Antibiogram of Bacteria and Fungi isolated from Medical and Non-medical Dumpsites in Rivers State

Abstract

Waste dumpsites could serve as reservoir for the transmission of antimicrobial resistant pathogenic microorganisms. The antibiogram of bacteria and fungi isolated from medical and non-medical dumpsites was investigated. Soil samples from the dumpsite of University of Port Harcourt teachings hospital, Rivers State University teachings hospital, NDDC hostel and faculty of Law were collected aseptically into sterile containers and analyzed using standard microbiological techniques. The total heterotrophic bacterial counts ranged from 1.1±0.4 to 1.9±0.9×10^7 CFU/g, the total coliform counts ranged from 4.1±0.3 to 6.8±0.2×10^4 CFU/g, the staphylococci count ranged from 3.9±0.8×10^3 to 1.9±0.1×10^4 CFU/g while the fungal count ranged from 6.5±0.21×10^4 to 1.25±0.71×10^5 CFU/g. The percentage occurrence of the bacterial isolates was *E. coli* (16.7%), *Pseudomonas* sp (8.3%), *Staphylococcus* sp (20.8%), *Streptococcus* sp (4.2%), *Bacillus* sp (20.8%), *Enterobacter*sp (12.5%), *Klebsiella*sp (8.3%), *Flavobacterium*sp (4.2%) and *Micrococcus* sp (4.2%). While the percentage occurrence of the fungal isolates was *A. niger*(14.3%), *A. terreus*(10.7%), *Mucor*sp (14.3%), *Geotrichum*sp (10.7%), *Trichoderma*sp (7.1%), *A. nidulans*(3.6%), *A. flavus*(7.1%), *Rhizopus*sp (10.7%), *Blastomyces*sp (10.7%) and *Candida albicans* (10.7%). The antibiotic susceptibility pattern of Gram-negative bacterial isolates showed that *E. coli* was 100% resistant to Ampliclox and Augmentin, and 75% resistant to Cefuroxime, Cefotaxime, Imipenem, Gentamycin, Nalidixic acid, Cefuroxime and Cefixime. *Klebsiella* was 100% resistant to all the antibiotics except levofloxacin, cefuroxime and Imipenem. *Enterobacter*sp showed 66.7% resistance to cefotaxime, imipenem and cefixime. *Pseudomonas* sp was 100% resistant to all the antibiotics except gentamycin. *Staphylococcus*sp was 100% susceptible to erythromycin, tetracycline and ciprofloxacin. *Streptococcus* sp was 100% susceptible to co-trimazole and vancomycin but completely resistant to Ampicillin, Meropenem, Erythromycin, Tetracycline, Ceftriaxone and Chloramphenicol. The multi-antibiotic-resistant index ranged from 0.2 to 1.0. The dumpsites contained drug-resistant microorganisms that could be a public health significance.

Keywords: Antibiogram, waste dumpsites, bacteria, fungi

Introduction

The upsurge in industrialization due to the increasing human population has contributed to the disposal of wastes (domestic, industrial and commercial wastes) in the world and the management of these wastes has remained an inevitably an serious environmental issue in developing countries (Grillo *et al*., 2019). Medical wastes is defined by the World Health Organisation as end products of medical services such as medical devices, sharps, blood, body parts, chemicals, pharmaceuticals and radioactive materials (Egbenyah *et al.*, 2021) while non-medical wastes could be related to domestic and industrial wastes.Food-wastes, agricultural wastes, human wastes (faeces and urine), and medical wastes are mostly associated with domestic wastes (Odum *et al.*, 2020). Waste dumpsites are sites designated for the disposal of wastes from different sources and in Nigeria, wastes aredisposed unsegregated without consideration of recycling, reducing or reusing of the wastes (Grillo *et al*., 2019).

Waste dumpsites can serve as sources of pathogenic bacteria and fungi (Odeyemi, 2012). Most of the wastes generated in hospitals and schools are dumped in designated areas and could serve as breeding ground for microorganisms and vectors dumpsites, thus, generating a public health concern (Grillo *et al*., 2019). Globally, it has been estimated that 5.2 million people, including 4 million children die annually from waste-related diseases (Egbenyah *et al*., 2021) and about 57 to 85% of the wastes generated worldwide are deposited in dumpsites devoid of effective waste treatment (Owhoudue & Agbini, 2021).Pathogenic microorganisms from waste dumpsites could be transmitted in the air through dust or liquid droplets that is inhaled or enter the body through skin and mucous membranes (Oyedele and Oyedele, 2017). The Niger Delta Development Commission (NDDC) hostel and the faculty of Law dumpsites are open dumpsites were domestic wastes generated by students, visitors of the school as well as those within the school premises are deposited. In addition to habouring or encouraging microorganisms, wastes dumpsites could be potential source for the transfer of antimicrobial resistance (Maina *et al.*, 2018).The disposal of human faecal matter or animal sheds in dumpsites could encourage the occurrenceofantibiotic-resistant bacteria. Drug-resistant microbial strains emerge in the environment as a result of inappropriate drug disposal, increasing the risks to public health (Borquaye*et al.,* 2019).More so, Mwaikono*et al.* (2015) opined that multidrug resistance in microbial populations has grown to be a significant worldwide issue and that these microorganisms have evolved defence mechanisms against the effects of several commonly used antibiotics. Previous studies have shown that home dumpsites are home to sizable populations of drug-resistant microorganisms (Mwaikonoet al., 2015; Idahosa et al., 2017). This study therefore investigated the type of bacteria and fungi in dumpsites situated in tertiary hospitals and University hostels including the determination of their susceptibility to antimicrobial substances.

Materials and Method

Collection of Sample

Soil samples were collected from medical waste dumpsite [University of Port Harcourt Teaching hospital (UPTH), and the Rivers State University Teaching Hospital (RSUTH)] and non-medical waste dumpsites (NDDC hostel and the faculty of Law, Rivers state University). Soil samples were collected aseptically into well labelled sterile sample containers. The samples were then conveyed to the Department of Microbiology laboratory, Rivers State University for immediate analysis. The coordinates of the sample locations are UPTH: Latitude 4.901582 and longitude

6.929798; RSUTH: Latitude 4.7801and longitude 7.0136; NDDC hostel: Latitude 4.806136 longitude 6.986422; faculty of Law: Latitude 4.806136 longitude 6.986422.

Enumeration and Isolation of Microorganisms in Waste

The spread plate technique was used in the enumeration of bacteria and fungi (Prescott *et al.*, 2011). Aliquot (0.1 ml) of 10^{-4} dilution (from a 10-fold serial dilution) was inoculated onto the surface of dried nutrient agar plates in duplicates for the enumeration and isolation of the total heterotrophic bacteria while aliquot from a 10^{-2} dilution was inoculated on to the surface of a freshly prepared pre-dried Eosin methylene blue agar, mannitol salt agar and tetracycline fortified Sabouraud Dextrose Agar (SDA) plates in duplicates. With the aid of a flamed glass spreader, the aliquot was spread evenly on the plates. Bacteria isolates were incubated at 37 °C for 24 hours while the SDA plates were incubated at 25°C for 5 days. After incubation, bacterial and fungal colonies that appeared on the respective agar plates were counted and the mean calculated and expressed as CFU/g for the samples. Discrete colonies were then subcultured on freshly prepared nutrient agar and SDA plates for the isolation of pure cultures.

$$\text{CFU/g} = \frac{\text{number of colonies}}{\text{Dilution} \times \text{Volume plated (0.1)}} \quad \text{equation 1}$$

Characterization and Identification of Bacterial Isolates

Cultural methods of characterizations employed were colour, shape, texture, odour, and microscopy under an oil immersion light microscope. Biochemical tests adopted include; citrate utilization, oxidase, Methyl-Red, Voges Proskauer, indole, starch hydrolysis and sugar fermentation tests.

The fungal isolates were identified based on morphological features (such as shape of colony, texture, sporetype and reverse pigmentation) and microscopic features. The microscopic examination was done by placing a drop of lactophenol cotton blue stain on a cleangrease free slide after which white tape was used in picking the aerial mycelia from therepresentative fungi cultures and placed on the drop of lactophenol on the slide. The slide was thenmounted and viewedunder the light microscope at ×10 and ×40 objective lenses. Themorphological characteristics and appearance of the fungal isolates seen were identified inaccordance with standard scheme for identification of fungi and reference was made to fungal identification manual (Sarah *et al.*, 2016).

Antibiotic Susceptibility Testing

The Kirby-Bauer disc diffusion method (Prescott *et al.,* 2011) was used to determine the antibioticsusceptibility of the bacterial isolates. Cellsuspension of the bacterial isolates was prepared by inoculating 4ml sterilenormal saline in a test tube with a pure culture of the test organism. The turbidity of the cellsuspension was adjusted to match 0.5 Mc Farland standard. The standardized inoculum was swabbed evenly on the surface of the fresh MuellerHinton agar plates with sterile swab sticks and was allowed to dry for 3 minutes before introducing disk containing different antibiotic concentrations. The plates were then incubated for24hrs at 37 □. After incubation the zone ofinhibition was measured and the sensitivity of the organisms were determined. (CLSI, 2020).

Antifungal Susceptibility Testing

Three antifungal drugs: Nystatin (12.5mg), Griseofulvin (500mg) and Ketoconazole (200mg) which were bought from Pharm care pharmacy were used in the antifungal testing. The drug concentration was prepared using the two-fold dilution method (Prescott *et al.,* 2011). Two hundred milligrams of ketoconazole was dissolved in 30mL sterile distilled water, 500mg Griseofulvin was dsolved in 75mL distilled water while 12.5mg Nystatin was dissolved in 1.9mL distilled water. The resulting concentration was 6.6mg/mL. subsequent two-fold dilution was carried out to obtain a concentration of 3.3mg/mL. This concentration was impregnated on sterile perforated discs and used for the testing.

Forty-eight hours old fungal isolates were standardized according to the Clinical Laboratory Standard Institute (Berkow *et al.,* 2020). The inoculum size of the yeast 2.5×10^{3}cells/ml while the filamentous fungi had the inoculum size of 5.0×10^{4}cells/mL. Sterile swabs were dipped into the standardized broth and swabbed on the surface of the SDA plates. Plates were allowed to dry before discs containing the antifungal agents were placed aseptically and incubated at 25°C for 24-48 hours. The plates were observed after incubation. Plates with which exhibited clear zone diameter were collected and zones were measured and reported.

Statistical Analysis

The microbial counts obtained during the study was subjected to statistical analysis. The mean and standard deviations were determined. The Anlysis of variance (ANOVA) was used in

checking for significant differences while Duncan multiple range test was used in mean separation. The percentages of the zone diameter (antibiotic susceptibility) were determined using descriptive statistics. All the analysis was done using SPSS version 27.

Results

The microbial counts of the dumpsites showed that the total heterotrophic bacterial counts ranged from 1.1±0.4 to $1.9\pm0.9\times10^{7}$CFU/g, the total coliform counts ranged from 4.1±0.3 to $6.8\pm0.2\times10^{4}$ CFU/g, the staphylococci count ranged from $3.9\pm0.8\times10^{3}$ to $1.9\pm0.1\times10^{4}$ CFU/g while the fungal count ranged from $6.5\pm0.21\times10^{4}$ to $1.25\pm0.71\times10^{5}$ CFU/g (Table 1).

The distribution of the bacterial isolates across the samples (Table 2a) showed inhomogeneity especially with some of the bacterial isolates being prevalent in all dumpsites while some rarely prevailed in three of the dumpsites. *E. coli, Staphylococcus* sp and *Bacillus* sp were isolated in all the dumpsites. *Pseudomonas* sp was isolated from the UPTH, RSUTH and NDDC hostel dumps only while *Streptococcus* sp was only isolated from the UPTH dump. *Enterobacter*sp and *Klebsiella*sp were isolated from only two of the dumpsites while *Flavobacterium*sp and *Micrococcus* sp were isolated in only NDDC hostel dump. The dump in the NDDC hostel had more of the bacterial types than the other dumpsites.

The distribution of the fungal isolates in the dumpsites (Table 2b) showed that *A. niger*and *Mucor*sp were isolated from all the dumps. *A. terreus*was isolated from dumps in UPTH, NDCC hostel and Law faculty while *Geotrichum*sp was isolated from dumps in RSUTH, NDDC hostel and Law faculty. *Trichoderma*sp was only isolated from RSUTH dump while *A. nidulans*and *A. flavus* was isolated from UPTH dump. *Blastomyces*sp were isolated from the dumps in UPTH and RSUTH while *Candida albicans* were isolated from UPTH, RSUTH and NDDC hostel dumps.

The percentage occurrence of the bacterial isolates (Fig. 1) was *E. coli* (16.7%), *Pseudomonas* sp (8.3%), *Staphylococcus* sp (20.8%), *Streptococcus* sp (4.2%), *Bacillus* sp (20.8%), *Enterobacter*sp (12.5%), *Klebsiella*sp (8.3%), *Flavobacterium*sp (4.2%) and *Micrococcus* sp (4.2%). While the percentage occurrence of the fungal isolates (Fig. 2) was *A. niger*(14.3%), *A. terreus*(10.7%), *Mucor*sp (14.3%), *Geotrichum*sp (10.7%), *Trichoderma*sp (7.1%), *A. nidulans*(3.6%), *A. flavus*(7.1%), *Rhizopus*sp (10.7%), *Blastomyces*sp (10.7%) and *Candida albicans* (10.7%).

Table 1: Microbial counts (CFU/g) of the Dumpsites

Location	THB ($\times 10^7$)	TCC ($\times 10^4$)	TSC ($\times 10^4$)	Fungal count ($\times 10^4$)
LAW faculty	1.2±0.2[a]	4.2±0.6[a]	1.1±0.1[a]	9.5±0.35[ab]
NDDC Hostel	1.9±0.9[a]	4.6±0.3[a]	1.4±0.4[a]	12.5±0.71[b]
RSUTH	1.1±0.4[a]	6.8±0.2[a]	0.39±0.8[a]	6.5±0.21[a]
UPTH	1.3±0.1[a]	4.1±0.3[a]	1.9±0.1[a]	9.0±0.14[ab]
p-value	0.85	0.603	0.357	0.04

*Means with similar superscript down the group showed no significant difference (P>0.05)(THB-Total Heterotrophic Bacteria, TCC-Total coliform count, TSC – Total staphylococcus count)

Table 2a: Distribution of Bacterial Isolates in the Samples

ISOLATE	UPTH	RSUTH	NDDC HOSTEL	LAW
Escherichia coli	+	+	+	+
Pseudomonas sp	+	+	+	-
Staphylococcus sp	+	+	+	+
Streptococcus sp	+	-	-	-
Bacillus sp	+	+	+	+
Enterobacter	+	-	+	-
*Klebsiella*sp	-	+	-	+
*Flavobacterium*sp	-	-	+	-
Micrococcus sp	-	-	+	-

Keys: + = isolated; - = not isolated

Table 2b: Distribution of Fungal Isolates in the Samples

ISOLATE	UPTH	RSUTH	NDDC HOSTEL	LAW
Aspergillus niger	+	+	+	+
Aspergillus terreus	+	-	+	+
*Mucor*sp	+	+	+	+
*Geotrichum*sp	-	+	+	+
*Trichoderma*sp	-	+	-	+
Aspergillus nidulans	+	-	-	-

Aspergillus flavus	+	-	-	+
*Rhizopus*sp	+	+	-	+
*Blastomyces*sp	+	+	-	+
Candida albicans	+	+	+	-

Keys: + = isolated; - = not isolated

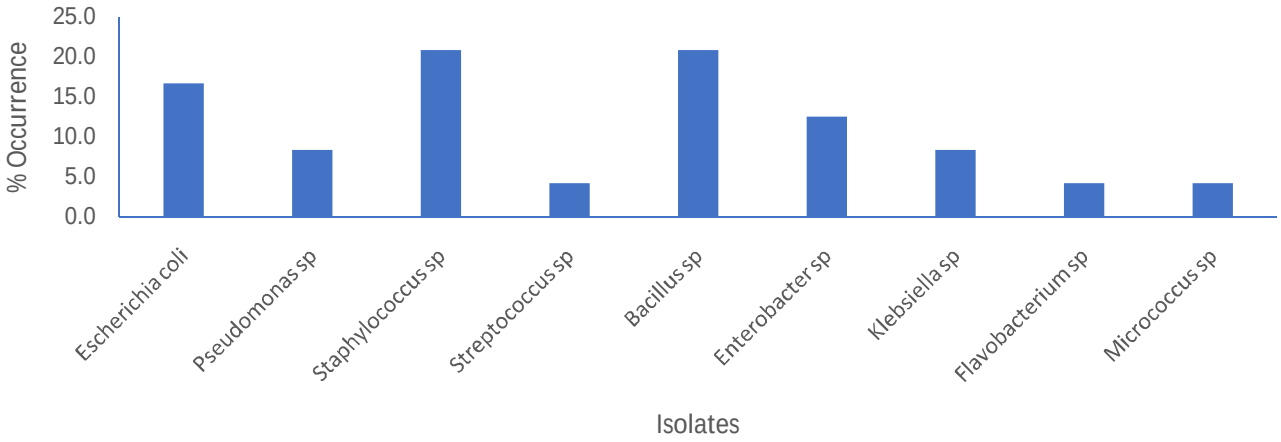

Fig. 1: Percentage occurrence of Bacterial Isolates

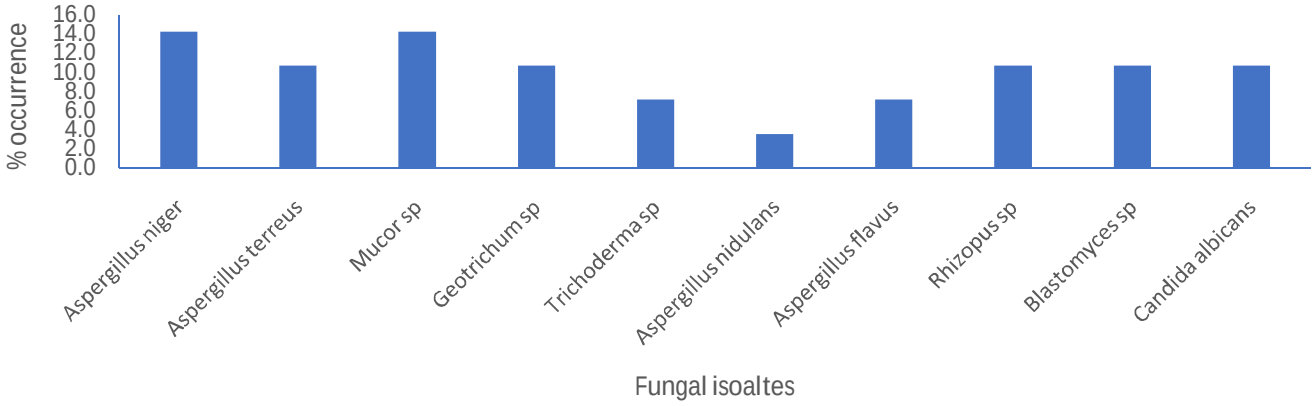

Fig. 2: Percentage Occurrence of fungal isolates

The antibiotic susceptibility pattern of Gram-negative bacterial isolates (Table 3a) showed very high resistance of the isolates to the antibiotic agents. *E. coli* while exhibiting 100% resistance to Ampliclox and Augmentin, displayed 75% resistance to Cefuroxime, Cefotaxime, Imipenem, Gentamycin, Nalidixic acid, Cefuroxime and Cefixime. Percentage resistance to ofloxacin and levofloxacin was 50%. All the *Klebsiella* isolates were 100% resistant to all the antibiotics except levofloxacin, cefuroxime and Imipenem. Susceptibility to levofloxacin was 100%. The *Enterobacter*sp. also displayed high resistance with 66.7% resistance displayed against cefotaxime, imipenem and cefixime. The isolates were 100% susceptible to levofloxacin,

gentamycin and nitrofurantoin. For the *Pseudomonas* isolates, they were 100% resistant to all the antibiotics except gentamycin which completely (100%) inhibited their growth.

The antibiotic susceptibility pattern of the Gram-positive isolates (Table 3b) showed that the *Staphylococcus*sp were 100% susceptible to erythromycin, tetracycline and ciprofloxacin while susceptibility to vancomycin was 50%. The results also showed that *Streptococcus* sp. which was 100% susceptible to co-trimazole and vancomycin were completely (100%) resistant to Ampicillin, Meropenem, Erythromycin, Tetracycline, Ceftriaxone and Chloramphenicol.

The multiple antibiotic-resistant index (MARI) of the isolates in Table 4a showed that all the isolates resisted more than two antibiotics with MAR index ranging from 0.2 to 1.0. More so, the isolates having displayed resistance against more than two antibiotic classes, displayed multi-drug resistance (Table 4b).

The antifungal susceptibility of *Aspergillus*, *Geotrichum*, *Blastomyces*and *Candida* sp showed that *Aspergillus* sp, *Geotrichum*sp and *Blastomyces*sp were not inhibited by ketoconazole or griseofulvin (Table 5).

Table 3a: Antibiotics susceptibility pattern of Gram-negative isolates

Antibiotics	***Escherichia coli* (n =4)**			***Klebsiella*sp (n=2)**			***Enterobacter*sp (n=3)**			***Pseudomonas sp* (n=2)**		
	S	I	R	S	I	R	S	I	R	S	I	R
Levofloxacin	1 (25)	1 (25)	2 (50)	2(100)	0	0	3(100)	0	0	0	0	2(100)
Cefuroxime	1 (25)	0	3 (75)	0	1(50)	1(50)	2(66.7)	0	1(33.3)	0	0	2(100)
Ampliclox	0	0	4(100)	0	0	2(100)	0	0	3(100)	0	0	2(100)
Cefotaxime	1(25)	0	3(75)	0	0	2(100)	1(33.3)	0	2(66.7)	0	0	2(100)
Imipenem	0	1(25)	3(75)	1(50)	0	1(50)	0	1(33.3)	2(66.7)	0	0	2(100)
Ofloxacin	2(50)	0	2(50)	0	0	2(100)	2(66.7)	0	1(33.3)	0	0	2(100)
Gentamycin	1(25)	0	3((75)	0	0	2(100)	3(100)	0	0	2(100)	0	0
Nalidixic acid	0	1(25)	3(75)	0	0	2(100)	1(33.3)	1(33.3)	1(33.3)	0	0	2(100)
Nitrofurantoin	1(25)	1 (25)	2(50)	0	0	2(100)	3(100)	0	0	0	0	2(100)
Cefuroxime	1 (25)	0	3(75)	0	0	2(100)	2(66.7)	1 (33.3)	0	0	0	2(100)

Cefixime	1(25)	0	3(75)	0	0	2(100)	1(33.3)	0	2(66.7)	0	0	2(100)
Augmentin	0	0	4(100)	0	0	2(100)	0	0	3(100)	0	0	4(100)

Table 3b: Antibiotics Susceptibility Pattern for Gram Positive Isolate

ANTIBIOTICS	***Staphylococcus sp* (n =4)**			**Streptococcus sp (n=1)**		
	S	I	R	S	I	R
Ampicillin	0	0	4(100)	0	0	1(100)
Meropenem	0	0	4(100)	0	0	1(100)
Erythromycin	4(100)	0	0	0	0	1(100)
Tetracycline	4(100)	0	0	0	0	1(100)
Co-trimoxazole	0	2(50)	2(50)	1(100)	0	0
Ceftriaxone	0	0	4(100)	0	0	1(100)
Ciprofloxacin	4(100)	0	0	0	1(100)	0
Amoxicillin	0	0	4(100)	0	1(100)	0
Chloramphenicol	0	0	4(100)	0	0	1(100)
Vancomycin	2(50)	2(50)	0	1(100)	0	0
Chlorpromazine	0	0	4(100)	0	0	1(100)

S-Susceptible, R- Resistance, I-Intermediate

Table 4a: Multiple Antibiotic-Resistant Index (MARI)

MARI	*Escherichia coli* (n =4) %	*Klebsiellasp* (n=2)	*Enterobactersp* (n=3)	*Pseudomonas sp* (n=2)	*Staphylococcus* sp (n =4) %	*Streptococcus* sp (n=1) %
0.2	1 (25)	0	0	0	0	0
0.3	0	0	1 (33.3)	0	0	0
0.4	0	0	1 (33.3)	0	0	0
0.5	0	0	1 (33.3)	0	2 (50)	0
0.6	0	0	0	0	2 (50)	0
0.7	0	0	0	0	0	1 (100)

0.8	1 (25)	2 (100)	0	2 (100)	0	0
0.9	1 (25)	0	0	0	0	0
1.0	1 (25)	0	0	0	0	0

Table 4b: Classes of Antibiotics Resisted by the Isolates

Isolates	Phenotypic resistance	Classes of Antibiotics	Multi-drug resistance
E. coli	LBC-CXM-ACX-CTX-IMP-OFX-GN-NA-NF-CRO-ZEM-AUG	Quinolone-cephalosporin-Penicillin-carbapenem-aminoglycoside-nitrofuran	+
*Klebsiella*sp	CXM-ACX-CTX-IMP-OFX-GN-NA-NF-CRO-ZEM-AUG	Quinolone-cephalosporin-Penicillin-carbapenem-aminoglycoside-nitrofuran	+
*Enterobacter*sp	CXM-ACX-CTX-IMP-OFX-GN-NA-NF-CRO-ZEM-AUG	Quinolone-cephalosporin-Penicillin-carbapenem	+
Pseudomonas sp	LBC-CXM-ACX-CTX-IMP-OFX-NA-NF-CRO-ZEM-AUG	Quinolone-cephalosporin-Penicillin-carbapenem-	+

		nitrofuran	
Staphylococcus sp	AMP-MEM-ERY-TET-COT-CRX-GEN-CIP-AUG-CP-VAN-CPZ	Penicillin-carbapenem-macrolide-tetracyclines-sulfonamides-cephalosporins-aminoglycoside-quinolones-glycopeptide	+
Streptococcus sp	AMP-MEM-ERY-TET-COT-CRX-GEN-CIP-AUG-CP-VAN-CPZ		+

LBC-CXM-ACX-CTX-IMP-OFX-GN-NA-NF-CRO-ZEM-AUG

Table 5: Antifungal Susceptibility of the Isolates

Antifungal agent	**Zone diameter (mm)**			
	Aspergillus sp	*Geotrichum*sp	*Blastomyces*sp	*Candida*sp
Ketoconazole	0.0±0.0 [a]	0.0±0.0 [a]	0.0±0.0 [a]	10.5±0.71 [b]
Griseofulvin	0.0±0.0 [a]	0.0±0.0 [a]	0.0±0.0 [a]	0.0±0.0 [a]
Nystatin	11.5±0.71 [b]	19.0±1.41 [b]	6.0±4.24 [b]	19.5±0.71 [c]

***Means with similar superscript down the group showed no significant difference (P>0.05)**

Discussion

Waste dumpsites is known to be one of the environmental issues in Nigeria and other developing countries due to the indiscriminate disposal and lack of facilities to contain or process these wastes (Odum *et al*., 2020). The dumpsites located in the NDDC hostel had the highest total heterotrophic bacterial and fungal count, it also had the second highest coliform counts while the RSUTH dumpsite had the highest total coliform count and the least staphylococcal count. The fungal counts in the dumpsite located in the NDDC hostel was significantly higher ($P<0.05$) than counts recorded in other dumpsites. More so, despite the variation in the counts in the total heterotrophic bacteria, total coliform and staphylococci, there was no significant differences ($P>0.05$) across the various dumpsites. The variation in the bacterial and fungal populations in the respective dumpsites could be a reflection of the extent of the pollution in that environment which is an indication of the amount of organic matter present(Ndimele *et al*., 2014). More so, the disparity could be attributed to the level of wastes dumped, the accessibility of the dumpsites and other rodents occupying these dumps. The dumpsites in the NDDC hostel and the Law faculty are not just accessed by students but also by visitors, hawkers and disposal of wastes is not restricted like wastes in the health institutions. The fungal counts in the present study are higher than fungal counts (3.8×10 to 3.5×10^3) reported by (Owhoudue & Agbini, 2021). They also opined that the increased fungal counts was a reflection of the microbial population in the dumpsites. The bacterial and fungal population of the waste dumpsites in the present study are higher than the THB (2.81 ± 1.01 to $6.38\pm1.78\times10^4$cfu/g), and fungal counts (2.00 ± 0.73 to $7.03\pm0.86\times10^3$cfu/g) reported by (Eghomwanre *et al.*, 2020). The total heterotrophic bacterial, coliform, staphylococcal and fungal counts reported by Ndimele *et al.*, (2014) in hospital waste dumpsites are higher than those reported in the present study. Nonetheless, the high microbial counts in the present study could have public health implications. The risk of infection may rise since these organisms are easily transported by foot or by other means into hospital, class rooms, and hostels as well as eateries. Additionally, rainwater can carry them into the hospitals' or hostel subterranean water, contaminating the water and spreading diseases that are transmitted by water(Ndimele *et al.*, 2014). The high total coliform in the present study could be attributed to the disposal of faecal matter in the dumpsites. Faecal matters in the hospital waste could result from the disposal of specimens (faecal) while in the hostels, faecal matter could be deposited directly or indirectly. Previous study have reported the disposal of faecal matters in dumpsites especially by individuals who defaecate directly in these dumpsites (Grillo *et al*., 2019).

The bacteria and fungi isolated from the dumpsites in this study have been reported in previous studies to be associated with waste dumpsites (Egbenyah *et al.,* 2021; Emmanuel *et al.,* 2017; Odum *et al*., 2020). *Staphylococcus* sp. and *Bacillus* sp. had the highest percentage occurrence (20.8%) followed by *E. coli* (16.7%). In a previous study, *Staphylococcus* sp. was reported as the most prevalent bacteria in the bioaerosols of waste dumpsites (Grillo *et al.*, 2019). The presence of these microorganisms in the dumpsites could imply that they could be transmitted by air. *Staphylococcus* sp. are regarded as sanitary indicators of atmospheric pollution which signify the presence of pathogenic microorganisms (Fraczek and Ropek,2011).*Staphylococcus* sp. have also been reported to cause bacteremia, skin and soft tissues infections, food poisoning and toxic shock syndrome (Oliveira*et al.,* 2018; Prescott *et al.,* 2011). The occurrence of *Bacillus* and *Micrococcus* species in waste dumpsites have been attributed to the presence of damp organic materials, food and food products in the dumpsites (Grillo *et al.*, 2019). More so, some species of *Bacillus* especially*B. cereus* have been implicated in food poisoning (Prescott *et al.,* 2011) while *Micrococcus* sp. could become opportunistic pathogens especially in immune compromised individuals ((Dada and Aruwa, 2014). The presence of *E. coli* and *Klebsiella* species could be the reflection of the disposal of faecal matters in the dumpsites especially since these isolates especially *E. coli* is an indicator microorganism which resides in the intestines of the human and other warm-blooded animals (Prescott *et al.,* 2011). *Pseudomonas* sp have been reported to be associated with varying diseases including being and opportunistic pathogen in hospitals (Maina *et al.,* 2018).

Fungi are mostly attributed to cause allergies as well as affecting individuals with weak or compromised immune system (Mbata, 2008). Furthermore, *Aspergillus* sp. have been reported to cause lung diseases (Matthew, *et al.*,2013) while species of *Candida* and *Blastomyces*sp have been implicated to cause candidiasis and blastomycosis, respectively (Prescott *et al.,* 2011). Thus, the indiscriminate dumping of trash near schools and hospitals may also serve as a haven for pests and disease-carrying insects like cockroaches, rats, flies, and mosquitoes. The public health risks associated with these dumpsites could affect students, teachers, patients and the surrounding communities whose food and water supplies could be tainted by waste dumping or leaks from dumpsites during rainy seasons and this could result in a higher chance of infectious disease transmission, including water- and food-borne illnesses (Eghomwanre *et al*., 2020).

The antibiogram of the bacterial isolates from these dumpsites showed the presence of multiple drug resistance. This agreed with Odum *et al.*, (2020) and Odjadjare*et al.* (2012). The prevalence of multi-drug-resistant bacterial isolates could be attributed to the indiscriminate disposal of wastes including faecal wastes into these dumpsites. Thus, wastes containing isolates that possess antimicrobial resistant genes could transfer them to other isolates (Odjadjare*et al.*, 2012) thereby increasing the isolates with the ability to resist drugs. More so, disposal of antimicrobials into dumpsites could aid in the development of resistant isolates especially since microorganisms could become sensitized with these antimicrobials and incorporate them into their metabolic cycles. The present study agreed with Grillo *et al.*,(2019) who reported resistance of *E. coli* to gentamycin, cefuroxime and ofloxacin. Although they reported 50% resistance which is comparable to the 75% reported in the present study. The presence of multi-drug-resistant *E. coli* from waste dumpsites in Tanzania has been reported (Mwaikono*et al.*,2015). Additionally, Andy & Okpo, (2018) has reported resistance of *E. coli, Klebsiella* and *Pseudomonas* sp to cefuroxime and Augmentin which agreed with the present study. Contrary to their study which reported complete susceptibility of *Klebsiella pneumoniae* to ofloxacin and gentamycin while exhibiting 33.3% resistance to levofloxacin, the present study showed that *Klebsiella*sp were completely susceptible to levofloxacin and were completely resistant to ofloxacin and gentamycin. Resistance of *Staphylococcus* and *Streptococcus* sp to vancomycin has been reported (Andy & Okpo, 2018). More so, self-medication which is a common practice in Nigeria could contribute to high prevalence of antibiotics resistance especially since treatments are stopped immediately they feel well (Andy & Okpo, 2018). Thus, disposing off the remaining antimicrobials.

The fungal isolates had varying antifungal susceptibility to nystatin while the *Candida* isolates showed susceptibility to ketoconazole and nystatin but were not inhibited by griseofulvin. *Aspergillus, Geotrichum*and *Blastomyces*species were completely resistant ketoconazole. It is commonly known that *Aspergillus* species are resistant to azole compounds specifically, through altered 14α-sterol demethylase, which is encoded by the cyp51A and cyp51B genes, and decreased intracellular concentration brought on by the expression of efflux pumps (Zeina and John,2008). Thus, this mechanism could have been adopted by *Geotrichum* and *Blastomyces*sp.

Conclusion

This study has shown that the dumpsites habour high bacterial and fungal population and the bacterial and fungal load could be dependent on the accessibility as well as the wastes disposed.

Additionally, the study showed that bacterial and fungal isolates in the dumpsites were highly resistant to commonly used antimicrobial agents. Thus, the upsurge of multi-drug-resistant bacteria and fungi. The dumpsites could also serve as a reservoir for the distribution of opportunistic bacterial and fungal isolates. Further studies on the evaluation of antimicrobial resistant genes in waste dumpsites in hospital and tertiary institutions is recommended for further study. Proper waste disposal and cleanup of waste is highly recommended to prevent seepage or distribution of microorganisms in these areas to other environments.

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