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Comparative evaluation of nosocomial infections in two major hospitals in Calabar Metropolis, Cross River State

Abstract

This study comparatively evaluates nosocomial infections in two major hospitals in Calabar metropolis, Cross River State. Bacteria and fungi were isolated using settle plate technique. A total mean load of 1002 cfu/m^2/hr was recorded of which 612.1cfu/m^2/hr was recorded in General hospital and 389.9cfu/m^2/hr was recorded in Infectious Disease hospital (IDH). Out of a total of 187 isolates characterized, 98 (54.4%) were gram negative, 33 (17.6%) were gram positive bacteria while 56(29.9%) were fungi. Furthermore, in General hospital, 99(52.9%) organisms were isolated of which 51 (51.5%), 16(16.2%) and 32(32.3%) were gram negative, gram positive bacteria and fungi respectively while in IDH, 47(53.4%), 17 (19.3%) and 24 (27.3%) out of 88 (47.1%) organisms isolated were gram negative, gram positive and fungi respectively. The test isolates when subjected to antimicrobial susceptibility testing exhibited varied patterns of resistance to antibiotics/antifungal agents. This calls for effective monitoring of the air quality in healthcare settings in a bid to reducing nosocomial infections.

Keywords: Nosocomial infections, airborne, microbial load, resistant profile, Hospitals, Calabar

Introduction

Airborne sources of possible bacterial contamination of the environment of hospitals have long been debated as potential causes of increasing incidence of nosocomial infections. This has contributed to the already existing burden of nosocomial infections in the health care setup [1]. Nosocomial Infections (NI) also known as healthcare-associated infections (HCAI) or Hospital-acquired infections (HAI) are infections that arise within few hours of admission into the hospital and were not present at the time of admission. They have been reported globally in hospital environment resulting in major hazard confronting patients and personnel who are hospitalized [2]. These infections have been reported by Witherspoon [3] to be most often silent while the patient is still in the hospital and account for significant morbidity and mortality due to the daily interaction existing among personnel and asymptomatic individuals assembled under one roof, thereby encouraging the proliferation, spread and transmission of nosocomial infections among patients and hospital workers.

The healthcare environment including its units as revealed by Gupta [4] constitute a significant facility in the healthcare settings, providing segregation, special care, accommodation, succor and protection for the sick. Despite advances in human capacity and technology development in the healthcare sector, many hospitals especially in developing countries are still faced with the challenges of nosocomial infections [5]. This may be due largely to the poor infection control practices in these hospitals [6]. The development of nosocomial infections and its severity involves locally recognized agents. However, the emergence and re-emergence of highly virulent infectious agents further compound the menace, contributing to the increase morbidity and mortality observed in hospitalized patients; increased burden of discomfort and high socio-economic cost [7].

Poor disinfection practices, ineffective use of antibiotics, monitoring of the hospital's air and units against overcrowding, management and inadequate surveillance teams to manage, sustain and ensure that aseptic hospital ethics has further aggravated the problem [8]. In developing countries including Nigeria, these inadequacies abound in the hospital settings, creating a safe haven for nosocomial infections [9]. This has been confirmed by several reports including the one recorded by Muhammed *et al* [11] who reported high frequency of

UNDER PEER REVIEW

pathogenic bacteria including *Staphylococcus aureus, Proteus species, Pseudomonas aeruginosa*, *Escherichia coli, Bacillus cereus*, *Klebsiella species, Salmonella species* and *Shigella species* from hospital sinks, floors, bed covers, toilets and ward walls. Despite the clinical implications associated with nosocomial infections, few studies if any, have evaluated the impact of nosocomial infections within the major hospitals of the state. This study therefore was aimed at evaluating nosocomial infections in two major hospitals in Calabar metropolis, Cross Rivers State.

MATERIALS AND METHODS

Study site

This study was carried out in two major hospitals including General Hospital and Infectious Disease Hospital, all in Calabar metropolis, Cross River State, Nigeria which are located on latitude 4^{o}59N and longitude 8^{o}15E.

Sources of samples

Samples were collected using settle plate technique from various units including pharmacy, theatre, laboratory, blood bank and patient wards of General Hospital and Infectious disease hospital, all in Calabar metropolis, Cross River State.

Microbiological analysis

The air qualities of five units of each hospital was assessed by exposing plates in triplicates containing Nutrient agar, Sabouraud dextrose agar and blood agar, respectively for 1hour following procedures described by Centre for Disease Centre [11] after which plates were aseptically packaged and immediately transported to microbiology laboratory where they were incubated at 37^{o}C for 24-48hours. After incubation, the plates were examined for growth and microbial load determined. Purified colonies were identified and characterized following standard microbiological procedures [12].

Antimicrobial susceptibility testing

This was done following procedures described by CLSI, (2004) and CLSI (2014) [13][14] for fungi and bacteria, respectively. Standardized inoculums were inoculated into plates containing freshly prepared Muller Hinton agar and allowed to stand for 15minutes. Then, antibiotic discs were placed aseptically on the surface of the inoculated plate using sterile forceps and pressed lightly to ensure contact with the agar surface and the plates were incubated at 35^{o}C for 24-48hours. After incubation, zones of inhibition were measured and compared with appropriate interpretive chats.

Determination of MIC and MBC

This was performed following procedures described CLSI (2014)[14]. Briefly, 2-3 colonies of the test isolate was inoculated into 5ml of sterile peptone broth/SDB and incubated for 30 minutes. Antibiotics of various concentrations were dissolved in sterile test tubes containing 5ml of diluents (distilled water and DMSO, respectively) to make stock solutions. Doubling dilutions of the antibiotics in the order of 1:2, 1:4, 1:8, 1:16, 1:32, 1:64, 1:128, 1:256, 1:512 and 1:1024 were carried prepared. Standardized inoculums were added to each of the tubes and incubated for 24-48hrs. The MICs were then determined. The MBCs were determined by sub-culturing tubes which showed no growth (turbidity) during the MIC tests into plates containing freshly prepared nutrient agar and sabouraud dextrose agar plates, respectively and incubated for 24-48hrs at 37^{0}C.

UNDER PEER REVIEW

Data analysis

Descriptive analysis such as simple percentages and student t-test was employed in this study.

RESULTS

Microbial load

The result of the microbial load and their percentages as observed in various units of GH and IDH are summarized in Table 1 and Table 2, respectively. In GH, pharmacy had a mean load of 128.9cfu/hr (21.1%) while ICU had a mean load of 129.9cfu/hr (21.2%). However, Laboratory, Blood bank and Ward had mean loads and percentages of 124cfu/hr(20.3%), 136cfu/hr(22.2%) and 93.7(15.3%), respectively. Similarly, in IDH, Pharmacy had a mean load of 67.4(17.4%), ICU 59.7(15.3%), Laboratory 115.8(29.7%), Blood bank 68.6(17.6%) and Ward78.4 (20.1%). Thus, a student t-test analysis of the sampled units revealed that only the intensive care unit was significant with a probability value of 0.02 at 0.05 significant levels.

Table 1: Microbial load in General Hospital (GH)

Units	Mean load	% load
ICU	129.9 cfu/hr	21.2%
Pharmacy	128.9 cfu/hr	21.1%
Ward	93.7cfu/hr	15.3%
Blood bank	135.6cfu/hr	22.2%
Laboratory	124cfu/hr	20.3%
Total mean load	612.1 cfu/hr	100%

Table 2: Microbial load in Infectious Disease Hospital (IDH)

Units	Mean load	% load
ICU	59.7 cfu/hr	15.3%
Pharmacy	67.4 cfu/hr	17.3%
Ward	78.4 cfu/hr	20.1%
Blood bank	68.6 cfu/hr	17.6%
Laboratory	115.8 cfu/hr	29.7%
Total mean load	389.9 cfu/hr	100%

UNDER PEER REVIEW

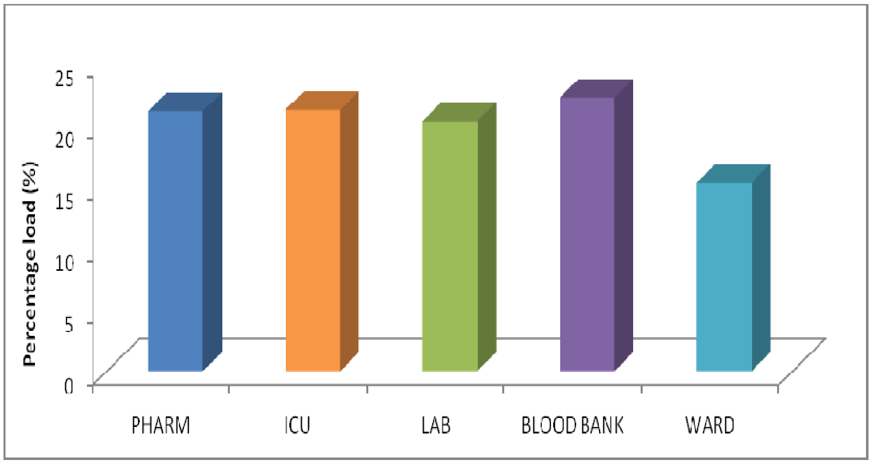

Figure 1: Percentage microbial load in General Hospital.

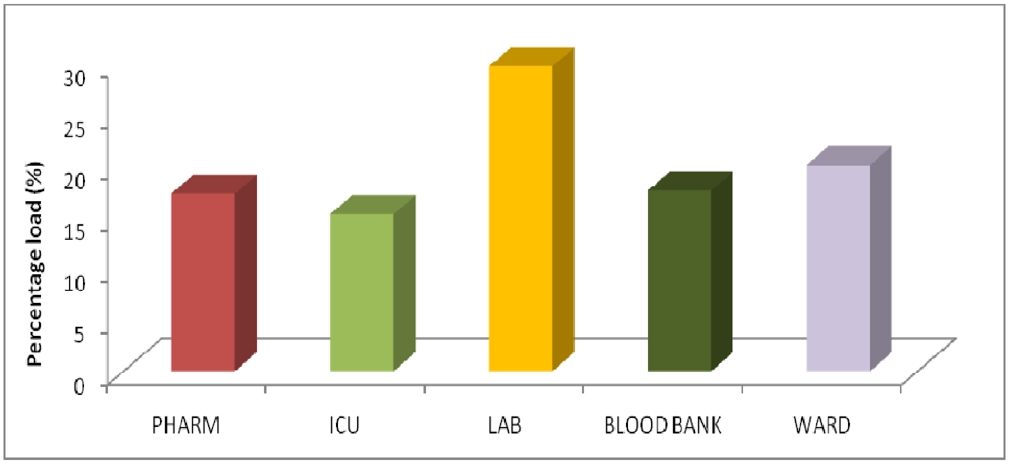

Figure 2: Percentage microbial load in Infectious Disease Hospital.

UNDER PEER REVIEW

Table 3: Mean bacteria load (CFU/m^2) of both locations

Units Sampled	GH	IDH
Intensive Care Unit (ICU)	129.90	59.70
Pharmacy	128.90	67.40
Ward	93.70	78.40
Blood Bank	135.60	68.60
Laboratory	124.00	115.80

*Represents significant probability at 0.05 level of significance.

A total of 187 isolates were recovered of which 99 (52.9%) and 88(47.1%) were recovered from General Hospital (Table 4) and Infectious Diseases Hospital (Table 5), respectively. In General hospital, the ward had the highest number of isolate of 23(23.2%) followed by, pharmacy 22 (22.2%), laboratory 21 (21.2%), Intensive care unit 17 (17.2%) and Blood bank 16 (16.1%). Similarly, in Infectious Diseases Hospital (Table 5), Blood bank and ward recorded the highest number of isolates 19 (21.6%), respectively followed by pharmacy 18(20.5%) while ICU and laboratory recorded 16 (18.2%), respectively.

Table 4: Distribution of Isolates in General Hospital units

	Units				
Isolates (n-99, 52.9%)	ICU (n-17, 17.2%)	Pharmacy (n-22, 22.2%)	Ward (n-23, 23.2%)	Blood Bank (16, 16.1%)	Laboratory (n-21, 21.2%)
Escherichia coli (9)	1(11.1)	3(33.3)	1(11.1)	1(11.1)	3(33.3)
Salmonella (9)	0(0.0)	3(33.3)	3(33.3)	1(11.1)	2(22.2)
Candida species(14)	3(21.4)	3(21.4)	2(14.3)	2(14.3)	4(33.3)
Klebsiella species(11)	3(27.3)	2(18.1)	3(27.3)	2(18.1)	1(9.1)
Proteus mirabilis (12)	2(16.7)	3(25.0)	3(25.0)	2(16.7)	2(16.7)
Pseudomonas aeruginosa(10)	3(30.0)	1(10.0)	2(20.0)	1(10.0)	3(30.0)
Staphylococcus aureus(11)	4(36.4)	1(9.1)	3(27.3)	1(9.1)	2(18.1)
Pencillum species(9)	0(0.0)	2(22.2)	3(33.3)	2(22.2)	2(22.2)
Streptococci species(5)	1(20.0)	1(20.0)	0(0.0)	2(40.0)	1(20.0)
Aspergillus sp(9)	0(0.0)	3(33.3)	3(33.3)	2(22.2)	1(11.1)

UNDER PEER REVIEW

TABLE 5

Distribution of Isolates in Infectious Disease Hospital (IDH)

	Units				
Isolates (n-88, 47.1%)	ICU (n-16, 18.2%)	Pharmacy (n-18, 20.5%)	Ward (n-19,21.6%)	Blood bank (n-19, 21.6%)	Laboratory (n-16,18.2%)
Escherichia coli (10)	3(30.0)	1(10.0)	3(30.0)	2(20.0)	1(10.0)
Salmonella species(12)	3(25.0)	1(8.3)	2(16.7)	2(16.7)	4(33.3)
Candida species (5)	1(20.0)	1(20.0)	2(40.0)	0(0.0)	1(20.0)
Klebsiella species (9)	2(22.2)	4(44.4)	1(11.1)	2(22.2)	0(0.0)
Proteus mirabilis (8)	0(0.0)	2(25.0)	3(37.5)	1(12.5)	2(25.0)
Pseudomonas aeruginosa(8)	1(12.5)	3(37.5)	1(12.5)	3(37.5)	0(0.0)
Staphylococcus aureus(7)	2(28.6)	2(28.6)	1(14.3)	0(0.0)	2(28.6)
Penicillium sp(10)	0(0.0)	2(20.0)	3(30.0)	2(20.0)	3(30.0)
Streptococci species(10)	3(30.0)	1(10.0)	1(10.0)	3(30.0)	2(20.)
Aspergillus species (9)	1(11.1)	1(11.1)	2(22.2)	4(44.4)	1(11.1)

Antimicrobial susceptibility pattern of isolates recovered from General hospital and IDH

Isolates employed in this study exhibited varying degrees of resistance to commonly used antibiotics as presented in Tables 6 and 7. In General hospital, *Salmonella species* showed resistance to tarivid and nalidixic acid. Other microbial isolates showed moderate to low resistance to antibiotics and antifungal agents as shown in table 6. However, in IDH as shown in Table 7, *Escherichia coli, Salmonella species, Klebsiella species, Proteus species and P. aeruginosa* exhibited a wide range of resistance against tarivid, reflacine, ciproflox, ceporex, nalidixic acid and moderately amplicin. These organisms however, showed low resistance to augmetin, gentamycin, septrin and streptomycin as shown in Table 6. In addition, *Staphylococcus aureus* strains exhibited marked resistance against norfloxacan, ciproflox, streptomycin and levofloxacin while *Streptococci* showed resistance to norfloxacin, amoxil, ciproflox, chloramphen, erythromycin, ampiclox and levofloxacin. Furthermore, *Penicillium* and *Aspergillus species* showed resistance to ketoconazole.

UNDER PEER REVIEW

Table 7: Resistant patterns of test organisms isolated from IDH

Gram negative Bacteria	OFX	PEF	CPX	AU	CN	S	CEP	NA	SXT	PN
Escherichia coli (10)	8(80.0)	9(90.0)	8(80.0)	4(40.0)	3(30.0)	2(20.0)	7(70.0)	7(70.0)	4(40.0)	5(50.0)
Salmonella sp (12)	8(67.0)	8(67.0)	7(58.0)	4(33.0)	6(50.0)	4(33.0)	6(50.0)	8(67.0)	8(67.0)	7(58.0)
Klebsiella sp (9)	8(89.0)	6(67.0)	7(78.0)	5(56.0)	6(67.0)	5(56.0)	6(67.0)	6(67.0)	5(56.0)	7(78.0)
Proteus mirabilis (8)	6(75.0)	7(88.0)	6(75.0)	5(63.0)	4(50.0)	3(38.0)	5(63.0)	6(75.0)	4(50.0)	6(75.0)
Pseudomonas sp (8)	6(75.0)	5(63.0)	5(63.0)	4(50.0)	6(75.0)	4(50.0)	5(63.0)	6(75.0)	5(63.0)	7(88.0)
Gram positive	NB	AML	CPX	RD	CN	S	CH	E	APX	LEV
Staphylococcus aureus (7)	6(86.0)	5(71.0)	6(86.0)	5(71.0)	4(57.0)	4(57.0)	6(86.0)	5(71.0)	5(71.0)	6(86.0)
Streptococcus sp (10)	6(60.0)	9(90.0)	6(60.0)	5(50.0)	5(50.0)	3(30.0)	7(70.0)	6(60.0)	6(60.0)	8(80.0)
Fungal Isolates	**K**	**NY**								
Candida albicans (5)	3(40%)	1(20%)								
Penicillium sp (10)	7(70%)	2(20%)								
Aspergillus sp (9)	6(67%)	2(22%)								

UNDER PEER REVIEW

Table 6: Summary of resistant patterns of test organisms isolated from GH

Gram negative	OFX	PEF	CPX	AU	CN	S	CEP	NA	SXT	PN
Escherichia coli (9)	4(44%)	5(56%)	2(22%)	2(22%)	1(11%)	0(0%)	2(22%)	3(33%)	1(11%)	4(44%)
Salmonella sp(9)	6(67%)	5(56%)	3(33%)	3(33%)	4(44%)	2(22%)	5(56%)	6(67%)	5(56%)	4(44%)
Klebsiella sp(11)	5(46%)	4(36%)	5(46%)	3(27%)	3(27%)	3(27%)	4(36%)	5(46%)	3(27%)	4(36%)
Proteus mirabilis(12)	4(33%)	5(42%)	5(42%)	2(17%)	2(17%)	1(8%)	3(25%)	4(33%)	2(17%)	3(25%)
Pseudomonas sp (10)	4(40%)	3(30%)	3(30%)	2(20%)	5(50%)	0(0%)	3(30%)	4(40%)	3(30%)	5(50%)
Gram positive	NB	AML	CPX	RD	CN	S	CH	E	APX	LEV
Staphylococcus aureus (11)	5(46%)	5(46%)	4(36%)	3(27%)	2(18%)	2(18%)	4(36%)	3(27%)	4(36%)	4(36%)
Streptococcus sp (5)	4(80%)	3(60%)	4(80%)	3(60%)	3(60%)	1(20%)	4(80%)	3(60%)	2(40%)	2(40%)
Fungal Isolates	K	NY								
Candida albicans (14)	2(14%)	0(0%)								
Penicillium sp (9)	5(56%)	1(11%)								
Aspergillus sp (9)	4(44%)	1(11%)								

Keys:
OFX = TARIVID
PEF = REFLACINE
CPX = CIPROFLOX
AU = AUGMETIN
CN = GENTAMYCIN
S = STREPTOMYCIN
NY=NYSTATIN
CEP = CEPOREX
NA = NALIDIXIC ACID
SXT = SEPTRIN
PN = AMPLICIN
NB = NORFLOXACIN
AML = AMOXIL
RD = RIFAMPCIN
E = ERYTHROMYCIN
CH = CHLORAMPHENICOL
APX = AMPICLOX
LEV = LEVOFLOXACIN
K = KETOCONAZOLE

UNDER PEER REVIEW

Minimum Inhibitory Concentrations (MIC) and Minimum Bactericidal Concentrations (MBC) of test isolates

The MICs and MBCs of microbial isolates from the various locations are as shown in Tables 8 and 9, respectively. The MICs and MBCs of *E. coli, Salmonella species* and *P. aeruginosa* to various antibiotics ranged from 1:16 - 1:64 and 1:8 - 1:32 while that of *Klebsiella species* ranged from 1:16- 1:128 and 1:8-1:64, respectively. Furthermore, *S. aureus* recorded MICs and MBCs of 1:32 and 1:16 respectively while *Streptococci* recorded 1:16-1:64 and 1:8-1:32 respectively. In addition, *Candida and Aspergillus species* recorded MICs and MBCs in the range of 1:16-1:32 and 1:8 and 1:16 respectively. However, in GH, *E. coli* and *Streptococci* recorded MICs and MBCs in the range of 1:32-1:512 and 1:16-256 respectively while *Salmonella species, Klebsiella species* and *Proteus species* exhibited MICs and MBCs in the range of 1:64-1:512 and 1:32-1:256 respectively. Meanwhile, *S. aureus* and *P. aeruginosa* had MICs and MBCs in the range of 1:64-1:512, 1:32-1:128 and 1:32-1:1024 and 1:16-1:64 respectively. *Aspergillus species* recorded 1:64 and 1:32 as MIC and MBC while *Candida albicans* recorded 1:32-1:64 and 1:16-1:32 as MICs and MBCs respectively as shown in Table 9.

UNDER PEER REVIEW

Table 8: Summary of MICs and MBCs of test isolate in IDH

Isolates	Test	OFX	PEF	CPX	AU	CN	S	CEP	NA	SXT	PN	NB	AML	RD	E	CH	APX	LEV	K	NY
Escherichia coli	MIC	1:32	1:32	1:12	1:64	1:16	1:32	1:16	1:16	1:64	1:32	NT	NT	NT	NT	NT	NT	NT	NT	NT
	MBC	1:16	1:16	1:64	1:32	1:8	1:16	1:8	1:8	1:32	1:16									
Salmonella species	MIC	I:32	1:32	1:32	1:16	1:32	1:64	1:64	1:32	1:32	1:64	NT	NT	NT	NT	NT	NT	NT	NT	NT
	MBC	1:16	1:16	1:16	1:8	1:8	1:32	1:32	1:16	1:16	1:32									
Candida species	MIC	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	1:16	1:32
	MBC																		1:8	1:16
Klebsiella species	MIC	I:64	1:128	1:64	1:64	1:16	1:32	1:64	1:16	1:32	1:64	NT	NT	NT	NT	NT	NT	NT	NT	
	MBC	1:32	1:64	1:32	1:32	1:8	1:16	1:32	1:8	1:16	1:32									
Proteus mirabilis	MIC	I:64	1:64	1:32	1:64	1:32	1:64	1:64	1:32	1:32	1:64	NT	NT	NT	NT	NT	NT	NT	NT	
	MBC	1:32	1:32	1:16	1:32	1:16	1:32	1:32	1:16	1:16	1:32									
Pseudomonas aeruginosa	MIC	I:32	1:32	1:64	1:16	1:16	1:16	1:128	1:64	1:64	1:32	NT	NT	NT	NT	NT	NT	NT	NT	
	MBC	1:16	1:16	1:32	1:8	1:8	1:8	1:64	1:32	1:32	1:16									
Staphylococcus aureus	MIC	NT	NT	1:32	NT	1:32	1:32	NT	NT	NT	NT	1:32	1:32	1:32	1:32	1:32	1:32	1:32	NT	
	MBC			1:16		1:16	1:16					1:16	1:16	1:16	1:16	1:16	1:16	1:16		
Penicillium species	MIC	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	1:64	
	MBC																		1:32	
Sreptococcus species	MIC	NT	NT	1:32	NT	1:32	1:64	NT	NT	NT	NT	1:16	1:64	1:32	1:16	1:32	1:32	1:64	NT	NT
	MBC			1:16		1:16	1:32					1:8	1:32	1:16	1:8	1:16	1:16	1:32		
Aspergillus species	MIC	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	1:32	1:16
	MBC																		1:16	1:8

Table 9: Summary of MICs and MBCs of test isolates in General hospital

Organisms	TEST	OFX	PEF	CPX	AU	CN	S	CEP	NA	SXT	PN	NB	AML	RD	E	CH	APX	LEV	K	NY
Escherichia coli	MIC	1:128	1:256	1:128	1:256	1:512	1:128	1:32	1:32	1:256	1:128	NT	NT	NT	NT	NT	NT	NT	NT	NT
	MBC	1:64	1:128	1:64	1:128	1:256	1:64	1:16	1:16	1:128	1:64									
Salmonella species	MIC	I:64	1:64	1:512	1:512	1:64	1:512	1:256	1:64	1:128	1:128	NT	NT	NT	NT	NT	NT	NT	NT	NT
	MBC	1:32	1:32	1:256	1:256	1:32	1:256	1:128	1:32	1:64	1:64									
Candia species	MIC	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	1:32	1:64
	MBC																		1:16	1:32
Klebsiella species	MIC	I:512	1:512	1:256	1:128	1:64	1:64	1:512	1:64	1:128	1:256	NT	NT	NT	NT	NT	NT	NT	NT	NT
	MBC	1:256	1:256	1:128	1:64	1:32	1:32	1:256	1:32	1:64	1:128									
Proteus mirabilis	MIC	I:64	1:64	1:512	1:64	1:256	1:256	1:64	1:64	1:64	1:256	NT	NT	NT	NT	NT	NT	NT	NT	NT
	MBC	1:32	1:32	1:256	1:32	1:128	1:128	1:32	1:32	1:32	1:128									
Pseudomonas aeruginosa	MIC	I:128	1:128	1:128	1:32	1:64	1:32	1:64	1:128	1:64	1:64	NT	NT	NT	NT	NT	NT	NT	NT	NT
	MBC	1:64	1:64	1:64	1:16	1:32	1:16	1:32	1:64	1:32	1:32									
Staphylococcus aureus	MIC	NT	NT	1:128	NT	1:128	1:128	NT	NT	NT	NT	1:128	1:64	1:64	1:256	1:64	1:128	1:512	NT	NT
	MBC			1:64		1:64	1:64					1:64	1:32	1:32	1:128	1:32	1:64	1:256		
Penicillum species	MIC	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	1:128	1:64
	MBC																		1:64	1:32
Streptococcus species	MIC	NT	NT	1:64	NT	1:32	1:32	NT	NT	NT	NT	1:64	1:32	1:64	1:64	1:64	1:64	1:512	NT	NT
	MBC			1:32		1:16	1:16					1:32	1:16	1:32	1:32	1:32	1:32	1:256		
Aspergillus species	MIC	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	1:64	1:64
	MBC																		1:32	1:32

UNDER PEER REVIEW

UNDER PEER REVIEW

Discussion

The hospital environment is a complex environment on its own and as such different microorganisms come to interact interchangeably resulting to infections and re-infections [16]. Several factors may determine which microorganism that will be responsible for a particular infection. Such factors may include the length and nature of which the patient was exposed, virulence, microbial load of microorganism and also the state of the patients defense [16]. Airborne source of possible bacterial contamination of the environment in the hospital setting has long been debated as potential threats for being an important cause of increasing incidence of nosocomial infections [16]. This can contribute to the already existing burden of nosocomial infections in health care set up [17].

This study revealed the total mean microbial load of various units in General hospital and Infectious disease hospital to be 612.1cfu/m^2/hr and 389.9 cfu/m^2/hr, respectively. The mean load observed in this study is higher than the results obtained by Omoigberale 18] in Ekpoma, Edo State, Nigeria. In addition, a higher mean load (612.1cfu/m2) was observed in General hospital (612.1cfu/m^2) compared to 389.9cfu/m^2recorded in IDH which is extremely above the acceptable 35cfu/m^3 per room [16]. In General hospital, blood bank had the highest mean load of 135.6cfu/m^2 (22.2%) whereas in IDH, the largest was in the laboratory unit which accounted for 115.8 cfu/m^2 (29.7%). The higher load in blood bank unit could be due in part to moisture properties of the unit as well as the temperature which is usually maintained at a somewhat lower rate and to a larger extent, contamination due to poor disinfection of the phlebotomy site [19]. In addition, the finding of a higher mean load in the laboratory may not be unconnected to the fact that clinical samples containing a vast majority of microorganisms are usually collected and processed there. The temperature, humidity, nutrient media used in the laboratories as well as storage conditions could be contributory factors [20]. Also, this high mean load could also be attributed to poor ventilation in the units. A mean load of 129.9cfu/m^2 (21.2%) observed in the intensive care unit of GH where patients with critical conditions are kept is worrisome and calls for urgent review of disinfection protocols. Studies have shown that air, temperature, relative humidity, ventilation systems, outdoor penetration and occupant density influence the quantity of airborne pathogens [16][21].

Furthermore, a total of 99 isolates were recovered from General hospital of which 67(67.7%) were bacteria and 32 (32.3%) were of fungal origin while in IDH, a total of 88 isolates were recovered of which 64(72.7%) were bacteria and 24 (27.2%) were fungal isolates. Organism including *Escherichia coli, Salmonella species, Klebsiella species*, *Candida species, Staphylococcus aureus, Aspergillus species*, *Penicillium species, Proteus mirabilis, Streptococcus species* and *Pseudomonas aeruginosa* were isolated in both hospitals [17]. The most isolated organisms in location one were *Candida sp* and *Staphylococcus aureus* were the most common in the laboratory and intensive care unit whereas in IDH, *Salmonella sp, Klebsiella sp,* and *Aspergillus sp* which showed high occurrence in laboratory, pharmacy and blood bank respectively whereas in location two, Generally, fungal isolates accounted for 29.9% of all microbial isolates. Though, 32.3% and 27.3% of fungi were isolated from General hospital and IDH, respectively.

In addition, gram negative organisms were more predominant (52.4%) in the environment of these two hospitals than gram positive organisms (17.6%) and fungi (29.9%). This is in line with researches conducted by Musaddiq [22] and Garcia-Cruz [23] where they observed that gram negative organisms were more common in the hospital environment than gram positive ones. The high percentage of gram negative organisms observed in this study is extremely higher than 4.9% reported by Lemmen [24]. The high occurrence of gram negative bacteria in the hospital environment may also be due to their ability to withstand

UNDER PEER REVIEW

adverse environmental conditions. Also, fungal isolates including *Aspergillus, Candida* and *Penicillum species* were the most dominant fungi isolated from these hospitals. This is consistent with findings of other researchers including Garcia-Cruz [23], and Abdollahi and Mahmoudzadeh [25] who confirmed the dominance of *Penicillum* and *Aspergillus species* in hospital units.

Furthermore, test isolates were subjected to a series of susceptibility testing in General hospital were observed to be less resistant to commonly used antibiotics than test organisms isolated in IDH. *E. coli* isolated from IDH showed considerable resistance to antibiotics including tarivid, reflacine, ciprolox, augmentin, gentamycin, streptomycin, ceporex, nalidixic acid, septrin and amplicin compared to *Escherichia coli* strains isolated in General hospital where the highest number (5) was observed with reflacine. The percentage of *P. aeruginosa* resistance (30-63%) to ciprofloxacin recorded in this study is in line with 60-70% reported by Kumari *et al* [25]. 33-80% resistance exhibited by gram negative organisms against tarivid in this study is somewhat lower than 91% reported by Gandham and Amatullah [27]. The resistance range of 27-71% of rifampicin against gram positive organism observed in this study is extremely higher than 14% reported by Omoigberale *et al* [18]. However, amoxil resistance of 100% against gram positive organism reported previously [18] is consistent with 46-90% observed in this study.

In IDH, *Salmonella species* showed more resistance (8) to tarivid, reflacine and nalidixic acid while in General hospital, the highest (6) was seen with tarivid and nalidixic acid, respectively. *Klebsiella species* and *Proteus mirabilis* isolates showed a peak resistance with tarivid and reflacine respectively in IDH while in General hospital, both isolates were high respectively. *Pseudomonas aeruginosa* from IDH showed a higher rate of resistance with amplicin compared to General hospital that showed resistance to both amplicin and gentamycin.

Also, gram positive and fungal isolates from IDH also displayed greater resistance patterns compared to General hospital. This marked resistance of isolates observed in IDH may be due to poor use and misuse of antibiotics in the hospital environments.

The MIC and MBC of the test isolates obtained in this study showed General hospital has the highest MIC and MBC values compared to IDH. *Escherichia coli* showed a maximum MIC and MBC with Ciprofloxacin (MIC 1:128; MBC 1:64) in IDH while in General hospital, gentamycin (MIC 1:512; MBC 256) were the known concentration. *Salmonella species* has a maximum concentration of MIC and MBC of 1:64, 1:32 with ceporex and amplicin respectively whereas in IDH, the highest concentration of *Salmonella species* isolates were with ceproflox, augmentin and Streptomycin at MIC 1:512 and MBC 1:256 respectively, *Klebsiella species* in General hospital showed MIC and MBC of 1:512 and 1:256 for tarivid, reflacine and ceporex respectively while in IDH, it was just reflacine at a concentration of 1:128 and 1:64. *Staphylococcus aureus* and *Streptococcus species* which were the gram positive showed the same concentration of MIC and MBC with levofloxacin in General hospital but this varied in IDH. For fungal isolates in IDH, the concentration of MIC and MBC was seen with ketoconazole (MIC 1:64, MBC 1:32) for *Penicillium species* whereas *Penicillium species* which is the highest also in General hospital were MIC1:128 and MBC1:64 with the same antibiotics.

Conclusion

The findings in this study highlight the fact that air quality of the hospital environment is an important reservoir of microbes and thus, there is need for monitoring of the hospital air especially in the units. Furthermore, hospital management, medical personnel and patients should be encouraged to imbibe good levels of hygiene in order to help reduce nosocomial infections.

UNDER PEER REVIEW

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