
5-Sulfonamides	R4	10 (14)	17 (22.7)	0 (0.0)	0 (0.0)	1 (12.5)	2 (9.1)	1 (10)
6-Colistin	R5	21 (15)	3 (4)	3 (9.7)	2 (6.7)	1 (12.5)	1 (4.5)	1 (10)
7-Carbapenem	R6	3 (4.2)	0 (0)	1 (3.2)	1 (3.3)	0 (0.0)	0 (0.0)	0 (0.0)
Total MDR=95 (37.8%)	R7	6 (8.5)	0 (0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
	MDR	41(57.7)	36 (48)	4 (12.9)	4 (13.3)	2 (25)	6 (27.3)	2 (20)

R0: Sensitive against all selected antibiotic class; R1: Resistant to at least one antibiotic class; R2: Resistant to two antibiotic class; R3: Resistant to three antibiotic class; R4: Resistant to four antibiotic class; R5: Resistant to five antibiotic class; R6: Resistant to six antibiotic class; R7: Resistant to all seven antibiotic class; MDR: Resistant to at least three antibiotic class.

Current research showed that, with the exception of *Proteus* spp., colistin (CST) is the most effective antibiotic in sensitivity tests for most gram-negative bacteria. More than 96% of *Proteus* species were discovered to be colistin resistant. Resistant was 2.8% to 12.5% for other gram-negative bacteria isolates. In a sensitivity test, the carbapenem group (imipenem and meropenem) and piperacillin-tazobactam displayed the highest levels of activity against *Proteus* spp. A low percentage of resistance to carbapenems was also demonstrated by several other kinds of bacteria. Additionally, our results are comparable to those of a recent systematic review and meta-analysis[35]. In the current analysis, it was observed that vancomycin (VAN) followed linezolid (LZD) were the most active antimicrobials in sensitivity against gram-positive bacteria species includes *S. aureus*, coagulase negative *staphylococci*, *S. pneumoniae* and *S. pyogens* in which there was no vancomycin resistant coagulase negative *staphylococci*, *S. pneumoniae* and *S. pyogens* observed; however 2 (0.83%), *S. aureus* were resistant to vancomycin (Table 6). Moreover, Al-Khawlany *et al.*, revealed that vancomycin was the most effective antibacterial against all the MRSA isolates recovered from infected wound[38]. Also, 1.2% *S. aureus* were found resistant against linezolid. Studies conducted in Bangladesh[28], India[36] and Colombia[37] also revealed similar findings, where *S. aureus* was found to be less than resistant to linezolid. Since isolates with resistance to more than three classes of tested antibiotics were referred to be multi-drug resistant (MDR) isolates, (MDR index>3)[9], therefore all isolated organisms from the wound specimens showed different level of MDR. This study also demonstrated that gram-positive bacteria from wound infections exhibit a very high percentage of MDR (92.1%) in comparison to gram-negative bacteria (37.8%).

Current study's overall MDR rate for gram-positive bacteria is higher than those done in Bangladesh (68.8%)[28], and Ethiopia[38]. The variation in the study population, where high MDR studies may have included hospitalized inpatients where greater MDR strains are anticipated, may be the likely explanation for such unevenness. In the current study patients consists of both hospitalized and non-hospitalized patients. All isolated organisms from the wound specimens displayed varying degrees of multi-drug resistance (MDR), which was defined as resistance to

>3 classes of antimicrobial tested (MDR index >3). This study also demonstrated that gram-positive bacteria from wound infections exhibit a very high percentage of MDR (92.1%) in comparison to gram-negative bacteria (37.8%). In comparison to studies done in Bangladesh (68.8%)[28] and Ethiopia[38], the total MDR rate of gram positive bacteria in our study is greater. The variation in the study population, where high MDR studies may have included hospitalized inpatients where greater MDR strains are anticipated, may be the likely explanation for such unevenness.

Among the gram-negative bacteria isolated, *E. coli* (57.7%), followed by *Citrobacter* spp (48%), Showed the highest percentage of MDR, while *Acinetobacter* spp (12.9%), *P. aeruginosa* (13.3%), *Klebsiella* spp (25%), *Proteus* spp (27.3%) and *Enterobacter* spp (20%) showed the lowest percentage of MDR. The overall MDR rate in the case of gram-negative bacteria in our study is (37.8%) is lower than the previously conducted studies in Yemen and elsewhere[39-44]. In Yemen, it is usual practice to provide antibiotics orally, which may limit bloodstream absorption of the drugs. Bacteria may acquire resistance if long-term oral antibiotic usage is undertaken. Inflamed wounds' MDR bacterial diversity may also be explained by a variety of factors, such as demography, age disparities, gender, length of hospitalization, and prior antibiotic use[2,9,13]. Hospitalization may also have a significant impact on the occurrence and type of MDR bacteria because patients are susceptible to nosocomial infections that are resistant to several prescription antibiotics[38,39].

Limitations of the study

This document focuses on bacterial wound infections, but other microorganisms such as fungi or viruses that may cause wound infections have not been studied and verified. It is known that the bacteria multiply, the healing is disrupted, and the wound tissues are damaged, and this leads to a local infection, but the bacteria present in the wound may cause other problems due to the spread of infection, which causes a systemic disease, and this was not studied in the current study. Further research is required to fully understand the factors involved in the transition from colonization to local infection and this may facilitate future guidance regarding the timing and nature of intervention for wound treatment.

CONCLUSIONS

This study has attempted to capture and address microbiological features that are crucial to the successful management of bacteria in wounds by giving a complete examination of wound microbiology, along with current opinion and issues regarding wound assessment and therapy. In the current study's wound bacteriological profile, *S. aureus* was shown to be highly prevalent, followed by *E. coli*, *S. epidermidis* (CoNS), *Acinobacter* spp., and *P. aeruginosa*. Their sensitivity to widely used antibiotics showed a pattern of decline. It is crucial to be informed of the current bacterial profile trend and to adjust the antibiotic schedule in accordance with sensitivity. Additionally, this study made the case for the necessity of routinely monitoring the clinical isolates' antibiotic sensitivity in order to control the spread of microorganisms that are resistant to antibiotics and to determine the most effective antibacterial treatments. Glycopeptide (vancomycin) and oxazolidinone (linezolid) antibiotics have been discovered to be efficient against gram-positive isolates. Contrarily, polypeptides and carbapenems were found to be effective against the majority of gram-negative isolates. Also, a significant proportion of MDR among frequently isolated bacteria was discovered in this investigation, which is a severe, worrying problem.

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AUTHOR’S CONTRIBUTIONS

Al-Shehari MM: writing, review, and editing. **Al-Khamesy KSA:** formal analysis investigation, conceptualization. **Al-Moyed KA:** formal analysis, writing. **Al-Shamahy HA:** supervision. **Al-Haddad AM:** methodology. **Al-Ankoshy AAM:** investigation. **Al-Shamahi EH:** formal analysis. All authors revised the article and approved the final version.

DATA AVAILABILITY

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

CONFLICT OF INTEREST

None to declare.

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