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Original Article

Surveillance of healthcare associated infections at a tertiary care teaching hospital from 2014 to 2016: Prevalence, microbiological spectrum and antibiogram

Savitha N[1*], Anitha D[1], PM Beena[2]

1. Assistant Professor, Department of Microbiology, Sri Devaraj Urs Medical College, Sri Devaraj Urs Academy of Higher Education and Research, Kolar.
2. Professor & HOD, Department of Microbiology, Sri Devaraj Urs Medical College, Sri Devaraj Urs Academy of Higher Education and Research, Kolar.

Abstract

Background: Healthcare-associated infections have emerged as a significant cause of mortality in the recent years. One of the major concerns in the prevalence of such infections is the development of multidrug-resistant microorganisms.
Aim: The present surveillance study was conducted to assess the prevalence, microbiological spectrum, and antimicrobial susceptibility aminoof the microorganisms at a tertiary care hospital.
Methods: The study was conducted between May 2014 and December 2016 including 466 patients (255 men and 211 women) diagnosed with healthcare-associated infections. Data related to sex, age, time of admission, type of surgery, and complication were collected. Samples of the pus, urine, and blood were collected and sent for isolation and characterization of microorganisms. Antimicrobial sensitivity was conducted by following the Clinical Laboratory Standards Institute (CLSI) guidelines. Data obtained were recorded in Microsoft Excel and analyzed using R 3.3.1; $P < 0.05$ indicative of significant differences.
Result: Mean age of the patients was 41.01 ± 18.11 years. Prevalence results were highest in surgical site infection (79.18%) and gram-negative organisms (80.92%) were the prevalent causes of infection. Escherichia coli (21.54%), Pseudomonas aeruginosa (15.76%), and Acinetobacter sp. (12.22%) were the predominant organisms with maximum sensitivity towards carbapenems, aminoglycosides, and cotrimoxazole, respectively. E. coli was the prevalent producer of AmpC and extended-spectrum beta-lactamases.
Conclusion: Reduced sensitivity to the majority of antimicrobials has led to the prevalence of gram-negative organisms in the healthcare-associated infections. However, carbapenems and chloramphenicol along with aminoglycosides remain the effective broad-spectrum antimicrobials. Further studies are required strategies to minimize antibiotic resistance, which can lead to improvement in therapeutic methods.
Keywords: Escherichia coli, Carbapenems, Surgical site infection, Lactamases

Introduction

Healthcare-associated infections (HAIs) are one of the most frequent causes of morbidity and mortality, globally.[1] Poor infrastructure and limited resources are the prominent factors responsible for the difference in prevalence of HAIs in developed and developing countries. The impact of HAIs leads to prolonged hospital stay and increased financial load. According to the 2014 HAI report of World Health Organization (WHO), prevalence of HAIs is more in middle and low income countries (5.7–19.1%), as compared to the high income countries (3.5–12%). In addition, the incidence of HAIs are most commonly observed in the intensive care units (ICU), with approximately 51% cases of HAIs in the high income countries and 4.4%-88.8% cases of HAIs in the middle and low income countries. Between 2004 and 2012, the rate of HAIs ranged from 4.36% to 83.09% in the Indian subcontinent.[2]

***Corresponding Author**
Dr. Savitha N
Assistant Professor, Department of Microbiology, Sri Devaraj Urs Medical College, Sri Devaraj Urs Academy of Higher Education and Research, Kolar-563101, Karnataka, India.
Mobile No : 9886998046
E-mail : drsavitha2003@gmail.com
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Inappropriate and inefficient use of invasive and life-support therapies in the healthcare facilities contribute to the development of HAIs.[3] Catheter-associated urinary tract infections (CAUTI) are the commonly encountered HAIs in the high income countries whereas surgical site infections (SSI) are prevalent in middle and low income countries.[2] In the Indian subcontinent, SSI accounts for 1.6%–21% of HAIs reported between 2003 and 2012.[4] However, the incidence of CAUTI in India was observed to be comparatively higher with approximately 49%–51% cases between 1998 and 2015.[5] Ventilator associated pneumonia (VAP) is another prominent HAI with an incidence rate of 52.7/1000 days in the developing countries and 40% in India.[6, 7]

Prolonged indiscriminate use of antibiotics plays a major role in the development of antibiotic-resistant strains.[2] Along with the drug-resistant strains of Staphylococcus aureus and Staphylococcus epidermidis, pathogens such as Escherichia coli, Pseudomonas aeruginosa, and Proteus sp. are commonly detected in HAIs.[4] Therefore, antimicrobial resistance and surveillance of drug usage in healthcare facilities may help in preparing a baseline data on the pattern of microbial susceptibility and infection control.[8] Apart from providing quality healthcare to the admitted patients, an effective surveillance may also help in ensuring better health of the hospital personnel and selection of an appropriate drug for treating the HAI cases.[9]

Studies on prevalence and microbiological spectrum of HAIs in India is limited. The present survey was undertaken to evaluate the prevalence and risk factors of HAI in a tertiary care teaching hospital, and analyze the spectrum of microorganisms associated with HAI and antibiotic sensitivity pattern of the respective isolates.

Methodology

Study design

This retrospective study was conducted at the Department of Microbiology in collaboration with other departments of a tertiary care teaching hospital, Kolar. Approval was obtained from the Institutional Ethics Committee.

Patient eligibility and assessment

A total of 466 patients diagnosed with HAIs including 255 men and 211 women of different age-groups were enrolled for the study. The study was conducted between May 2014 and December 2016. The patients were screened from the departments of Otolaryngology, medicine, neurosurgery, obstetrics and gynecology, orthopedics, pediatrics, plastic surgery, surgery and urology and classified with SSIs, CAUTIs and VAP infection based on the USA Centers for Disease Control and Prevention (CDC, Table 1). Data on age, sex, date of admission, preoperative and postoperative stay, and the reason for admission and type of surgery—emergency or elective were recorded in the case record form.

Samples of pus, urine, and endotracheal aspirate for HAIs were collected from the patients and transported to the laboratory for isolation and identification of the microorganisms.

Microbiological analysis

Prevalence of the isolates was recorded on the basis of the type of HAI and Gram stain. In vitro antimicrobial sensitivity of the isolated microorganisms was performed according to the Clinical Laboratory Standards Institute (CLSI) guidelines.[8] The antibiotics used in the survey include beta lactam antibiotics (penicillin, ampicillin, imipenem, meropenem, ertapenem and piperacillin), beta lactam drugs in combination with betalactamase inhibitors (amoxicillin-clavulanic acid, piperacillin-tazobactam, and ampicillin-sulbactam), inhibitors of protein synthesis (erythromycin, clindamycin, amikacin, gentamicin, tobramycin, chloramphenicol, tetracycline, vancomycin, linezolid, and doxycycline), fluoroquinolones (ciprofloxacin, levofloxacin, norfloxacin and ofloxacin), cephalosporins (ceftazidime, ceftriaxone, cefoxitin and cefotaxime), cotrimoxazole and nitrofurantoin. Production of lactamases (AmpC beta lactamases and extended-spectrum beta-lactamases or ESBL) by all the isolates was also analyzed using CLSI guidelines.[10]

Statistical analysis

Recorded data were coded using Microsoft Excel. R 3.3.1 software was used to perform the statistical analysis. Continuous data were expressed as mean ± SD and compared using one-way analysis of variance (ANOVA). Categorical data were analyzed using chi-square test. $P \leq 0.05$ was considered as statistically significant.

Results

Patient characteristics

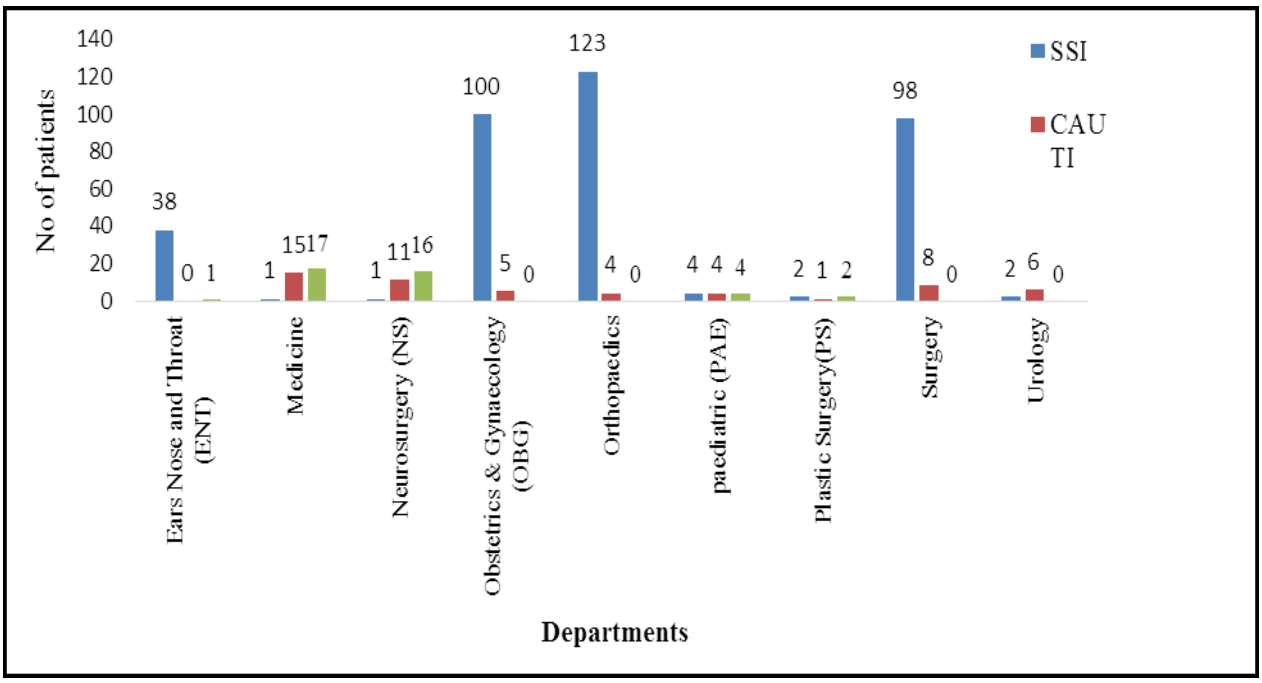
The mean age of the patients was 41.01 ± 18.11 years. Sex-wise distribution of the patients revealed a male predominance (54.5%) in the study. Age-wise distribution of the patients was significant ($P = 0.01$), in which the maximum number of patients were in the age-group of 20-39 years. Among the SSI patients,

mean duration of hospital stay was 25 days with the majority of the patients (58.60%) undergoing elective type of surgery. The demographic and clinical characteristics of the patients are shown in **Table 1**.

Table 1: Patient characteristics

Variable	n (%)	SSI	CAUTI	VAP	Mean ± SD	p-value
Sex						
Male	255 (54.5)	196 (52.7%)	32 (59.3%)	27 (67.5%)	-	0.16
Female	211 (45.3)	176 (47.3%)	22 (40.7%)	13 (32.5%)	-	
Age (Mean ± SD in years)						
Male	-	41.91± 17.27	47.97±22.14	40.58±17.32	41.01±18.11	0.06
Female	-	40±17.11	40.92±23.66	34.23±22.08		
Age group (years)						
<20	28 (6.14)	16 (4.40%)	6 (11.32%)	6 (15.38%)	-	0.01*
20-39	208 (45.61)	175 (48.10%)	17 (32.10%)	16 (41.02%)	-	
40-59	114 (25)	94 (25.82%)	11 (20.75%)	9 (23.08%)	-	
60-79	97 (21.27)	74 (20.33%)	16 (30.19%)	7 (17.95%)	-	
≥80	9 (1.97)	5 (1.37%)	3 (5.66%)	1 (2.56%)	-	

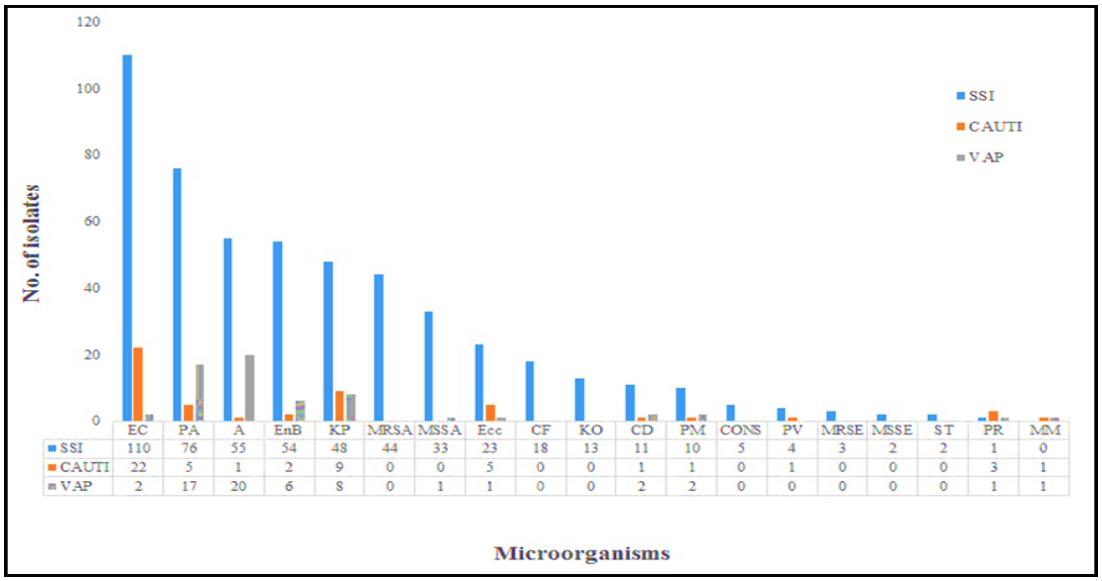
Figure 1. Department-wise characterization of HAIs



Identification and prevalence of isolates

Prevalence of SSIs (79.18%) was highest among HAIs. The prevalence of SSIs was maximum in the departments of ENT, obstetrics & gynecology, orthopedics and surgery **(Figure 1)**. Out of 466 clinical samples, 624 isolates were identified upon their growth in the culture media and Gram staining. Out of these isolates, 19.07% were gram-positive cocci (GPC), 53.04% were gram-negative bacteria (GNB), and 27.88% were non-fermenting gram-negative bacteria (NFGNB). Culture reports of the isolates revealed the predominance of GNB in all the cases of HAIs. The most common microorganisms causing HAIs were *Escherichia coli* (21.54%), *Pseudomonas aeruginosa* (15.76%), and *Acinetobacter* sp. (12.22%). In addition, *E. coli* was predominant in SSI (21.48%) and CAUTI (47.83%), whereas *Acinetobacter* sp. was predominant in VAP (33.33%) infection. The distribution of the isolates with respect to infection is shown in **Figure 2**.

Figure 2. Characterization of isolates with respect to HAIs



	EC	PA	A	EnB	KP	MRSA	MSSA	Ecc	CF	KO	CD	PM	CONS	PV	MRSE	MSSE	ST	PR	MM
SSI	110	76	55	54	48	44	33	23	18	13	11	10	5	4	3	2	2	1	0
CAUTI	22	5	1	2	9	0	0	5	0	0	1	1	0	1	0	0	0	3	1
VAP	2	17	20	6	8	0	1	1	0	0	2	2	0	0	0	0	0	1	1

Antimicrobial sensitivity test

Antimicrobial sensitivity pattern of the isolates is shown in **Table 2a** and **b**. *E. coli* was the most predominant isolate with high rates of sensitivity to imipenem (88.81%), amikacin (85.07%), meropenem (85.07%), chloramphenicol (70.15%), gentamicin (65.67%), ertapenem (65.67%), tobramycin (63.43%), piperacillin-tazobactam (51.49%), amoxicillin-clavulanic acid (40.30%), tetracycline (36.57%), cotrimoxazole (33.58%), and levofloxacin (30.60%). Least sensitivity was noted for ciprofloxacin (17.16%), nitrofurantoin (13.43%), ceftazidime (5.22%), piperacillin (3.73%), ampicillin (2.99%), doxycycline (2.99%), cefotaxime (2.24%) and ceftriaxone (2.24%). *P. aeruginosa* demonstrated high rate of sensitivity to meropenem (89.80%), imipenem (85.71%), piperacillin-tazobactam (75.51%), ceftazidime (69.39%), amikacin (67.35%), gentamicin (63.27%), piperacillin (62.24%), levofloxacin (60.20%), tobramycin (57.14%) and ciprofloxacin (57.14%). Reduced sensitivity of *P. aeruginosa* was observed to tetracycline (23.47%), cotrimoxazole (23.47%), doxycycline (22.45%), and ampicillin-sulbactam (21.43%). *Acinetobacter* sp., another predominant organism in HAIs in the present study, demonstrated sensitivity to levofloxacin (63.16%), meropenem (53.95%), imipenem (52.63%), and tetracycline (34.21%). On the other hand, reduced sensitivity was observed to ampicillin-sulbactam (25%), amikacin (23.68%), gentamicin (18.42%), tobramycin (18.42%), cotrimoxazole (14.47%), piperacillin-tazobactam (10.53%), doxycycline (9.21%), ciprofloxacin (5.26%), ceftazidime (1.32%), and piperacillin (1.32%).

In general, the GNB were highly sensitive to amikacin (75.53%), imipenem (87.01%), ertapenem (68.28%), and meropenem (85.80%) and least sensitive to ampicillin (3.02%), doxycycline (3.02%), piperacillin (4.23%), ceftazidime (4.23%), nitrofurantoin (6.65%), cefotaxime (1.81%), and ceftriaxone (1.51%). GPC were highly sensitive to Vancomycin (69.75%), Linezolid (77.31%), chloramphenicol (66.39%), tetracycline (67.23%), and doxycycline (68.07%) and least sensitive to nitrofurantoin was observed to be high in the case of carbapenems—imipenem (71.26%), meropenem (74.14%), and levofloxacin (61.49%).(1.68%); however,. In the case of NFGNB, sensitivity was observed to be high in the case of carbapenems—imipenem (71.26%), meropenem (74.14%), and levofloxacin (61.49%).

Table 2.a. Antimicrobial sensitivity pattern of isolates

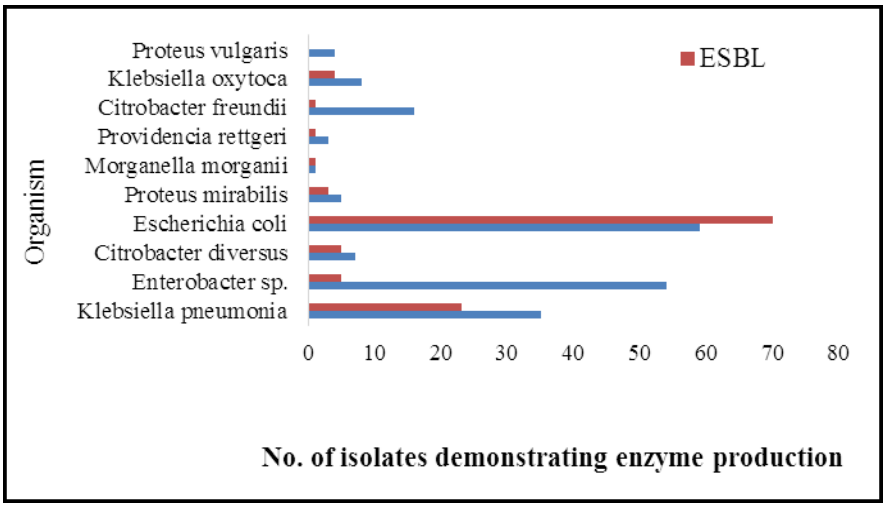
Nature of isolates	Organism	P	AMP	AMC	E	CD	VA	LZ	AK	GEN	TOB	IMP	MRP	ERP	C
GNB	*Escherichia coli*	-	4 (2.99)	54 (40.29)	-	-	-	-	114 (85.07)	88 (65.67)	85 (63.43)	119 (88.81)	114 (85.07)	88 (65.67)	94 (70.15)
	Klebsiella pneumoniae	-	1 (1.54)	19 (29.23)	-	-	-	-	43 (66.15)	33 (50.77)	33 (50.77)	55 (84.62)	55 (84.62)	46 (70.77)	37 (56.92)
	Enterobacter sp.	-	1 (1.61)	5 (8.06)	-	-	-	-	42 (67.74)	28 (45.16)	28 (45.16)	54 (87.1)	54 (87.1)	43 (69.35)	41 (66.13)
	Citrobacter freundii	-	0 (0)	1 (5.56)	-	-	-	-	13 (72.22)	11 (61.11)	11 (61.11)	11 (61.11)	14 (77.78)	5 (27.78)	11 (61.11)
	Klebsiella oxytoca	-	0 (0)	4 (30.77)	-	-	-	-	9 (69.23)	9 (69.23)	8 (61.54)	13 (100)	11 (84.62)	13 (100)	8 (61.54)
	Citrobacter diversus	-	0 (0)	3 (21.43)	-	-	-	-	12 (85.71)	9 (64.29)	8 (57.14)	11 (78.57)	11 (78.57)	10 (71.43)	11 (78.57)
	Proteus mirabilis	-	3 (23.08)	7 (53.85)	-	-	-	-	12 (92.31)	11 (84.62)	11 (84.62)	13 (100)	13 (100)	10 (76.92)	6 (46.15)
	Proteus vulgaris	-	0 (0)	1 (20)	-	-	-	-	4 (80)	3 (60)	2 (40)	5 (100)	5 (100)	5 (100)	1 (20)
	Providencia rettgeri	-	0 (0)	2 (40)	-	-	-	-	0 (0)	0 (0)	0 (0)	5 (100)	5 (100)	5 (100)	1 (20)
	Morganella morganii	-	1 (50)	1 (50)	-	-	-	-	1 (50)	1 (50)	1 (50)	2 (100)	2 (100)	1 (50)	0 (0)
GPC	Methicillin-resistant *Staphylococcus aureus*	0 (0)	0 (0)	0 (0)	13 (29.55)	25 (56.82)	31 (70.45)	38 (86.36)	0 (0)	20 (45.45)	-	-	-	-	39 (88.64)
	Methicillin-sensitive *Staphylococcus aureus*	5 (14.71)	1 (2.94)	31 (91.18)	20 (58.82)	23 (67.65)	20 (58.82)	23 (67.65)	0 (0)	30 (88.24)	-	-	-	-	29 (85.29)
	Enterococci sp.	12 (41.38)	16 (55.17)	0 (0)	0 (0)	0 (0)	26 (89.66)	25 (86.21)	0 (0)	6 (20.69)	-	-	-	-	2 (6.9)
	Coagulase negative Staphylococci	3 (60)	4 (80)	4 (80)	3 (60)	3 (60)	3 (60)	3 (60)	0 (0)	5 (100)	-	-	-	-	4 (80)
	Methicillin-resistant *Staphylococcus epidermidis*	0 (0)	0 (0)	0 (0)	2 (66.67)	2 (66.67)	1 (33.33)	1 (33.33)	0 (0)	2 (66.67)	-	-	-	-	2 (66.67)
	Methicillin-sensitive *Staphylococcus epidermidis*	0 (0)	0 (0)	2 (100)	2 (100)	2 (100)	1 (50)	1 (50)	0 (0)	2 (100)	-	-	-	-	2 (100)
	Streptococci sp.	1 (50)	0 (0)	0 (0)	0 (0)	0 (0)	1 (50)	1 (50)	0 (0)	2 (100)	-	-	-	-	1 (50)
NFGNB	*Pseudomonas aeruginosa*	-	-	-	-	-	-	-	66 (67.35)	62 (63.27)	56 (57.14)	84 (85.71)	88 (89.8)	-	-
	Acinetobacter sp.	-	-	-	-	-	-	-	18 (23.68)	14 (18.42)	14 (18.42)	40 (52.63)	41 (53.95)	-	-

Table 2.b. Antimicrobial sensitivity pattern of isolates

Nature of isolates	Organism	COT	TE	DO	CIP	LEV	PIP	PI	CAZ	AS	NIT	CX	CTX	CRO	NOR	OFL
GNB	*Escherichia coli*	45 (33.58)	49 (36.57)	4 (2.99)	23 (17.16)	41 (30.6)	5 (3.73)	69 (51.49)	7 (5.22)	-	18 (13.43)	-	3 (2.24)	2 (1.49)	-	-
	Klebsiella pneumoniae	11 (16.92)	29 (44.62)	1 (1.54)	30 (46.15)	38 (58.46)	1 (1.54)	27 (41.54)	1 (1.54)	-	2 (3.08)	-	0 (0)	0 (0)	-	-
	Enterobacter sp.	15 (24.19)	41 (66.13)	1 (1.61)	30 (48.39)	35 (56.45)	2 (3.23)	7 (11.29)	1 (1.61)	-	0 (0)	-	0 (0)	0 (0)	-	-
	Citrobacter freundii	1 (5.56)	13 (72.22)	1 (5.56)	12 (66.67)	8 (44.44)	0 (0)	1 (5.56)	0 (0)	-	0 (0)	-	0 (0)	0 (0)	-	-
	Klebsiella oxytoca	5 (38.46)	4 (30.77)	0 (0)	3 (23.08)	5 (38.46)	0 (0)	3 (23.08)	0 (0)	-	0 (0)	-	0 (0)	0 (0)	-	-
	Citrobacter diversus	2 (14.29)	5 (35.71)	0 (0)	3 (21.43)	6 (42.86)	0 (0)	7 (50)	1 (7.14)	-	1 (7.14)	-	0 (0)	0 (0)	-	-
	Proteus mirabilis	4 (30.77)	4 (30.77)	3 (23.08)	10 (76.92)	13 (100)	5 (38.46)	9 (69.23)	4 (30.77)	-	0 (0)	-	3 (23.08)	3 (23.07)	-	-
	Proteus vulgaris	0 (0)	0 (0)	0 (0)	2 (40)	3 (60)	0 (0)	2 (40)	0 (0)	-	1 (20)	-	0 (0)	0 (0)	-	-
	Providencia rettgeri	0 (0)	2 (40)	0 (0)	1 (20)	3 (60)	1 (20)	1 (20)	0 (0)	-	0 (0)	-	0 (0)	0 (0)	-	-
	Morganella morganii	0 (0)	1 (50)	0 (0)	0 (0)	1 (50)	0 (0)	0 (0)	0 (0)	-	0 (0)	-	0 (0)	0 (0)	-	-
GPC	Methicillin-resistant *Staphylococcus aureus*	22 (50)	39 (88.64)	41 (93.18)	6 (13.64)	-	-	-	-	-	0 (0)	0 (0)	0 (0)	-	-	-
	Methicillin-sensitive *Staphylococcus aureus*	19 (55.88)	30 (88.24)	30 (88.24)	17 (50)	-	-	-	-	-	0 (0)	33 (97.06)	0 (0)	-	-	-
	Enterococci sp.	1 (3.45)	1 (3.45)	1 (3.45)	1 (3.45)	-	-	-	-	-	2 (6.9)	1 (3.45)	0 (0)	-	-	-
	Coagulase negative Staphylococci	4 (80)	5 (100)	5 (100)	3 (60)	-	-	-	-	-	0 (0)	3 (60)	0 (0)	-	-	-
	Methicillin-resistant *Staphylococcus epidermidis*	0 (0)	2 (66.67)	2 (66.67)	1 (33.33)	-	-	-	-	-	0 (0)	3 (100)	0 (0)	-	-	-
	Methicillin-sensitive *Staphylococcus epidermidis*	0 (0)	2 (100)	2 (100)	1 (50)	-	-	-	-	-	0 (0)	0 (0)	0 (0)	-	-	-
	Streptococci sp.	0 (0)	1 (50)	0 (0)	0 (0)	-	-	-	-	-	0 (0)	0 (0)	0 (0)	-	-	-
NFGNB	*Pseudomonas aeruginosa*	23 (23.47)	23 (23.47)	22 (22.45)	56 (57.14)	59 (60.2)	61 (62.24)	74 (75.51)	68 (69.39)	21 (21.43)	-	-	-	-	-	-
	Acinetobacter sp.	11 (14.47)	26 (34.21)	7 (9.21)	4 (5.26)	48 (63.16)	1 (1.32)	8 (10.53)	1 (1.32)	19 (25)	-	-	-	-	-	-

Production of AmpC lactamases and ESBL were also detected in the isolates with *E. coli* being the highest producer of AmpC and ESBL lactamases **(Figure 3)**.

Figure 3: Production of ESBL and AmpC lactamases by isolates



Discussion

The retrospective study was performed at a tertiary care hospital to analyze the prevalence and risk factors of HAIs. The antimicrobial sensitivity and lactamase production assay was also performed to prepare a baseline data of microbial susceptibility.

Bacterial infections have been commonly encountered in the hospitals due to the ability of the causative agent to survive extreme conditions such as the dry surfaces of hospitals. The spread of these organisms through patients (infected or carrier) and hospital personnel play a major role in the increased incidence of HAIs.[11] The majority of the isolates, identified in the present study, were GNB (53.04%), with E. coli being the most frequently encountered strain. The predominance of E. coli in HAIs had also been reported in earlier studies.[3, 12] However, in the recent years, NFGNB have also emerged as the prominent pathogens in HAIs. These microorganisms are usually encountered on the skin surfaces of hospital staffs, as well as in ventilators and hospital linens.[8] In support of this statement, the present study reported the predominance of NFGNB (27.88%), especially P. aeruginosa and Acinetobacter sp. in SSI, CAUTI, and VAP. In contrast to the incidence of GNB and NFGNB, the prevalence of GPC was minimal (19.07%) and drug-resistant S. aureus (12.5%) was the predominant microorganism. Previous studies have observed the predominance of GNB in HAIs, as compared to the GPC.[13, 14]

In the present study, the GNB belonged to Enterobacteriaceae family and were highly sensitive to carbapenems (ertapenem, meropenem, and imipenem). Carbapenems, being broad spectrum beta lactam antibiotics, have been reported to be highly active against the Enterobacteriaceae family of microorganisms, including those possessing the ability to produce AmpC beta lactamases[15] and hence were highly active against the GNB isolates in the present study. NFGNB were also sensitive to carbapenems in the present study. Carbapenems have been used against infections caused by Acinetobacter sp. and P. aeruginosa; however, recent studies have demonstrated the development of carbapenems-resistant strains of NFGNB due to its extensive use in the hospitals.[16, 17]

According to the observations of the present study, aminoglycosides, such as amikacin are highly effective against several GNB, as well as GPC infections, especially the multidrug resistant forms. These antimicrobials inhibit protein synthesis by binding to 16S rRNA leading to disruption of the integrity of bacterial cell membrane.[18-20] Similar rates of sensitivity against GNB, as well as the majority of GPC has been exhibited by chloramphenicol in the present study. Chloramphenicol acts by reversible binding to the 50S ribosome leading to inhibition of protein synthesis. It is especially effective against multidrug-resistant pathogens, [21] which can be a possible cause of its high rate of sensitivity in the present study. Tetracycline, doxycycline, and gentamicin are the inhibitors of protein synthesis, which have shown similar activities in the present study. These antimicrobials have demonstrated maximum activity towards Staphylococcal sp. in the present surveillance study. Tetracycline acts by inhibiting the binding of tRNA to mRNA [22], doxycycline binds to 30S subunit of the bacterial ribosome, and

aminoglycoside and gentamicin bind to 30S subunit of the ribosome and 16S rRNA for limiting the synthesis of proteins.[23] However, extensive use of these antimicrobials has led to the reduction of sensitivity and increase in the development of multidrug-resistant strains.[22]

Fluoroquinolones, especially ciprofloxacin and levofloxacin, have demonstrated effective activity against GNB and P. aeruginosa in the present surveillance study. Fluoroquinolones interact with DNA gyrase (especially in GNB) and topoisomerase IV (especially in GPC) leading to inhibition of DNA synthesis.[24] Positive interaction of ciprofloxacin and levofloxacin with DNA gyrase may possibly be the reason of the effectiveness demonstrated in the present study. The majority of the isolates in the current surveillance study demonstrated sensitivity toward cotrimoxazole, which is a combination of trimethoprim and sulfamethoxazole. The effectiveness of the antimicrobial drug can be attributed to its ability of selectively inhibiting microbial reductases and synthesis of tetrahydrofolate leading to restricted cellular growth and survival.[25]

The isolates in the present study have demonstrated low levels of sensitivity toward beta lactam antibiotics. This may be due to the ability of AmpC and ESBL lactamases production, as observed in the GNB isolates of the present study. The reduced sensitivity can also be due to the utilization of cell wall transpeptidases in the synthesis of the cell wall, which are beta lactam resistant. Apart from the production of lactamases, GNB can also resist the adverse actions of beta lactam antibiotics by actively expelling the antimicrobials from within the cells with the help of efflux pumps.[26] The sensitivity to cephalosporins also reduced due to the similar reasons, which could be the possible reason for its reduced activity towards the isolates of the present study.[27]

These findings support the increasing and undesirable trend in the development of multidrug-resistant strains, indicating decreased efficacy of beta lactam antibiotics, cephalosporins, fluoroquinolones, and inhibitors of protein synthesis. Production of lactamases has become the major cause of reduced sensitivity along with repetitive exposure of the microorganisms to the same antimicrobials over the years. Such findings have led to extensive research over the factors contributing to the development of resistance, the alternative modes of treatment, and performance of similar surveillance study in the same hospital, with a gap of few years.

Conclusion

The current research finding indicated that the isolated microorganisms were susceptible to carbapenems, aminoglycosides, and chloramphenicol. The majority of the microorganisms demonstrated minimal sensitivity to cephalosporins and fluoroquinolone. In addition, the GNB were found to produce AmpC and ESBL, which might have played a role in their resistance to several antimicrobials along with other inherent factors of the microorganisms. Thus, this surveillance study could facilitate the preparation of baseline data for providing an effective and improved healthcare facility to patients. In addition, studies involving factors responsible for virulence and resistance of the microorganism to drugs could be performed to monitor the drug administration and improve the therapeutic methods for treatment of HAIs.

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