ORIGINAL RESEARCH

Microbiological Profile and Drug-Resistance Pattern of Pathogens Among Patients Who Visited the University of Gondar Comprehensive Specialized Hospital, Ethiopia

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Background: The emergence of antimicrobial resistance (AMR) is a public health threat in developing countries including Ethiopia; and there is a paucity of information regarding antimicrobial resistance patterns of commonly isolated pathogens, particularly in the study area. Hence, this study aimed to assess the microbiological profiles and resistance patterns of pathogens among patients who visited a tertiary hospital in the study setting.

Methods: This study was based on secondary data sources from the hospital microbiology database and culture reports between September 2019 and August 2020 at the University of Gondar comprehensive specialized hospitals, Ethiopia. Data about socio-demographic characteristics and clinical parameters, types of specimens collected, culture results, and antibiotic resistance pattern were collected manually by using a data abstraction format from the department of clinical bacteriology registration book and electronic database.

Results: A total of 5328 culture results were included in the final analysis. Bacterial growth was documented only in 803 (15.1%) samples. From the positive culture results documented, the highest positivity rate was reported from abscess (47.8%) followed by blood (26.2%) and urine (15.1%) samples. Among the bacterial isolates *S. aureus* (32.5%), *Klebsiella* species (17.9%), *E. coli* (14.8%) and *Streptococcus* species (7.4%) were the commonly identified organisms. Of the 803 bacterial isolates, about 672 (83.6%) isolates were resistant to at least one antibiotic and 19.7% isolates were MDR.

Conclusion: This study showed that *Staphylococcus aureus, Klebsiella pneumonia* species, and *Escherichia coli* were the commonest isolated pathogens. Antimicrobial resistance among common isolates was high for most routinely used antibiotics, and some reserved drugs like carbapenems and fourth-generation cephalosporin. Thus, this study may have implications on patient management, drug procurement, local treatment guideline development, and rational use of antibiotics. Furthermore, this finding could also help to facilitate the implementation of antimicrobial stewardship and infection prevention and control interventions within the hospital.

Keywords: microbiological profile, antimicrobial resistance, Ethiopia

Background

Infectious diseases are the leading cause of morbidity and mortality and the major public health concern in developing countries.[1] Different pathogens are responsible for infectious diseases that cause morbidity and mortality and highly resistant to commonly used antibiotics. Moreover, antibiotic resistance (AR) is a global health

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threat and the current agenda of the World health organization (WHO) and other international organizations. In 2015 WHO released the Global Action Plan (GAP) on antimicrobial resistance which outlines five different objectives that aimed at ensuring treatment and prevention of infectious diseases with quality-assured, safe, and effective medicines.[2]

Antimicrobial resistance (AMR) threatens the effective prevention and treatment of an ever-increasing range of infections caused by bacteria, parasites, viruses, and fungi strains.[3–6] Irrational use of antibiotics, suboptimal quality drugs, and empirical treatment of infections without adequate laboratory evidence contributed to the occurrence of antimicrobial resistance.[7–10] Evidences showed that 25,000 annual deaths, and 2.5 million extra days of hospital stays are attributed to antimicrobial resistance. Irrational use of antibiotics, poor drug quality, and the smuggling of substandard drugs are the major drivers of rising antimicrobial resistance in developing countries.[11–13] Besides, poor infection prevention control practices in the health facilities also contributed to the increased occurrence of antimicrobial resistance. In addition, the transmission of healthcare-associated infections in hospitals is also responsible to the widespread of antimicrobial-resistant germs.

Recently, a group of bacteria has been described by the acronym of ESKAPE which refers *Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa*, and *Enterobacter species* predominantly causes most of the nosocomial infections in healthcare settings.[7,8,11–14]

Developing countries are characterized by poor health facility infrastructures and overwhelmed by high burdens of infectious diseases like tuberculosis and HIV/AIDS. Additionally, there is a lack of information about the bacteriologic profile and antimicrobial susceptibility patterns in health facilities of resource-limited settings including the study area. Therefore, this study aimed to assess the microbiological profile and resistance pattern of pathogens isolated from patients who visited the University of Gondar comprehensive specialized hospital.

Method
Study Design, Setting, and Period
This study was a descriptive cross-sectional based on secondary data from the hospital microbiology database and culture reports between September 2019 and August 2020 at the University of Gondar Comprehensive Specialized Hospitals, Ethiopia. The hospital is one of the tertiary hospitals in Northwest Ethiopia and serves more than seven million people in the catchment area. The University hospital has separated microbiological and tuberculosis culture units; and a functioning antimicrobial stewardship and infection prevention and control committee. As an average, close to 6000 cultures are being performed in the hospital annually.

Data Collection and Specimen Processing
Data about socio-demographic characteristics and clinical parameters such as age, sex, names of wards and departments, types of samples collected, culture results, and antibiotic susceptibility pattern were collected manually by using a pre-prepared data abstraction format from secondary data sources obtained from the department of clinical bacteriology registration book and electronic database whereby all the necessary clinical and microbiology-related information were recorded.

After a request by the treating physician, different culture samples were collected from respective units of the hospital. The standard operating procedures of collection, storage, and transport of samples were implemented. After culture samples get collected by the microbiology unit; culture Media were tested for sterility and performance according to CLSI standard procedures.[15]

A drop of different specimens was placed on chocolate, blood, and MacConkey agar plates; and stroked over the culture media. The chocolate and blood agar plates were incubated in a CO_2 enriched atmosphere at 35–37°C for up to 72 hours, on the other hand, MacConkey agar plates were incubated aerobically. After overnight incubation, culture media were checked for growth manually; and whenever there was any growth after overnight incubation, the definitive biochemical identification of the organism and antimicrobial susceptibility test was performed. Colony morphology, hemolytic pattern, Gram stain, and biochemical tests including lactose fermentation, lysine, citrate and urea utilization, motility, and gas production were used to identify types of bacteria.[16]

Susceptibilities to common antibiotics were determined by the Kirby-Bauer disc diffusion method.[17] The drugs tested for both gram-negative and gram-positive bacteria were: Amoxicillin/clavulanic acid (10μg), Ciprofloxacin (10μg), Gentamicin (10μg), Trimethoprim/sulfamethoxazole (10μg), chloramphenicol (10μg), cefotaxime (30μg), Cefepime (10μg) and ceftriaxone (30μg). Moreover,

penicillin (10µg), Tetracycline (10µg), cefoxitin (10µg), clindamycin (10µg), vancomycin (30 µg), and erythromycin (15µg) drugs were exclusively used to test gram-positive bacteria whereas, Ampicillin (10µg), ceftazidime (30µg), Norfloxacin (30 µg), Amikacin (10µg), Imipenem (10µg) and meropenem (10µg) were used for gram-negative bacterial isolates. The zones of inhibition were measured and compared with the National Committee for Clinical Laboratory Standards (NCCLS) guidelines.[18] International reference bacteria strains: *Escherichia coli* (ATCC 25922) and *Staphylococcus aureus* (ATCC 25923) were used as controls.[19]

For this study, intermediate antimicrobial susceptibility was considered as resistance and multi-drug resistance (MDR) was defined as the resistance of bacterial isolates to at least two or more different antibiotics tested.

Data Analysis and Interpretation

The data were checked for inconsistencies, coding errors, completeness, clarity, and missing values before entry. The data entry was done using Epi-data version 4.64.0 and then it was exported to SPSS version 22 for further analysis. Descriptive statistics were carried out and presented using tables, text, and graphs. In addition, cross-tabulation of culture results with socio-demographic variables was done to check if there was any association with culture positivity. Thus, variables having less than 0.05 P-value were considered to have a statistically significant association.

Result
Socio-Demographic Characteristics

A total of 5340 culture samples were collected during the study period, of which 12 samples were excluded due to incomplete information. As a result, the final samples analyzed for this study were 5328, close to 60% of the patient samples included were from male patients. More than half (55%) patients aged above 15 years; and about 8.3% of them were neonates below the age of 28 days. Additionally, the majority of culture samples were obtained from the pediatric emergency unit, adult emergency unit, and medical wards contributing about 30.3%, 24%, and 18.2%, respectively (Table 1).

Microbiological Profile of Culture Isolates

Out of the total 5328 cultures performed, more than a quarter (27.4%) of the samples constituted blood cultures followed by CSF (25.5%) and other body fluids (16.3%) (Figure 1).

Table 1 Socio-Demographic Characteristics of Patients Whose Samples Were Included (N=5328)

Characteristics	Frequency	Percentages
Age category		
Less than 28 days	443	8.3
1 month to 5 years	1264	23.7
5–15 years	650	12.2
>15 years	2971	55.8
Sex		
Male	2195	58.8
Female	3133	41.2
Departments		
Pediatric wards	1614	30.3
Adult emergency	1277	24
Medical wards	971	18.2
NICU	432	8.1
ICU (adult and pediatric)	336	6.3
Surgical wards	338	6.3
Outpatient Department	229	4.3
Pediatric emergency	81	1.5
Gynecology and obstetrics	50	0.9

Abbreviations: ICU, intensive care unit; NICU, neonatal intensive care unit.

From all the cultures analyzed during one year period, bacterial growth was documented only in 803 (15.1%) samples and contaminants were also isolated among 132 (2.5%) samples. Culture samples collected from the pediatric ward accounted for the highest positivity result (27.9%) followed by samples collected from medical wards (19.3%), surgical wards (17.8%), and ICU (10.2%) respectively. More than half (57.3%) of positive culture results were obtained from samples collected from the age group of above 15 years. From the positive culture results documented, the highest positivity rate was obtained from abscess (47.8%) followed by blood (26.2%) and urine (15.1%) samples (Figure 2). Findings also revealed that culture positivity had statistically significant association with the types of samples collected (P=0.0001) and place of sample collection (P=0.0001). However, no statistically significant association was noted with the other variables including, age (P= 0.705) and sex of patients (P= 0.475). Among the bacterial isolates: *S. aureus* (32.5%), *Klebsiella* species (17.9%), *E.coli* (14.8%), and *Streptococcus* species (7.4%) were the most commonly identified organisms (Figure 3) and (Tables 2 and 3).

Antimicrobial Resistance Pattern

Of the 803 culture isolates about six hundred seventy-two (83.6%) isolates were resistant to at least one antibiotic and
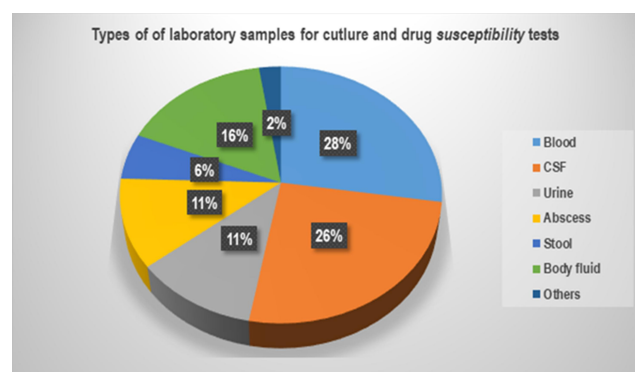
Figure 1 A pie chart showing the types of laboratory samples for culture and drug susceptibility tests.

19.7% isolates were multidrug-resistant (MDR). More specifically, 34.8%, 28.7%, 26.8%, and 22.6% of isolated *S. aureus* species were resistant to Penicillin, Erythromycin, TTC, and clindamycin, respectively.

From the gram-negative isolates, *Klebsiella* species showed resistance to ceftazidime (59%), Cefuroxime (44.4%), Ceftriaxone (38.2%), ciprofloxacin (45.1%), and trimethoprim or sulfamethoxazole (SXT) (58.3%). On the other hand, out of the 119 *E.coli* isolates, most were resistant to widely used antimicrobials like fluoroquinolones and cephalosporin including ciprofloxacin (47.9%),

ceftazidime (50.4%), ceftriaxone (39.5%), and cefuroxime (35.3%).

In addition, about 47.3%, 43.7%, 25%, 25% of *Pseudomonas* species were resistant to trimethoprim or sulfamethoxazole (SXT), ceftazidime, ceftriaxone, and amoxicillin/clavulanic acid antibiotics, respectively. Notably, out of all gram-negative isolates, only three hundred twenty-two gram-negative pathogens had been tested for Carbapenems susceptibility from which 39 (12.1%) of the bacteria isolates were resistant to either imipenem or meropenem. The details of antimicrobial resistance patterns of isolates are presented in Tables 4–6.

Discussion

This study showed that more than half (55.8%) of patients aged above 15 years and 8.3% of the patients were neonates. Blood (28%), Cerebrospinal fluid (CSF) (26%), and body fluid (16%) were the most frequently collected samples. From 5328 patient cultures during one year period, bacterial growth was documented only in 803 (15.1%) culture samples. The rate of culture positivity in this study was comparable with other previous findings reported from Jimma medical center (15.8%).[20] However, this study finding was lower than other similar studies
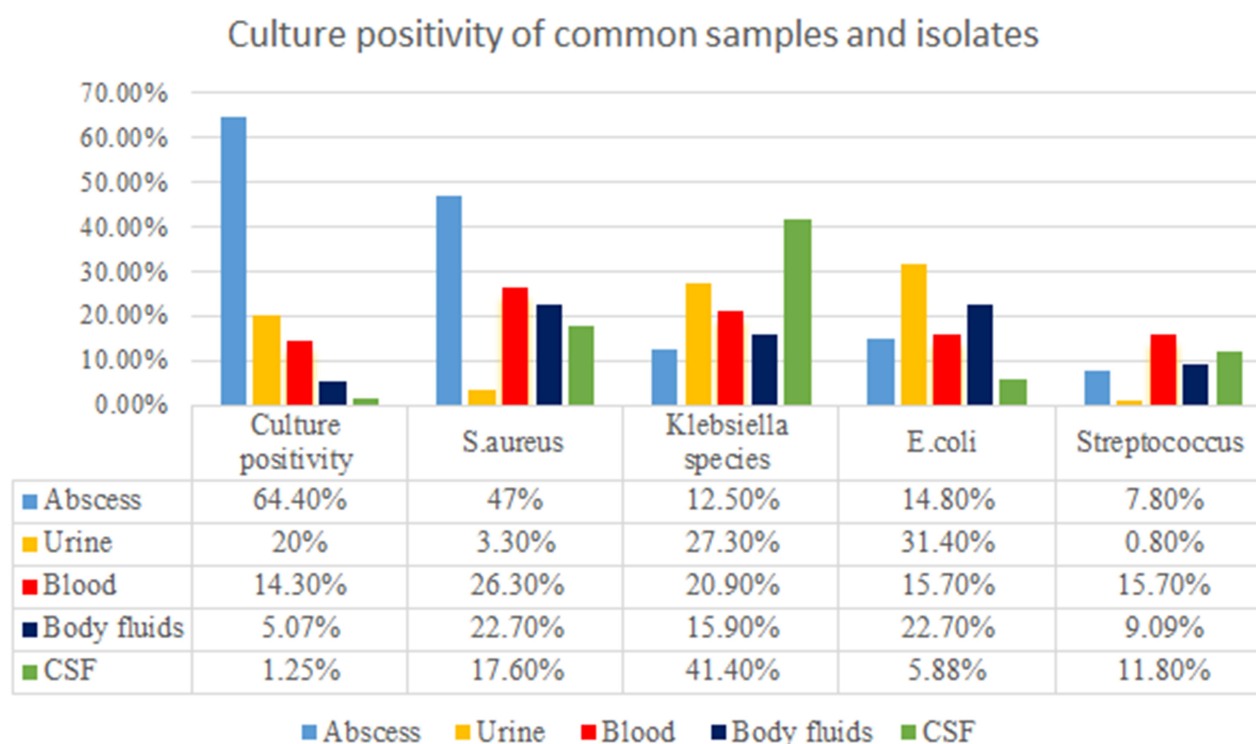

Figure 2 Culture positivity of common samples and isolates at the University of Gondar comprehensive specialized hospital.
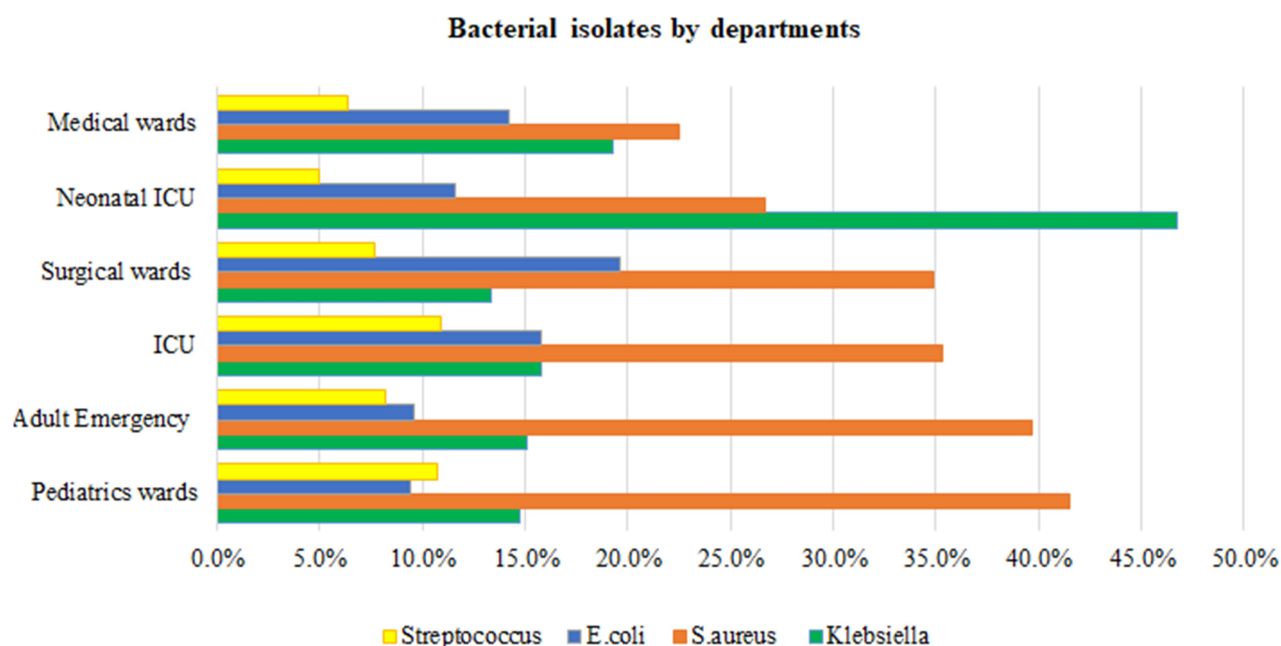
Bacterial isolates by departments

Figure 3 Graph showing the bacterial isolates by hospital departments.

conducted in Ethiopia, particularly in Addis Ababa (27.9%)[21] and Dessie (22.7%);[22] and a study done in India (22.5%).[23] In addition, this study showed that about 132 (2.5%) samples grew contaminants. The rate of contamination in this study appeared to be within acceptable ranges recommended by WHO.[24] Regarding

Table 2 Bacterial Isolates from Clinical Samples (N=5328)

Characteristics	Frequency	Percentages
Bacterial isolates		
Yes	803	15.1
No	4393	82.4
Contaminant	132	2.5
Isolates (n=803)		
S.aureus	261	32.5
Klebsiella species	144	17.9
E.coli	119	14.8
Streptococcus species	68	7.4
Acinetobacter species	52	6.5
Enterobacter cloacae	45	5.6
Pseudomonas species	32	4
Citrobacter species	25	3.1
Enterococcus species	19	2.4
LFGNR (Undifferentiated)	15	1.9
Shigella species	12	1.5
Others*	11	1.4

Note: Others*: (Salmonella, Serratia, and Neisseria).
Abbreviation: LFGNR, lactose ferments Gram-negative rods.

the place of collection, culture samples collected from the pediatric ward accounted for the highest positivity result (27.9%) followed by medical wards (19.3%), surgical wards (17.8%) and ICU (10.2%), adult emergency (9.1%) and neonatal ICU (7.5%). As depicted in Figure 2 *Klebsiella* species was the most common isolate from CSF (41.4%) and Urine (27.3%) samples, whereas, *S. aureus* was the commonest isolate from Abscess (47%) and Blood (26.3%) samples. These findings were consistent with the studies mentioned above.[11,25] Regarding the rate of culture positivity related to the type of samples, the highest percentage of bacterial growth was documented from abscess samples (47.8%) followed by blood (26.2%) and urine (15.1%). Overall, S. aureus (32.5%), Klebsiella species (17.9%), E.coli (14.8%), and Streptococcus species (7.4%) were the commonest identified organisms. This finding was consistent with systematic review findings in Africa and similar studies conducted in Ethiopia.[5,7,11] Regarding the specific age groups, Klebsiella species (46.7%) was the commonest bacteria isolated among the neonatal age group followed by S. aureus (26.7%), whereas, S. aureus (26.9%), E.coli (18.3%), and Klebsiella species (16.1%) were the most common isolates in adults. This finding was consistent with the previously mentioned studies.[5,25,26] This finding might suggest that the source of infections to neonates might be the mother or acquired in the hospitals during or after delivery as a result

Table 3 Bacteriological Isolates by Socio-Demographics and Hospital Departments (Place of Specimen Collection)

Characteristics	S. aureus	Klebsiella Species	E. coli	Streptococcus Species	Acinetobacter Species	Enterobacter cloacae	Pseudomonas Species	Citrobacter Species	Enterococcus Species	Shigella Species	Others
Age											
Less than 28 days (n=60)	16 (26.7)	28 (46.7)	7 (11.7)	3 (5)	1 (1.7)	2 (3.3)	1 (1.7)	0 (0)	1 (1.7)	0 (0)	1 (1.7)
1mon to 5 years (n=189)	76 (40.2)	33 (17.5)	17 (9)	20 (10.6)	10 (5.3)	9 (4.8)	2 (0.1)	6 (3.2)	8 (4.2)	5 (2.6)	1 (0.5)
5–15 years (n=94)	45 (47.9)	9 (9.6)	9 (9.6)	9 (9.6)	3 (3.2)	4 (4.2)	10 (10.6)	2 (2.1)	4 (4.2)	1 (1.01)	1 (1.01)
>15 years (n=460)	124 (26.9)	74 (16.1)	86 (18.7)	36 (7.8)	38 (8.3)	30 (6.5)	19 (4.1)	17 (3.7)	29 (6.3)	6 (1.3)	8 (1.7)
Sex											
Male (n=340)	145 (42.6)	87 (25.6)	64 (18.8)	3 (5)	38 (10.3)	32 (9.4)	16 (4.7)	17 (5)	7 (2)	3 (2.6)	7 (2)
Female (n=463)	116 (25)	53 (11.4)	55 (11.9)	20 (10.6)	14 (2.8)	13 (2.8)	16 (3.4)	8 (1.7)	12 (2.6)	9 (1.9)	2 (0.4)
Place of collection											
Adult emergency (n=73)	29 (39.7)	11 (15.1)	7 (9.6)	6 (8.2)	4 (5.5)	5 (6.8)	5 (6.8)	1 (1.3)	0 (0)	2 (2.7)	1 (1.3)
Pediatric wards (n=224)	93 (41.5)	33 (14.7)	21 (9.4)	24 (10.7)	11 (4.9)	11 (4.9)	8 (3.6)	6 (2.6)	7 (3.1)	6 (2.6)	1 (0.4)
Medical wards (n=155)	35 (22.5)	30 (19.3)	22 (14.2)	10 (6.4)	14 (9)	15 (9.6)	6 (3.8)	8 (5.2)	8 (5.2)	2 (1.3)	3 (1.9)
NICU (n=60)	16 (26.7)	28 (46.7)	7 (11.6)	3 (5)	1 (1.7)	2 (3.3)	1 (0)	0 (0)	1 (1.7)	0 (0)	1 (1.7)
ICU (n=82)	29 (35.3)	13 (15.8)	13 (15.8)	9 (10.9)	5 (6.1)	2 (2.4)	4 (4.9)	5 (6.1)	2 (2.4)	0 (0)	0 (0)
Surgical wards (n=143)	50 (34.9)	19 (13.3)	28 (19.6)	11 (7.7)	14 (9.8)	6 (4.2)	4 (2.8)	3 (2.1)	1 (0.7)	0 (0)	2 (1.4)
OPD (n=50)	6 (12)	5 (10)	19 (38)	4 (8)	3 (6)	4 (8)	1 (2)	2 (4)	0 (0)	2 (4)	2 (4)
Pediatric emergency (n=9)	3 (33.3)	0 (0)	0 (0)	1 (11.1)	0 (0)	0 (0)	2 (22.2)	0 (0)	0 (0)	0 (0)	0 (0)
Gynecology and obstetrics (n=7)	0 (0)	2 (28.6)	2 (28.6)	1 (14.2)	0 (0)	0 (0)	1 (14.2)	0 (0)	0 (0)	0 (0)	0 (0)

Table 4 Drug Susceptibility Test Results of Bacteriological Isolates at the University of Gondar Comprehensive Specialized Hospital

Pathogens Isolated	Frequency of Antibiotic Resistance, n (%)									
	Tazo	Cefa	CAF	Cefta	Genta	SXT	Amik	Amo/Clv	Nal	Cefu
S.aureus (n=261)	0 (0)	0 (0)	2 (0.8)	1 (0.4)	31 (11.9)	61 (23.4)	1 (0.4)	0 (0)	0 (0)	0 (0)
Klebsiella species (n=144)	22 (15.3)	11 (7.6)	14 (9.7)	85 (59)	63 (43.5)	84 (58.3)	9 (6.2)	33 (22.9)	23 (16)	64 (44.4)
Streptococcus species (n=68)	0 (0)	0 (0)	1 (1.4)	1 (1.4)	0 (0)	5 (7.3)	0 (0)	0 (0)	0 (0)	0 (0)
E.coli (n=119)	18 (15.1)	10 (8.4)	4 (3.4)	60 (50.4)	27 (22.7)	68 (57.1)	3 (2.5)	31 (26)	21 (17.6)	42 (35.3)
Acinetobacter species (n=52)	8 (15.4)	4 (7.7)	0 (0)	28 (53.8)	26 (50)	29 (55.7)	3 (5.8)	9 (17.3)	2 (3.8)	24 (46.1)
Enterobacter cloacae (n=45)	8 (17.8)	7 (15.6)	3 (6.7)	25 (55.5)	15 (33.3)	24 (53.3)	2 (4.4)	0 (0)	7 (15.6)	17 (37.8)
Pseudomonas species (n=32)	1 (3.1)	1 (3.1)	0 (0)	14 (43.7)	1 (3.1)	14 (43.7)	0 (0)	8 (25)	2 (6.2)	0 (0)
Citrobacter species (n=25)	2 (8)	1 (4)	3 (12)	7 (28)	5 (20)	10 (40)	0 (0)	6 (24)	2 (8)	8 (32)
Enterococcus species (n=19)	11 (57.9)	0 (0)	2 (10.5)	1 (5.3)	1 (5.3)	1 (5.3)	0 (0)	0 (0)	0 (0)	1 (5.3)
Shigella species (n=12)	0 (0)	1 (8.3)	0 (0)	1 (8.3)	0 (0)	8 (66.7)	0 (0)	0 (0)	0 (0)	3 (25)

Abbreviations: Tazo, piperacillin/tazobactam; Cefa, cefazolin; CAF, chloramphenicol; Cefta, ceftazidime; Genta, gentamycin; SXT, trimethoprim/sulfamethoxazole; Amik, amikacin; Amo/clv, amoxicillin/clavulanic acid; Nal, nalidixic acid; Cefu, cefuroxime.

Table 5 Drug Susceptibility Test Results of Bacteriological Isolates at the University of Gondar Comprehensive Specialized Hospital (Continued)

Pathogens Isolated	Frequency of Antibiotic Resistance, n (%)								
	Pen	Cefo	Ery	TTC	AZT	Nrf	Dxy	Cft	Cipr
S.aureus (n=261)	91 (34.8)	45 (17.2)	75 (28.7)	70 (26.8)	14 (5.4)	0 (0)	5 (1.9)	0 (0)	34 (13)
Klebsiella species (n=144)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	5 (3.5)	0 (0)	55 (38.2)	65 (45.1)
E.coli (n=119)	1 (0.8)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.8)	0 (0)	47 (39.5)	57 (47.9)
Streptococcus species (n=68)	7 (10.3)	1 (1.4)	9 (13.2)	6 (8.8)	6 (8.8)	0 (0)	0 (0)	9 (13.2)	0 (0)
Acinetobacter species (n=52)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	21 (40.4)	2 (3.8)
Enterobacter cloacae (n=45)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	16 (35.6)	19 (42.2)
Pseudomonas species (n=32)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (3.1)	8 (25)	5 (15.6)
Citrobacter species (n=25)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (4)	0 (0)	5 (20)	7 (28)
Enterococcus species (n=19)	4 (21)	0 (0)	1 (5.2)	9 (47.4)	1 (5.2)	0 (0)	1 (5.2)	1 (5.2)	3 (15.8)
Shigella species (n=12)	0 (0)	0 (0)	0 (0)	1 (8.3)	0 (0)	0 (0)	0 (0)	0 (0)	2 (16.7)

Abbreviations: Pen, penicillin; Cefo, cefoxitin; Ery, erythromycin; TTC, tetracycline; Azt, azithromycin; Nrf, norfloxacin; Dxy, doxycycline; Ceft, ceftriaxone; Cipr, ciprofloxacin.

Table 6 Drug Susceptibility Test Results of Bacteriological Isolates at the University of Gondar Comprehensive Specialized Hospital for Selected Antibiotics

Pathogens	Frequency of Antibiotic Resistance, n (%)								
	Cefo	Cefe	Imp	Mer	Pipe	Torb	Clin	Van	Nitr
S.aureus (n=261)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	59 (22.6)	1 (0.4)	0 (0)
Klebsiella species (n=144)	18 (12.5)	2 (1.4)	6 (4.2)	13 (9.03)	24 (16.7)	59 (41)	0 (0)	0 (0)	8 (5.5)
E.coli (n=119)	8 (6.7)	0 (0)	2 (1.6)	3 (2.5)	16 (13.4)	32 (26.9)	0 (0)	0 (0)	4 (3.4)
Streptococcus species (n=68)	0 (0)	4 (5.9)	0 (0)	0 (0)	0 (0)	0 (0)	7 (10.3)	9 (13.2)	0 (0)
Acinetobacter species (n=52)	11 (21.1)	0 (0)	4 (7.7)	9 (17.3)	0 (0)	20 (38.5)	0 (0)	0 (0)	1 (1.9)
Enterobacter cloacae (n=45)	4 (8.9)	1 (2.2)	3 (6.6)	2 (4.4)	4 (8.9)	19 (42.2)	0 (0)	0 (0)	1 (2.2)
Pseudomonas (n=32)	0 (0)	1 (3.1)	0 (0)	3 (9.3)	3 (9.3)	3 (9.3)	0 (0)	0 (0)	3 (9.3)
Citrobacter species (n=25)	6 (24)	0 (0)	0 (0)	0 (0)	4 (16)	5 (20)	0 (0)	0 (0)	1 (4)
Enterococcus species (n=19)	0 (0)	0 (0)	1 (5.2)	0 (0)	0 (0)	1 (5.3)	1 (5.2)	1 (5.2)	2 (10.5)
Shigella species (n=12)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (8.3)	0 (0)	0 (0)	1 (8.3)

Abbreviations: Cefo, cefotaxime; Cefe, cefepime; Imp, imipenem; Mer, meropenem; Pipe, piperacillin; Torb, tobramycin; Clin, clindamycin; Van, vancomycin; Nitr, nitrofurantoin.

of poor infection prevention and control activities within the hospital.

Regarding the resistance pattern, out of all culture isolates, about six hundred seventy-two (83.6%) pathogens were resistant to at least one antibiotic. The *S.aureus* species isolates showed resistance to routinely prescribed antibiotics like: penicillin (34.8%), Erythromycin (28.7%), Tetracycline (26.8%), clindamycin (22.6%), SXT (23.4%) and Cefoxitin (17.2%). This current study also revealed that gram-negative pathogens like pseudomonas, Klebsiella, and E.coli were highly resistant to commonly used antibiotics such as cephalosporin, fluoroquinolones, aminoglycosides, and trimethoprim or sulfamethoxazole (SXT). This finding was consistent with the finding from the antimicrobial resistance surveillance study from Ethiopia.[25]

In addition, this study also showed that *Acinetobacter* species identified were commonly resistant to antibiotics like Trimethoprim/Sulfamethoxazole (SXT) (55.7%), Ceftazidime (53.8%), Gentamycin (50%), and Cefuroxime (46.1%).

Generally, our study finding revealed that most isolated pathogens were highly resistant to the commonly utilized antibiotics in the hospital which may directly affect the quality of patient care, efficiency of the hospital, and cost of patient treatment. Hence, the development of evidence-based local guidelines, modification of treatment protocols, and leveraging antimicrobial stewardship and IPC interventions are relevant to mitigate the high burden of antimicrobial resistance in the study setting.[25,26]

Limitation of the Study

The retrospective nature of the study has led missing of some clinical and laboratory variables; and most importantly, our study did not support the integration of microbiology findings with stewardship and IPC interventions; and was not well incorporated in the routine patient care. Shortage of some required materials and supplies in the hospital might harm the quality of culture result. For instance, susceptibility tests to some important antibiotics like Carbapenems, methicillin, and vancomycin were not consistently being performed in the hospital during the study period. Generally, only those antibiotics tested in the hospital laboratory were included in this study. Thus, it may not include all antibiotics used in routine clinical practice. Since the majority of the samples were collected from Internal medicine and Pediatrics departments, the finding of this study might not be representative of the whole units of the hospital.

Conclusion

This study showed that *Staphylococcus aureus, Klebsiella pneumonia* species, and *Escherichia coli* were the commonest isolated pathogens. Antimicrobial resistance among common isolates was high for routinely used antibiotics; particularly to cephalosporin, fluoroquinolones, aminoglycosides, and trimethoprim or sulfamethoxazole; and to some reserved drugs like Carbapenems and fourth-generation Cephalosporin.

In general, this study has just revealed an overview of common pathogens isolated in our hospital and their resistance profile which may guide clinicians, hospital stewardship and IPC committees, policymakers, and hospital managers for future measures. In addition, the findings of this study could also be used as a baseline by researchers for further prospective studies and interventions.

Abbreviations

CSF, cerebrospinal fluid; ICU, intensive care unit; IPC, infection prevention and control; MDR, multi-drug resistant; NCCLS, National Committee for Clinical Laboratory Standards; NICU, Neonatal Intensive Care Unit; TB, tuberculosis; OPD, outpatient department; trimethoprim/sulfamethoxazole (SXT) WHO, World Health Organization.

Data Sharing Statement

The datasets used during the current study are available from the corresponding author.

Ethical Considerations

Ethical clearance was obtained from the University of Gondar ethical review board. In addition, permission was also obtained from the hospital chief clinical director and microbiology unit head of the hospital. Patient identifiers were not used to ensure the privacy of study participants. All information obtained during this study was kept confidential and used merely for the research purpose. Regarding ethical issues, this study protocol was conducted in accordance with the World Medical Association (WMA) Declaration of Helsinki.

Consent for Publication

Not applicable as there is no image or other confidentiality related issues.

Acknowledgment

Author Contributions

All authors contributed to data analysis, drafting or revising the article, have agreed on the journal to which the article will be submitted, gave final approval of the version to be published, and agree to be accountable for all aspects of the work.

Funding

Disclosure

The authors declared that they have no conflicts of interest for this work.

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