

Antibiogram of bacterial isolates from clinical specimens during 2018-2020 at Al-Aqsa hospital, Gaza, Palestine

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Abstract

Background: The increased resistance of microorganisms to widely prescribed antibiotics in current medical practice has become a major challenge. Healthcare-associated infections (HAIs) are complications of healthcare and are associated with high morbidity and mortality. This study aims to investigate the susceptibility pattern of bacteria isolated from different bacterial infections to commonly used antimicrobials from Al-Aqsa hospital in Gaza Strip, Palestine.

Methods: A total of 8062 various clinical specimens were collected from August 2018 to February 2020 and sent to Al-Aqsa medical microbiology laboratory for bacteriological culture. Specimens were processed based on the recommended microbiology procedures. The modified Kirby-Bauer disc diffusion method was used for antimicrobial susceptibility testing on Muller Hinton agar (MHA) according to the Clinical Laboratory Standards Institute (CLSI) guideline.

Results: *Enterobacteriaceae* were the most frequent of all isolated pathogens (58.3%), followed by *Staphylococcus* spp (24.6%), *Pseudomonas* and non-fermenters (6.9%), *Streptococcus* and *Enterococcus* (6.2%), and others (4.0). *E. coli* was the most frequent of all isolated pathogens (38.2%), followed by *Coagulase Negative Staphylococci* (14.9%), *Klebsiella* spp (14.2%), and *Staphylococcus aureus* (9.4%). The resistance of Gram-negative isolates to piperacillin, cephalixin, cefuroxime, cefotaxim, ceftazidim, ceftriaxone, cefazolin, co-trimoxazole, nalidixic acid, aztreonam, amoxicillin/clavulanic acid, meropenem, and teicoplanin was between 62% and 92%. On the other hand, Gram-positive isolates (*Staphylococcus* spp) were found to be susceptible to

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cloxacillin (65.0%), erythromycin (47.3%), and clindamycin (81.7%), levofloxacin (100.0%), rifampicin (95.2%) and vancomycin (89.2%).

Conclusions: High resistance rates were found among bacterial pathogens isolated from the Al-Aqsa hospital. Regular antimicrobial resistance surveillance should be a continuous process to provide up-to-date information to physicians with local antimicrobial resistance data. This approach will decrease to some extent the emergence of local antimicrobial resistance.

Keywords

Antimicrobial Resistance, Healthcare-Associated Infections, Gaza, Palestine.

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Introduction

Increased resistance of microorganisms to widely prescribed antibiotics in current medical practice has become a major challenge. The World Health Organization (WHO) states that antibiotic resistance is "a significant threat to global public health [1]. This rising antibiotic resistance pattern will leave routine infections with no effective treatment [2].

The problem of antimicrobial resistance is not only the development of resistance but also the transmission of the resistant strains from one person to another, especially in health facility settings. Transmission may occur due to routine daily interaction of people or the movement of animals or with different types of packed foods and drinks [3].

Healthcare-associated infections (HAIs) are complications of healthcare and are linked to high morbidity and mortality. Each year, about 1 in 25 U.S. hospital patients is diagnosed with at least one infection related to hospital care alone; additional infections occur in other healthcare settings [4].

Many HAIs are caused by the most recent and serious antibiotic-resistant bacteria (ARB) and can lead to sepsis or death. Central for Disease Control and Prevention (CDC) uses antimicrobial resistance data

for action to prevent infections, improve antibiotic use, and protect patients. This led to a 50% decrease in central line-associated bloodstream infections (CLABSI) between 2008 and 2014, a 36% decrease in healthcare-associated invasive Methicillin Resistant *Staphylococcus aureus* (MRSA), 2008–2014. Furthermore, National Healthcare Safety Network (NHSN) data reported a 13% decrease (2011–2014) for hospital-onset MRSA bacteremia bloodstream infections, confirming overall trends [4].

Antimicrobial resistance in the Gaza strip is escalating at an alarming pace, as evident by several published reports [5-8]. This increase is attributed to the uncontrolled use, misuse, and overuse of antimicrobials. In addition, poor infection control practices in health care settings contribute to the spread of antibiotic resistant bacteria (ARB).

This study aims at determining the most common bacterial pathogens from various infections in the Al_Aqsa hospital and their antimicrobial profiles. Area-specific monitoring studies aimed at gaining knowledge about the type of pathogens responsible for bacterial infection and their resistance patterns may help clinicians prescribe the appropriate empirical treatment.

Methods

Study setting, design, population, and sampling techniques

An institution-based cross-sectional study was conducted at Al Aqsa Hospital, Deir Al Balah, Gaza city. The antimicrobial resistance patterns of the bacterial isolates among the patients who attended all hospital clinics from August 2018 to February 2020 were determined.

Deir Al Balah is located in the center of the Gaza Strip, 14 kilometers south of the city of Gaza. Based on the Palestinian Central Bureau of Statistics, this city has a total population of 83,192 [9]. The hospital was purposely selected because it is one of the largest hospitals in the region. Currently, it provides inpatient and outpatient services for its catchment area and surrounding regions.

A total of 8062 clinical specimens were collected from outpatients and inpatients of Al-Aqsa hospital in Gaza, during the study period and sent to Al-Aqsa medical microbiology laboratory for bacteriological culture. The collected clinical specimens were processed according to the recommended microbiological procedures (Microbiology SOP). Identification of clinical isolates was performed using commercial systems (API 20 E) for Gram negative isolates, and Gram staining, catalase, coagulase, hemolytic activity, and other conventional tests for the identification of Gram-positive isolates. The Kirby-Bauer disk diffusion method was used for antimicrobial susceptibility testing on Muller Hinton agar (MHA) as per the Clinical Laboratory Standards Institute (CLSI) guideline [10].

Data analysis

Data were checked for completeness and consistency, and they were entered and analyzed using SPSS version 23. Descriptive statistics were used to describe the demographic characteristics of the patients and the bacteriological and antimicrobial resistance profile of the isolates. Statistical significance was considered at $P < 0.05$.

Ethical approval

A letter of ethical approval (IUG-28) was obtained from the Ethical Research Committee of the Islamic University of Gaza.

Results

The sources of the 8062 clinical specimens were as follow: ENES (Ear, Nose and Eye Swabs) 67.7%, Pus 67.3%, Body fluid 41.9%, Urine 35.7%, Blood 8.5%, Other 5.9%, Stool 1.5%, and CSF 0.6%. Out of the total cases (8062), 52.6% ($n=4242$) were males and 43.6% were adults, while infants constituted only 16% of the study subjects (**Table 1**).

Table 1. Demographic characteristics of the study participants ($n = 8062$).

Age group	Frequency	Percent
Adult	3519	43.6
Child	3256	40.4
Infant	1287	16.0
Total	8062	100.0

The overall percentage of positive cultures is 22.1% ($n=1781$). The highest percentage rate of positive culture was among eye, ear, and nose swabs (67.6%) followed by pus specimen (67.3%). The lowest positive rate was for CSF samples (0.6%), followed by stool sample (1.5%) as shown in **Table 2**. No statistically significant variation between males and females with regard to percentage of positive culture in any of the specimen groups

The hospital records classified the age of patients into adults, children, and infants. **Table 3** lists the percentage of positive cultures from various samples distributed by age groups. It could be noticed that there are variations among the various groups.

The results showed that members of the family *Enterobacteriaceae* were the most frequent of all isolated pathogens (58.3%), followed by *Staphylococcus* spp (24.6%), *Pseudomonas* and Non-fermenters (6.9%), *Streptococcus* and *Enterococcus* (6.2%) and others (4.0%) (**Table 4**).

Table 2. Culture positive specimens distributed by gender at Al-Aqsa hospital, August 2018–February 2020.

Specimen group	Male						Female						Culture positivity %
	Negative		Positive		Total		Negative		Positive		Total		
	N	%	N	%	N	%	N	%	N	%	N	%	
Blood	629	92.0	55	8.0	684	100.0	440	90.9	44	9.1	484	100.0	8.5
Body Fluid	76	55.9	60	44.1	136	100.0	43	62.3	26	37.7	69	100.0	42
C.S.F	854	99.4	5	0.6	859	100.0	642	99.4	4	0.6	646	100.0	0.6
ENES	7	53.8	6	46.2	13	100.0	4	53.8	17	46.2	24	100.0	67.6
Others	482	98.0	10	2.0	492	100.0	124	81.6	28	18.4	152	100.0	5.9
Pus	111	32.3	233	67.7	344	100.0	95	33.2	191	66.8	286	100.0	67.3
Stool	617	98.7	8	1.3	625	100.0	193	98.0	4	2.0	197	100.0	1.5
Urine	720	66.1	369	33.9	1089	100.0	1244	63.3	721	36.7	1965	100.0	35.7
Total	3496	82.4	746	17.6	4242	100.0	2785	72.9	1035	27.1	3820	100.0	22.1

ENES: Ear Nose and Eye Swabs.

Table 3. Frequency of the major bacterial groups isolated from Al-Aqsa hospital, August 2018–February 2020.

Specimen group	Adult				Child				Infant				Total percentage			
	Negative		Positive		Negative		Positive		Negative		Positive		Negative		Positive	
	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%
Blood	73	91.3	7	8.8	358	88.2	48	11.8	638	93.5	44	6.5	1069	91.5	99	8.5
Body Fluid	111	63.1	65	36.9	6	23.1	20	76.9	2	66.7	1	33.3	119	58.0	86	41.9
C.S.F	57	91.9	5	8.1	1264	99.7	4	0.3	175	100	0	0.0	1496	99.4	9	0.6
ENES	3	15.8	16	84.2	8	53.3	7	46.7	0	0.0	0	0.0	11	32.3	23	67.6
Others	583	94.6	33	5.4	19	95.0	1	5.0	4	50.0	4	50.0	606	94.0	38	5.9
Pus	165	33.1	334	66.9	35	34.3	67	65.7	6	20.7	23	79.3	206	32.7	424	67.3
Stool	637	99.7	2	0.3	156	94.0	10	6.0	17	100	0	0.0	810	98.5	12	1.5
Urine	811	56.8	617	43.2	868	69.3	385	30.7	285	76.4	88	23.6	1964	35.7	1090	35.7

ENES: Ear Nose and Eye Swabs.

Table 4. Frequency of the major bacterial groups isolated from Al-Aqsa hospital, August 2018–February 2020.

Isolated microorganisms	Frequency	Percent
<i>Enterobacteriaceae</i>	1037	58.3
<i>Pseudomonas</i> spp.	98	5.5
None fermenters other than <i>Pseudomonas</i>	24	1.35
<i>Staphylococcus</i> spp.	438	24.6
<i>Streptococcus</i> spp.	80	4.5

Isolated microorganisms	Frequency	Percent
<i>Enterococcus</i> spp.	31	1.7
Others bacterial isolates	71	4.0
<i>Candida</i> spp.	64	3.6
<i>Xanthomonas</i> spp.	2	0.1
<i>Haemophilus</i> spp.	4	0.2
<i>Neisseria meningitidis</i>	3	0.2
Total	1779	100.0

Table 5. Frequency of the major bacterial isolates from the Al-Aqsa hospital, August 2018–February 2020.

Organism isolated	N	%
Enterobacteriaceae		
<i>E. coli</i>	679	38.2
<i>Klebsiella</i> spp.	253	14.2
<i>Proteus</i> spp.	74	4.2
<i>Enterobacter</i>	14	0.8
<i>Salmonella</i> spp.	7	0.4
<i>Shigella</i>	5	0.3
<i>Serratiamarcescens</i>	3	0.2
<i>Citrobacter</i> spp.	1	0.1
<i>Morganellamorganii</i>	1	0.1
Pseudomonas and Non-fermenters		
<i>Pseudomonas</i> spp.	98	5.5
<i>Acinetobacter</i>	17	1.0
Others	5	0.3

Organism isolated	N	%
<i>Staphylococcus</i> spp		
<i>Staphylococcus aureus</i>	167	9.4
<i>Staphylococcus haemolyticus</i>	6	.3
Coagulase Negative <i>Staphylococci</i>	265	14.9
<i>Streptococcus</i>		
<i>Streptococcus viridans</i>	64	3.6
<i>Streptococcus pneumonia</i>	12	0.7
<i>Streptococcus pyogenes</i>	3	0.2
<i>Streptococcus agalactiae</i>	1	0.1
<i>Enterococcus</i> spp.	31	1.7
Others		
<i>Candida</i> spp.	64	3.6
<i>Xanthomonas</i> spp.	2	0.1
<i>Haemophilus</i> spp.	4	0.2
<i>Neisseria meningitides</i>	3	0.2
Total	1779	100.0

Table 5 contains a list of the isolated pathogens during the study period. The results showed that *E. coli* was the most frequent of all isolated pathogens (38.2%), followed by *Coagulase Negative Staphylo-*

cocci (14.9%), *Klebsiella*spp (14.2%), and *Staphylococcus aureus* (9.4%).

The overall AMR profile of the isolates is presented in **Table 6**. Resistance rates of Gram-negative

Table 6. Antimicrobial resistance profile (AMR) of the Gram-negative isolates.

Specimen group	Enterobacteriaceae						Pseudomonas spp.						Other Non-fermenters					
	S		I		R		S		I		R		S		I		R	
	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%
Amikacin	543	93.6	7	1.2	30	5.2	67	88.2	1	1.3	8	10.5	7	46.5	1	7.0	7	46.5
Amoxicillin	1	0.7	0	0.0	137	99.3	1	8.3	0	0.0	11	91.7	0	0.0	0	0.0	5	100
Ampicillin	3	5.2	0	0.0	55	94.8	0	0.0	0	0.0	1	100	0	0.0	0	0.0	2	100
Aztreonam	24	37.5	0	0.0	40	62.5	3	42.9	0	0.0	4	57.1	0	0.0	0	0.0	3	100
Cefazolin	173	36.5	1	0.2	300	63.3	9	16.6	0	0.0	45	83.4	1	9.0	0	0.0	10	91.0
Cefotaxime	226	45.1	7	1.4	268	53.5	24	39.3	1	1.6	36	59.0	3	23.0	1	8.0	9	69.0
Ceftazidime	443	57.7	28	3.6	297	38.7	49	61.3	0	0.0	31	38.7	5	31.0	2	12.5	9	56.0
Ceftriaxone	234	45.4	4	0.8	277	53.8	32	46.4	2	2.9	35	50.7	3	25.0	0	0.0	9	75.0
Cefuroxime	317	41.9	10	1.3	430	56.8	12	14.9	0	0.0	69	85.1	4	25.0	0	0.0	12	85.0
Cephalexin	170	21.4	25	3.2	598	75.4	4	7.0	0	0.0	53	94.8	4	11.0	0	0.0	31	89.0
Chloramphenicol	30	53.6	0	0.0	26	46.4	5	29.4	0	0.0	12	70.5	2	50.0	0	0.0	2	50.0

Specimen group	Enterobacteriaceae						Pseudomonas spp.						Other Non-fermenters					
	S		I		R		S		I		R		S		I		R	
	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%
Ciprofloxacin	626	70.7	7	0.8	253	28.6	60	79.0	0	0.0	27	31.0	9	50.0	0	0.0	9	50.0
Co Trimoxazole	257	29.5	2	0.2	612	70.3	15	19.5	0	0.0	62	80.5	4	25.0	1	6.0	11	69.0
Doxycycline	25	41.0	1	1.6	35	57.4	5	33.3	0	0.0	10	66.6	1	14.0	0	0.0	6	86.0
Gentamicin	369	70.0	8	1.5	150	28.5	33	63.5	0	0.0	19	36.5	5	45.5	0	0.0	6	54.5
Meropenem	11	37.9	2	6.9	16	55.2	5	50.0	3	30.0	2	20.0	6	66.6	0	0.0	3	33.3
Nalidixic acid	278	49.3	5	0.9	281	49.8	5	18.5	0	0.0	22	81.5	2	100	0	0.0	0	0.0
Nitrofurantoin	145	84.8	2	1.2	24	14.0	15	68.2	1	4.6	6	27.3	3	33.3	0	0.0	6	66.6
Piperacillin	13	16.9	1	1.3	63	81.8	4	50.0	0	0.0	4	50.0	0	17.0	0	0.0	5	83.0
Piperacillin-Tazobactam	1	12.5	0	0.0	7	87.5	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	4	100
Tetracycline	3	16.7	0	0.0	15	83.3	0	0.0	0	0.0	2	100	0	0.0	0	0.0	1	100

to piperacillin, cephalixin, cefuroxime, cefotaxime, ceftazidime, ceftriaxone, cefazolin, co-trimoxazole, nalidixic acid, aztreonam, co amoxiclav, meropenem and teicoplanin were between 62%-92%.

On the other hand, Gram-positive isolates (*Staphylococcus* spp) were found to be sensitive to

cloxacillin (65%), erythromycin (47.3%), clindamycin (81.7%), levofloxacin (100%), rifampicin (95.2%) and vancomycin (89.2%) (Tables 7).

Table 7. Antimicrobial resistance profile (AMR) of the Gram-positive isolates.

	Staphylococcus spp.						Streptococcus spp.						Enterococcus spp.					
	S		I		R		S		I		R		S		I		R	
	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%
Amikacin	104	90.4	6	42.8	0	0.0	8	57.2	0	0.0	11	9.6	14	100	0	0.0	0	0.0
Amoxicillin	6	10.5	0	0.0	0	0.0	1	100	0	0.0	51	89.5	0	0.0	0	0.0	3	100.0
Ampicillin	8	47.1	1	100	0	0.0	0	0.0	0	0.0	9	52.9	3	60.0	0	0.0	2	40.0
Augmentin	94	38.1	12	54.6	0	0.0	10	45.4	7	2.8	146	59.1	22	46.8	0	0.0	25	53.2
Cefazolin	107	75.9	7	41.2	0	0.0	10	58.8	4	2.8	30	21.3	21	84	0	0.0	4	16.0
Cefotaxime	119	65.7	7	36.8	0	0.0	12	63.2	11	6.1	51	28.2	28	87.5	0	0.0	4	12.5
Ceftazidime	7	23.3	0	0	0	0.0	2	100	1	3.3	22	73.3	4	80.0	0	0.0	1	20.0
Ceftriaxone	101	52.1	4	23.5	0	0.0	13	76.5	7	3.6	86	44.3	28	73.8	0	0.0	10	26.2
Cefuroxime	232	75.8	9	40.9	0	0.0	13	59.1	6	2.0	68	22.2	46	82.1	0	0.0	10	17.9
Cephalexin	146	48.2	4	17.4	0	0.0	19	82.6	17	5.6	140	46.2	26	48.1	1	1.9	27	50.0
Chloramphenicol	52	81.3	2	66.7	0	0.0	1	33.3	1	1.6	11	17.2	6	85.7	0	0.0	1	14.3
Ciprofloxacin	254	81.2	16	66.7	0	0.0	8	33.3	2	0.6	57	18.2	50	86.2	0	0.0	8	13.8
Clindamycin	187	81.7	2	14.3	0	0.0	12	85.7	1	0.4	41	17.9	35	74.5	0	0.0	12	25.5

	Staphylococcus spp.						Streptococcus spp.						Enterococcus spp.					
	S		I		R		S		I		R		S		I		R	
	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%
Cloxacillin	212	65.0	5	21.7	0	0.0	18	78.3	6	1.8	108	33.1	29	51.8	1	1.8	26	46.4
Co Trimoxazole	152	50.2	6	35.3	0	0.0	11	64.7	0	0.0	151	49.8	25	48.1	0	0.0	27	51.9
Doxycycline	51	79.7	1	25.0	0	0.0	3	75.0	1	1.6	12	18.8	5	55.5	0	0.0	4	44.4
Erythromycin	172	47.3	9	37.5	0	0.0	15	62.5	2	0.5	190	52.2	40	67.8	0	0.0	19	32.2
Gentamicin	112	81.8	4	36.4	0	0.0	7	63.6	0	0.0	25	18.2	12	45.8	1	4.2	11	45.8
Levofloxacin	3	100	0	0.0	0	0.0	2	100.0	0	0.0	0	0.0	0	0.0	0	0.0	1	100.0
Nalidixic acid	3	42.9	2	57.0	0	0.0	1	25.0	0	0.0	4	57.1	0	0.0	0	0.0	1	100.0
Nitrofurantoin	20	83.3	6	50.0	0	0.0	6	50.0	0	0.0	4	16.7	3	75.0	0	0.0	1	25.0
Penicillin G	5	23.8	5	62.5	1	12.5	2	25	0	0.0	16	76.2	14	53.8	0	0.0	12	46.2
Rifampicin	219	95.2	0	0.0	0	0.0	0	0.0	1	0.4	10	4.3	38	95	0	0.0	2	5.00
Tetracycline	2	50.0	19	82.6	0	0.0	4	17.4	0	0.0	2	50.0	0	0.0	0	0.0	0	0.0
Vancomycin	298	89.2	8	2.4	28	8.4	55	90.2	0	0.0	6	9.8	20	83.4	0	0.0	4	16.6

Discussion

Over a 3-year period, this research was conducted to assess the distribution of bacterial pathogens in various types of clinical specimens at Al-Aqsa Hospital, Gaza, Palestine, and to determine their antimicrobial resistance profile.

In the present study, the overall proportion of positive results was 22.0%. Of all isolates, Gram-negative (65.2%) were more frequent than others. It has been previously reported that Gram-negative isolates were predominantly found in different clinical specimens since they are an important cause of nosocomial infections, UTI, sepsis, pneumonia, and meningitis, and they generally cause severe disease [3]. Blood was the most prevalent infection site (32.37%) followed by sputum and urine [11].

The prevailing isolation of Gram-negative bacteria might be due to their simple nutritional requirements, frequent existence in the clinical setting, and their ability to resist many antibiotics and detergents in the hospital area. This was consistent with previous reports from other countries such as Ethiopia [12] India [13], China [14], and Egypt [11, 15].

In our study, ENES specimens showed the highest incidence of total isolates (67.6%) followed by Pus (76.3%), while C.S.F specimens exhibited the least frequency (0.6%). Also, contrary to our results, Sheblet *al.*, in their study, found that out of 554 bacterial isolates, urine specimens showed the highest incidence of total isolates (41.5%, n = 230) followed by blood (23.1%, n = 128), while sputum specimens exhibited the least frequency (17%, n = 94) [16].

The overall prevalence of culture-confirmed bacterial infection was significantly higher in males than females in the present study. In this study, the majority of the clinical isolates were recovered from urine, pus, and blood cultures. Among urine culture isolates, *E. coli* and *Klebsiella* spp. were the main etiologic agents identified. This finding is in agreement with other studies conducted in Ethiopia [17], Tanzania [18, 19], and Sudan, while *P. aeruginosa* was reported to be the predominant ICU isolates recently reported from Saudi Arabia [20]. Also, both two studies from Pakistan and Iraq reported that *Acinetobacter* and *E. coli* were the predominant ICU isolates, respectively [21].

Our results showed that *E. coli* was the most frequent of Gram-negative isolated pathogens (38.2%), followed by *Klebsiella* spp (14.2%), which is similar with results of many studies from various countries [22-24]. A study from Egypt showed that *Pseudomonas* (37.5%), *Klebsiella* (25%), *Staphylococcus* (20.8%), and methicillin-resistant *S. aureus* (4.2%) were the most commonly isolates from ventilator-associated pneumonia [25], whereas a second study from Egypt, reported that *E. coli* was the second most common isolate from neonatal sepsis [26].

Staphylococcus spp. was the most common isolate in our study and has constituted nearly one-third of all bacterial isolates, and this result is similar to a study reported from Tanzania [9]. Regarding the antimicrobial resistance profile *Staphylococcus* spp., they were found resistant (52.9%) to ampicillin. Other studies from Ethiopia, [17, 27, 28] have fully resistant (100%) to ampicillin. In other studies, we found the highest antimicrobial resistance was against ampicillin (89%) [29]. This means that ampicillin resistance increases with the rise of its use over time [29].

Our study showed 83.3% tetracycline resistance to *Enterobacteriaceae* and also showed high resistance to third-generation cephalosporins (53.8% ceftriaxone). Other study showed 33% tetracycline-resistance to *E. coli*, and showed high resistance to third-generation cephalosporins (93% ceftazidime and 90% ceftriaxone) [21].

It is very serious to note in this study that resistance to the relatively new introduced meropenem was 55.2% and 20.0% among *Enterobacteriaceae* and *Pseudomonas* and Non-fermenters isolates, respectively, which is similar to 66.2% for *Enterobacteriaceae* and very much lower than 55.2% for *Pseudomonas* and non-fermenters reported from Tanzania [30], and Jordan [9, 31]. Another study from Jordan showed that the highest resistance rates among *E. coli* isolates were 69.8%, 57.6% and 57.3%, to nalidixic acid, augmentin, and co-

trimoxazole, respectively [32]. 85% intermediate or resistant to imipenem and/or meropenem [33].

In the current study, the resistant rate of *Staphylococcus* spp for the first, second, and third generation was 7.5-16.2%, 11.3%, 13.4-20%, respectively. By 2017, treatment failure with third-generation cephalosporin antibiotics had been confirmed in at least 10 countries worldwide; South Africa, Australia, United Kingdom, Canada, Japan, Norway, France, Slovenia, Sweden, and Northern Ireland [34].

In this study, the resistance to vancomycin was 8.4, 9.8, 16.6% for *Staphylococcus* spp and *Streptococcus* and *Enterococcus*, respectively. An old study from Gaza city published in 2009, investigated vancomycin resistance among hospitalized patients showed higher rates of VRE. *E. faecium* showed the highest resistance rate to vancomycin (86.5%), while *E. avium* has the lowest resistance rate (16.7%), whereas among non-hospitalized individuals *E. faecium* has the highest resistance rate to vancomycin, while *E. durans* has the lowest resistance rate (33.3%) [35].

The emergence and spread of multidrug resistant pathogens are one of the major challenges for providing high-quality health care in resource-constrained settings. The detection of bacterial pathogens and the proper selection of antimicrobials effective against the species are critical to the successful treatment of patients with various infectious diseases.

On the contrary, extended-spectrum beta lactamases (ESBL) and resistance to colistin are becoming a serious problem in animals. This is mainly due to the continuous use of colistin in veterinary medicine even though it has been abandoned in the human domain [36].

In conclusion, the high frequency of multidrug resistant bacteria in the Al-Aqsa hospital indicates the need to prescribe broad-spectrum antibiotics more wisely to reduce pressure on sensitive bacterial strains. This could be beneficial in saving patients and preventing the spread of resistant isolates in hospital

settings. Therapeutic protocols involving using antibiotics should be periodically reviewed and revised according to the most recent local data on AMR pathogens isolates. Variations in resistance rates for almost all pathogens exist even in the same geographical area. Therefore, continuous performance antimicrobial susceptibility surveys for healthcare associated as well as community-acquired pathogens are recommended.

Author statements

Islam M. El-Aydi and Naema Ferwana. Sample collections, processing, and laboratory work, Mariam R. Al-Reefi, Data analysis, contributed to preparation and reviewing of the manuscript. Abdelraouf Elmanama, Conceptualization, supervision, writing of the original draft, reviewing and editing.

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Conflict of interest

The authors declare that there is no conflict of interest

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