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Comparative Evaluation of Nosocomial Infections in Two Major Hospitals in Calabar Metropolis, Cross River State

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Authors' contributions

This work was carried out in collaboration between all authors. Authors UEG, CIM, ENM and UOE designed the study. All authors did sample collection, laboratory and data analysis. All authors read and approved the final manuscript.

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ABSTRACT

Aim: This study comparatively evaluates nosocomial infections in two major hospitals in Calabar metropolis, Cross River State.
Place and Duration of Study: This study was carried out in two major hospitals which were General Hospital (GH) and Infectious Disease Hospital (IDH) located in Calabar, Cross River State, Nigeria. The study lasted for 2 months from samples collection to report writing.
Methodology: Bacteria and fungi were isolated using settle plate technique and isolates were subjected to antibiotics sensitivity, minimum and bactericidal concentration tests. Resulting data were analysed using simple descriptive statistics and student t –test.

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Results: A total mean load of 1,002 cfu/m^2/hr was recorded of which 612.1cfu/m^2/hr was recorded in General hospital and 389.9 cfu/m^2/hr was recorded in Infectious Disease Hospital (IDH). Although the wards of both hospitals did not recorded the highest loads, they showed the highest microbial diversities of 23(23.2%) and 19 (21.6%) for GH and IDH, respectively. *Salmonella species* and *Escherichia coli* from GH showed resistance to taravid, nalidixic acid, reflacine and ciproflox. *E. coli, Salmonella, Klebsiella, Proteus species and P. aeruginosa* exhibited a wide range of resistance against tarivid, reflacine, ciproflox, ceporex, nalidixic acid and also moderately to amplicin. *Penicillium* and *Aspergillus species* from both hospitals showed higher resistance to ketoconazole than nystatin. Comparism of the mean loads in both hospital showed significance ($p = 0.01$). In IDH, *S. aureus* recorded MICs and MBCs of 1:32 and 1:16, respectively while for *Streptococci* species it was 1:16-1:64 and 1:8-1:32, 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.
Conclusion: 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; Nigeria.

1. INTRODUCTION

Airborne sources of possible bacterial contamination of the environment of hospitals have long been debated as potential causes of nosocomial infections. This has contributed to the already existing burden of nosocomial infections in the health care settings [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 environments and they constitute a major hazard confronting patients and personnel within hospital environments [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.

The units of healthcare environment as revealed by Gupta [4] represent 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 is linked to several microbial 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, poor 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 majorities of 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. [10] who reported high frequency of 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 isolated from Northern Nigeria. Despite the clinical implications associated with nosocomial infections, few studies exist that 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.

2. MATERIALS AND METHODS

2.1 Study Site

This study was carried out in two major hospitals in Cross River State, Nigeria. The hospitals were General Hospital (GH) and Infectious Disease

Hospital (IDH) and are located on latitude 4°59'N and longitude 8°15'E, respectively.

2.2 Sources of Samples

Samples were collected in December 2016 using settle plate technique from various units of these hospitals including pharmacy, theatre, laboratory, blood bank and intensive care units of both hospitals.

2.3 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 the plates were aseptically packaged and immediately transported to microbiology laboratory where they were incubated at 37℃ for 24-48 hours. After incubation, the plates were examined for growth and microbial load determined. Purified colonies were identified and characterized following standard microbiological procedures [12].

2.4 Antimicrobial Susceptibility Testing

This was done following procedures described previously by CLSI, (2004) and CLSI (2014) for fungi and bacteria, respectively [13,14]. Standardized inoculums were inoculated into plates containing freshly prepared Muller Hinton agar and allowed to stand for 15 minutes. Then, antibiotic discs were placed aseptically on the surface of the inoculated plates using sterile forceps and pressed lightly to ensure contact with the agar surface and the plates were incubated at 37℃ for 24-48 hours. After incubation, zones of inhibition were measured and compared with appropriate interpretive chats.

2.5 Determination of Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC)

This was performed following procedures described CLSI [14]. Briefly, 2-3 colonies of the test isolate was inoculated into 5ml of sterile peptone broth/sabouraud dextrose broth and incubated for 30 minutes. Antibiotics of various concentrations were dissolved in sterile test tubes containing 5ml of diluents (distilled water and dimethyl-sulphur oxide, 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 prepared. Standardized inoculums were added to each of the tubes and incubated for 24-48 hrs and the MICs 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 24-48 hrs at 37℃.

2.6 Data Analysis

Descriptive analysis such as simple percentages and student t-test was employed in this study. These were all done using Microsoft Excel office 2010.

3. RESULTS

3.1 Microbial Load

The result of the microbial load and their percentages as observed in various units of general hospital (GH) and infectious disease hospital (IDH) are summarized in Table 1 and Figs. 1 and 2, respectively. In GH, pharmacy had a mean load of 128.90 (21.1%) while ICU had a mean load of 129.9 (21.2%) cfu/m^2/hr. However, laboratory, blood bank and ward had mean loads and percentages of 124 (20.3%), 136 (22.2%) and 93.7 (15.3%) cfu/m^2/hr, respectively. Similarly, in IDH, pharmacy had a mean load of 67.40 (17.4%), ICU 59.70 (15.3%), laboratory 115.8(29.7%), blood bank 68.6(17.6%) and ward78.4 (20.1%). Student t-test analysis of the mean loads from the sampled units of both hospitals gave a significant probability value of 0.01 at 95% significance level.

Table 1. Mean bacteria loads (cfu/m^2/hr) of both hospitals

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

[a]*Represents significant p value (0.01) at 95% level of significance*

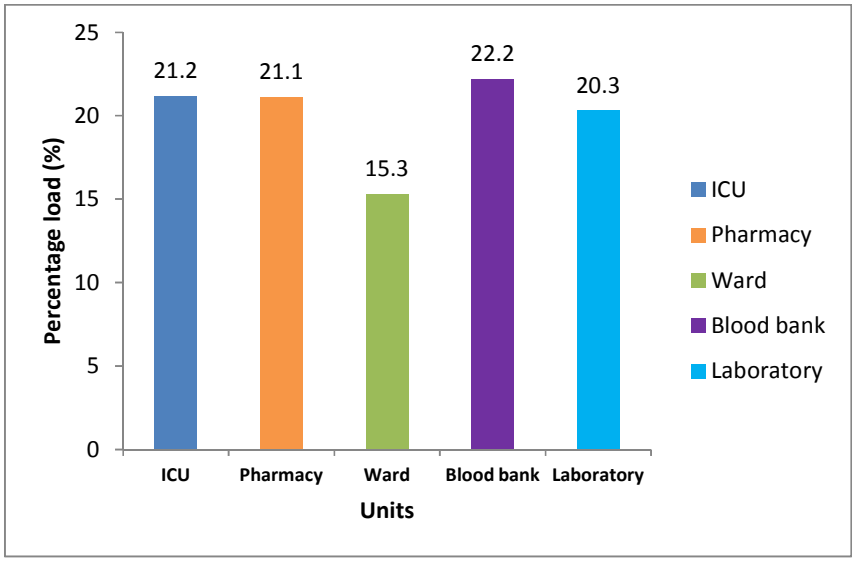

Fig. 1. Percentage microbial load in General Hospital

3.2 Number and Distribution of Microbial Isolates

A total of 187 isolates were recovered from both hospitals of which 99 (52.9%) and 88(47.1%) were recovered from General Hospital (Table 2) and Infectious Diseases Hospital (Table 3), 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.

3.3 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 4 and 5. 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 4. However, in IDH as shown in Table 4, *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 to amplicin. These organisms however, showed low resistance to augmentin, gentamycin, septrin and streptomycin as shown in Table 5. In addition, *Staphylococcus aureus* strains exhibited marked resistance against norfloxacan, ciproflox, streptomycin and levofloxacin while *Streptococci* showed resistance to norfloxacin, amoxil, ciproflox, chloramphenicol, erythromycin, ampiclox and levofloxacin. Furthermore, *Penicillium* and *Aspergillus species* showed resistance to ketoconazole.

3.4 Minimum Inhibitory Concentrations (MIC) and Minimum Bactericidal Concentrations (MBC) of Test Isolates

The MICs and MBCs of microbial isolates are as shown in Tables 6 and 7, 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.

4. DISCUSSION

The hospital environment is a complex environment on its own and interactions with different microorganisms lead to infections and re-infections. 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 and microbial load of microorganism, and also the state of the patients defense [15][16]. Airborne sources of bacterial contamination of the environment of hospital settings have long been debated as an important route of increasing incidence of nosocomial infections [16]. This can contribute to the already existing burden of nosocomial infections in health care set up [17].

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 (612.1 cfu/m^2/hr) was observed in General hospital (612.1 cfu/m^2/hr) compared to 389.9 cfu/m^2/hr in IDH which are higher the acceptable 35cfu/m^3 per room [16]. In General hospital, blood bank had the highest mean load of 135.6 cfu/m^2/hr (22.2%) whereas in IDH, the largest was in the laboratory unit which accounted for 115.8 cfu/m^2/hr (29.7%). The higher load in blood bank unit could be due in part to high moisture of the unit, low temperature and possibly poor disinfection of the phlebotomy unit [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 129.9 cfu/m^2/hr (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,*

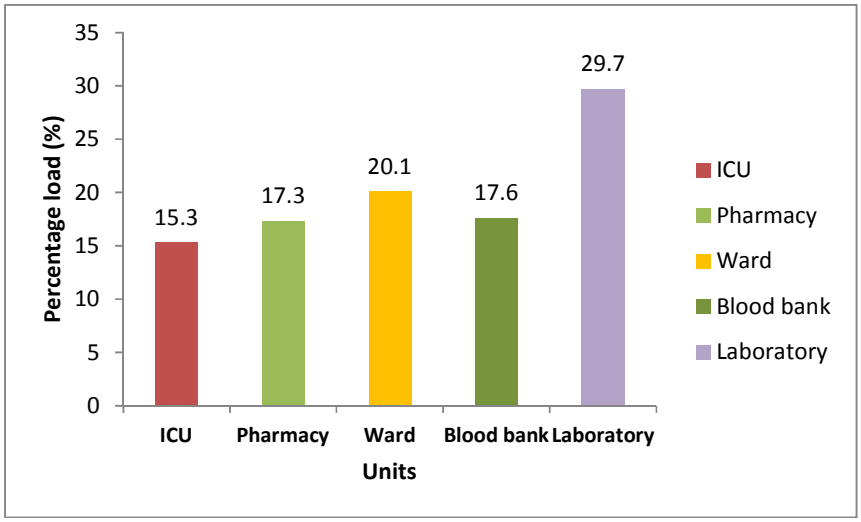

Fig. 2. Percentage microbial load in Infectious Disease Hospital

Table 2. Distribution of Isolates in General Hospital (GH) units

Isolates (n-99, 52.9%)	Units				
	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 species (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)
Penicillum 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 species(9)	0(0.0)	3(33.3)	3(33.3)	2(22.2)	1(11.1)

Table 3. Distribution of Isolates in Infectious Disease Hospital (IDH) units

Isolates (n-88, 47.1%)	Units				
	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 species(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)

Table 4. Resistant patterns of microorganisms 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%)								

Table 5. Resistant patterns of microorganisms isolated from GH

Gram negative bacteria	**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, CEP = CEPOREX, RD = RIFAMPCIN, PEF = REFLACINE, NA = NALIDIXIC ACID, E = ERYTHROMYCIN, CPX = CIPROFLOX, SXT = SEPTRIN, CH = CHLORAMPHENICOL, U = AUGMETIN, PN = AMPLICIN, APX = AMPICLOX, CN = GENTAMYCIN, NB = NORFLOXACIN, LEV = LEVOFLOXACIN S = STREPTOMYCIN, AML = AMOXIL, K = KETOCONAZOLE, NY=NYSTATIN*

Table 6. 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	1:128	1:64	1:16	1:32	1:16	1:16	1:64	1:32	ND	ND	ND	ND	ND	ND	ND	ND	ND
	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	ND	ND	ND	ND	ND	ND	ND	ND	ND
	MBC	1:16	1:16	1:16	1:8	1:8	1:32	1:32	1:16	1:16	1:32									
Candida species	MIC	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	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	ND	ND	ND	ND	ND	ND	ND	ND	
	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	ND	ND	ND	ND	ND	ND	ND	ND	
	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	ND	ND	ND	ND	ND	ND	ND	ND	
	MBC	1:16	1:16	1:32	1:8	1:8	1:8	1:64	1:32	1:32	1:16									
Staphylococcus aureus	MIC	ND	ND	1:32	ND	1:32	1:32	ND	ND	ND	ND	1:32	1:32	1:32	1:32	1:32	1:32	1:32	ND	
	MBC			1:16		1:16	1:16					1:16	1:16	1:16	1:16	1:16	1:16	1:16		
Penicillium species	MIC	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	1:64	
	MBC																		1:32	
Sreptococcus species	MIC	ND	ND	1:32	ND	1:32	1:64	ND	ND	ND	ND	1:16	1:64	1:32	1:16	1:32	1:32	1:64	ND	ND
	MBC			1:16		1:16	1:32					1:8	1:32	1:16	1:8	1:16	1:16	1:32		
Aspergillus species	MIC	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	1:32	1:16
	MBC																		1:16	1:8

ND= Not determined.

Table 7. 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	ND	ND	ND	ND	ND	ND	ND	ND	ND
	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	ND	ND	ND	ND	ND	ND	ND	ND	ND
	MBC	1:32	1:32	1:256	1:256	1:32	1:256	1:128	1:32	1:64	1:64									
Candia species	MIC	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	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	ND	ND	ND	ND	ND	ND	ND	ND	ND
	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	ND	ND	ND	ND	ND	ND	ND	ND	ND
	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	ND	ND	ND	ND	ND	ND	ND	ND	ND
	MBC	1:64	1:64	1:64	1:16	1:32	1:16	1:32	1:64	1:32	1:32									
Staphylococcus aureus	MIC	ND	ND	1:128	ND	1:128	1:128	ND	ND	ND	ND	1:128	1:64	1:64	1:256	1:64	1:128	1:512	ND	ND
	MBC			1:64		1:64	1:64					1:64	1:32	1:32	1:128	1:32	1:64	1:256		
Penicillum species	MIC	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	1:128	1:64
	MBC																		1:64	1:32
Streptococcus species	MIC	ND	ND	1:64	ND	1:32	1:32	ND	ND	ND	ND	1:64	1:32	1:64	1:64	1:64	1:64	1:512	ND	ND
	MBC			1:32		1:16	1:16					1:32	1:16	1:32	1:32	1:32	1:32	1:256		
Aspergillus species	MIC	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	1:64	1:64
	MBC																		1:32	1:32

ND = Not determined.

Staphylococcus aureus, Aspergillus species, *Penicillium species, Proteus mirabilis, Streptococcus species* and *Pseudomonas aeruginosa* were isolated in both hospitals [17]. The most isolated organisms in GH were *Candida species* and *Staphylococcus aureus* were the most common in the laboratory and intensive care unit. In IDH, *Salmonella sp, Klebsiella species,* and *Aspergillus species* 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. However, 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 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 susceptibility testing using a number of antibiotics. General hospital isolates were observed to be less resistant to commonly used antibiotics than test organisms isolated from 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 GH where the highest 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. [26]. The 33-80% resistance exhibited by gram negative organisms against tarivid in this study is 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 also high. *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 had 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. In IDH, the highest concentration was observed with *Salmonella species* isolates against ceproflox, augmentin and streptomycin with MIC and MBC of 1:512 and 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* 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 was MIC1:128 and MBC1:64 with the same antibiotics.

5. CONCLUSION

The findings in this study confirm the fact that air quality in hospital environments is an important reservoir of microbes. The mean microbial loads of 389.9 and 612.1 cfu/m^2/hr reported for both IDH and GH were far above recommended and safe means levels. A total of ninety-nine isolates recovered from both hospitals were distributed amongst bacteria and fungi groups routinely implicated in nosocomial infections. Furthermore, all the isolates showed varying levels of resistance to all the test antimicrobials used in this study. Given these findings, 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 high levels of hygiene in order to help reduce nosocomial infections.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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