Published by ECRTD-UK

ISSN 2054-6351 (print), ISSN 2054-636X (online)

# ASSESSMENT OF AIRBORNE MICRO-ORGANISMS (BIOAEROSOLS) IN THE VICINITY OF SOME WASTE DUMPSITE IN UMUDIKE, ABIA STATE

Stephen, A.C\*., Nwanmuo, C.C. and Mbagwu, C.F

Department of Environmental Management and Toxicology, Michael Okpara University of Agriculture, Umudike, Nigeria \*Corresponding Author: Austinchigz@gmail.com

**ABSTRACT:** Environmental pollution from waste dump sites is a major concern to both environmental scientists and individual citizens. The study aimed at determining the microbial loads of air in the vicinity of various dumpsites in Michael Okpara University of Agriculture, Umudike using standard pour plate and spread plate microbiological techniques. Air samples were collected from selected dumpsites in the study area. The sampling time was 5 to 10 minutes interval and the sampling was 5 to 10meters at 26°c and 37° c temperature ranges for both bacterial and fungal load. The results shows that DUB for 37°c nutrient agar count recorded the lowest microbial load of 15333.33±3785.94 (cfu/m<sup>3</sup>) at distance 5meters in 5mins while DUB had the highest microbial load of 82333.33±5859.47 (cfu/m<sup>3</sup>) in 5mins. DUA for 26°c nutrient agar count in 10mins recorded the lowest microbial load mean± standard deviation values of 4366.67 $\pm$ 3412.23 (cfu/m<sup>3</sup>) while DUB in 10mins has the highest microbial load of 47666.67±2516.61 (cfu/m<sup>3</sup>) at distance 5 meters. At 37°c potato dextrose agar, distance 5 meters has the lowest microbial load value at DUC in 10mins  $5633.33\pm57.74$  (cfu/m<sup>3</sup>) while the highest microbial load count level is in DUB in 5mins  $34166.67 \pm 47500.98$  (cfu/m<sup>3</sup>). There is no significant increase in the mean values of DUA in 5min, DUA in 10mins and DUC in 5mins with respective values of 5166.67±1724.34, 4700.00±300.00 and 1866.67±665.83 (cfu/m<sup>3</sup>). The microbial loads of the air samples taken from the dumpsites were higher than the normal atmospheric concentration of the microorganisms as the reported average level of the microbes in the ambient air is 3.0 log10 cfu/ml. The bacterial genera isolated were Bacillus sp, B. subtilis, B. cereus, Staphylococcus sp, Streptococcus sp and Micrococcus sp., while the fungal isolates were Aspergillus fumigatus, Aspergillus niger, Penicillium notatum and Fusarium sp. This study indicates that potential airborne pathogens not only abound in the vicinity of waste dumpsites but also decreased with increasing distance from the dump sites. It is therefore recommended that students should be educated on alternative waste management options, so that gradually the dumpsites can be closed.

**KEYWORDS:** microbial loads, dumpsites, heterotrophic bacteria count, heterotrophic fungal count, residential quarters

# **INTRODUCTION**

In Nigeria as well as in most developing countries, the urban landscapes are littered with garbage, plastics, bottles, disposable cups, discarded tires and even human and livestock faeces. These wastes are aesthetically unpleasant, constitute eyesores, produce unpleasant odour especially when

# ISSN 2054-6351 (print), ISSN 2054-636X (online)

their organic compositions are acted upon by putrefying bacteria. These refuse dumps thus constitute a habitat for vector and other nuisance organisms capable of transmitting or causing diseases such as typhoid, infantile diarrhoea and cholera in humans and animals (Siboe *et al.*, 2006). Refuse dumps include both municipal solid wastes and industrial wastes including liquid effluents containing heavy metals (Olanrewaju, 2002). Refuse dumps provide a rich source of microorganisms most of which are pathogenic (Odeyemi *et al.*, 2011). This is usually as a result of the attraction of rodents and vector insects for which the dump serves as shelter and food source (Donderski *et al.*, 2000). A refuse disposal site is an area or land sites where material wastes from several sources and processes are deposited. It is an arena specifically used for the disposal of wastes. It is an old traditional method of waste disposal similar to landfill method of waste management (Adama, 2007). A refuse disposal site can also be referred to as a waste dumpsite.

Airborne microbes are biological airborne contaminants (also known as bioaerosols) like bacteria, viruses or fungi as well as airborne toxins passed from one victim to the next through the air, without physical contact, causing irritation at the very least. Microorganisms are transported from refuse dumps to the atmosphere with the wind. Their survival depends on their resistance, meteorological conditions, air pollution and time spent in the atmosphere (Marthi *et al.*, 1990). According to various studies, the range of bioaerosol emission is considerable and may reach 1000–1200 m from the border of the site (Adamiak *et al.*, 2001; Frączek *et al.*, 2003; Traversi *et al.*, 2011). Emissions from waste facilities are issues from occupational health and safety as well as environmental hygiene aspects (Kummer *et al.*, 2008; Giusti, 2009). Airborne microorganisms may cause respiratory diseases and other health effects in the facility workers and neighbouring residents (Wouters *et al.*, 2002; Douwes *et al.*, 2003; Heldal *et al.*, 2003; Curtis *et al.*, 2006; Schrapp *et al.*, 2010). The World Health Organization estimates that about two million people die prematurely every year as a result of air pollution, while many more suffer from breathing ailments heart disease, lung infections and even cancer (Madhukar and Srikantaswamy, 2013).

Indoor air in buildings located in close vicinity of refuse disposal sites may be polluted by microorganisms emitted from the refuse disposal site. Atmospheric transport is a key mode of microbial dispersal (Stetzenbach *et al.*, 2004) and the transmission of airborne plant and animal pathogens can have significant impacts on ecosystems, human health and agricultural productivity. In order to develop appropriate air quality management plans, it is necessary first to have reliable information about the state of airborne bacteria and fungi especially in the vicinity of waste dumpsites. Therefore, this study was undertaken to determine the microbial load of air in dump sites in Michael Okpara University of Agriculture Umudike (MOUAU), Abia State.

#### MATERIALS AND METHODS

#### **Study Area**

The study area is Michael Okpara University of Agriculture, Umudike which is located in the Ikwuano local government area of Abia state. It is essentially between latitude 05°28'N and 05°30'N and longitude 7°31'E and 7°33'E. The vegetation of the study area is typical of the rain forest type having an altitude of 122mm above sea level. The mean monthly temperature is always around 25°C with peak at about 32°C around April-October. The mean annual rainfall is 2200mm

# British Journal of Environmental Sciences Vol.8, No.3, pp. 1-12, October 2020 Published by ECRTD-UK

## ISSN 2054-6351 (print), ISSN 2054-636X (online)

annually distributed over 9-10 months in a bimodal rainfall pattern; these are early rain (April-July) and late rain (August-October) with five months dry season and a short heat period in August particularly called August break. The relative humidity varies from 84% to 87%. The disposal of solid waste in the study area is presently a serious problem and will become increasingly serious as the options for disposal become more limited and the amount of such waste generated becomes greater. The current disposal practice in the study area is the use of unsanitary dump sites (open dump site). Composition of waste generated in the study area includes: garbage, paper, plastics, kitchen waste etc. Student hotels are located some distance away from the dumpsites (study area). The occupations of the people in the study area are students, civil servants, farmers, traders etc.



FIG 1: MAP OF THE STUDY AREA (SOURCE: ESRI ARC MAPVERSION 10.0)

# SAMPLE COLLECTION

Air samples were collected from three selected dumpsites in the study area. Dumpsite A (DUA) which is located in front of Goodluck Jonathan female hostel, Dumpsite B (DUB) which is located in front of Goodluck Jonathan male hostel and dumpsite C (DUC) which is beside college of natural resources and environmental management. At each sampling area, sterile plates containing culture media were exposed in the dumpsite. In all one hundred and eight air samples were collected from three different dumpsites. From each dumpsite, thirty-six samples were collected. The isolates were collected from different locations around the dumpsites, the locations included the dump site DUA (5m and 10m away from the dumpsite), dumpsite DUB (5m and 10m away from the dumpsite). After which plates were closed and taken to the laboratory for analysis.

#### **Culturing and Enumeration of Bacteria in Air Samples**

Freshly prepared Nutrient agar plates and MacConkey agar were exposed to air. The plates were inverted and incubated at 37°C and 26°C. 8 plates containing Nutrient agar were incubated for 48 hours at 37°C, 8 plates containing Nutrient agar were incubated for 72 hours at room temperature (26°C) and 4 plates containing MacConkey agar were incubated at 37°C for 48 hours after which the plates were examined for growth. The colonies which developed were counted and the average counts for duplicate cultures were recorded as aerobic bacteria in the sample.

# ISOLATION, CHARACTERIZATION AND IDENTIFICATION OF BACTERIA IN THE AIR SAMPLES

Pure cultures of bacteria were obtained by aseptically streaking representative colonies of different morphological types, which appeared on the cultured plates onto freshly prepared Nutrient agar plates and MacConkey agar plates and incubated at 37°C for 24 hrs. Discrete bacteria colonies which developed were sub cultured onto Nutrient agar slopes and incubated at 28°C for 24 hrs. These will serve as pure stock cultures for subsequent characterization and identification via physiological and biochemical tests [Cheesbrough, 2006].

# **Culturing and Enumeration of Fungi in Air Samples**

Freshly prepared Potato dextrose agar plates were exposed to air. The plates were inverted and incubated at 37°C and 26°C. 8 plates were incubated for 48 hours at 37°C and another 8 plates containing Potato dextrose agar were incubated for 72 hours at room temperature after which the plates were examined for growth. The colonies which developed were counted and the average counts for duplicate cultures were recorded as viable fungal counts in the sample.

# Isolation, Characterization and Identification of Fungi in Air Samples

Pure cultures of fungi were obtained by sub-culturing discrete colonies onto freshly prepared Potato Dextrose Agar plates and inoculated at room temperature  $(28\pm 2^{0}C)$  for 5 days. The fungal isolates which developed were further sub cultured onto agar slopes and incubated at room temperature. The isolates which developed were pure cultures which were stored in the refrigerator (4°C) as stock cultures for subsequent characterization via macroscopic and microscopic examination. The identification of fungal isolates was done by comparing the result of their cultural and morphological characteristics with those of known taxa (Harrigan and McCance 1990).

# RESULTS

# Microbial Load (cfu/m<sup>3</sup>) at 37°c for Nutrient agar

The table below indicates an increase in the mean $\pm$  standard deviation values of the microbial load from dumpsite DUA to DUC at distance 5meters. DUC recorded the lowest microbial load of 15333.33 $\pm$ 3785.94 (cfu/m<sup>3</sup>) at distance 5meters in 5mins while DUC had the highest microbial load of 82333.33 $\pm$ 5859.47 (cfu/m<sup>3</sup>) in 5mins. There is no significant difference at p  $\leq$ 0.05 in the microbial load mean  $\pm$  standard deviation values between DUA in 5mins, DUA in 10mins, DUB in 5mins and DUC in 10mins. A significant difference at p  $\leq$ 0.05 is seen between the aforementioned dumpsites and DUB in 10mins, DUC 5mins. Distance 10meters, DUC in 5mins

Published by ECRTD-UK

ISSN 2054-6351 (print), ISSN 2054-636X (online)

recorded the lowest microbial load of  $5700.00\pm100.00$  (cfu/m<sup>3</sup>) while DUB in 10mins had the highest microbial load mean± standard deviation value of  $27666.67\pm577.35$  (cfu/m<sup>3</sup>). No significant difference is seen in DUC in 5mins and DUC in 10mins. There is a significant difference at p  $\leq 0.05$  between DUA in 5mins and DUA in 10mins also between DUB in 5mins and DUB in 10mins.

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Dumpsite	Time	5 Meters ( $cfu/m^3$ )	10 Meters ( $cfu/m^3$ )		
DUA	5 MINS	15666.67±4041.45 <sup>a</sup>	15666.67±4932.88 <sup>c</sup>		
	10 MINS	21666.67±8504.91 <sup>a</sup>	10333.33±577.35 <sup>d</sup>		
DUB	5 MINS	24000.00±2645.75 <sup>a</sup>	16333.33±3785.94 °		
	10 MINS	36333.33±6110.10 <sup>b</sup>	27666.67±577.35 <sup>b</sup>		
DUC	5 MINS	82333.33±5859.47 <sup>c</sup>	5700.00±100.00 a		
	10 MINS	15333.33±3785.94 <sup>a</sup>	5000.00±1100.00 <sup>a</sup>		

Table 1: Microbial Load	(cfu/m <sup>3*</sup>	) at 37°c for Nutrient agar
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Different alphabetical superscripts in the same column means there is a significant difference at  $P \le 0.05$  between treatments according to Duncan test while same alphabetical superscripts in the same column means no significant difference at  $P \le 0.05$  between treatments according to Duncan test.

#### **Microbial Load** (cfu/m<sup>3</sup>) at 26°c for Nutrient Agar

From the table below, DUA in 10mins recorded the lowest microbial load mean± standard deviation values of 4366.67±3412.23 (cfu/m<sup>3</sup>) while DUB in 10mins has the highest microbial load of 47666.67±2516.61 (cfu/m<sup>3</sup>) at distance 5 meters, There is no significant difference at P<0.05 between DUC in 10mins, DUA in 5mins and DUA in 10mins with values of  $13000.00\pm1000.00$ ,  $14000.00\pm0.00$  and  $4366.67\pm3412.23$  (cfu/m<sup>3</sup>) respectively. This is also applicable to DUB in 5mins, DUB in 10mins and DUC in 5mins with respective microbial load mean± standard deviation values of 43000.00±1000.00, 47666.67±2516.61 and 47000.00±33181.32 (cfu/m<sup>3)</sup>. For 10meters distance, DUC in 5mins recorded the lowest microbial load of 4366.67±57.74 (cfu/m<sup>3</sup>), while DUB in 10mins had the highest microbial load count of 29666.67 $\pm$ 6027.71 (cfu/m<sup>3</sup>). There is no significant difference at p $\leq$ 0.05 between DUA in 5mins, DUA in 10mins, DUC in 5mins and DUC in 10mins. Also, there is a significant difference between DUB in 5mins and DUB in 10mins with respective values of 24000.00±3605.55 (cfu/m<sup>3</sup>) and 29666.67±6027.71 (cfu/m<sup>3</sup>).

#### Published by ECRTD-UK

#### ISSN 2054-6351 (print), ISSN 2054-636X (online)

#### Table 2: Microbial Load (cfu/m<sup>3</sup>) at 26°c for Nutrient agar

Dumpsite	Time	5 Meters(cfu/m <sup>3</sup> )	$10 Meters(cfu/m^3)$
DUA	5 MINS	14000.00±0.00 ª	8400.00±556.78 <sup>a</sup>
	10 MINS	4366.67±3412.23 a	6900.00±700.00 <sup>a</sup>
DUB	5 MINS	43000.00±1000.00 <sup>b</sup>	24000.00±3605.55 b
	10 MINS	47666.67±2516.61 b	29666.67±6027.71 °
DUC	5 MINS	47000.00±33181.32 <sup>b</sup>	4366.67±57.74 <sup>a</sup>
	10 MINS	13000.00±1000.00 <sup>a</sup>	4466.67±2916.05 a

Different alphabetical superscripts in the same column means there is a significant difference at  $P \le 0.05$  between treatments according to Duncan test while same alphabetical superscripts in the same column means no significant difference at  $P \le 0.05$  between treatments according to Duncan test.

#### Microbial Load (cfu/m<sup>3</sup>) at 37°<sup>c</sup> for Potato Dextrose agar

The table below at distance 5meters has the lowest microbial load value at DUC in 10mins  $5633.33\pm57.74$  (cfu/m<sup>3</sup>) while the highest microbial load count level is in DUB in 5mins  $34166.67\pm47500.98$  (cfu/m<sup>3</sup>). There is no significant difference at P $\leq$ 0.05confidence interval in DUA in 5mins, DUA in 10mins, DUB in 5mins, DUB in 10mins and DUC 5mins, DUC 10mins. For distance 10meters, DUC in 5mins had the lowest microbial load count mean $\pm$  standard deviation value of 1866.67 $\pm$ 665.83 (cfu/m<sup>3</sup>) while DUC in 10mins recorded the highest microbial load mean value of 23666.67 $\pm$ 3785.94 (cfu/m<sup>3</sup>). There is no significant increase in the mean values of DUA in 5min, DUA in 10mins and DUC in 5mins with respective values of 5166.67 $\pm$ 1724.34, 4700.00 $\pm$ 300.00 and 1866.67 $\pm$ 665.83 (cfu/m<sup>3</sup>).

#### **Table 3: Microbial Load** (cfu/m<sup>3</sup>) at 37°c for Potato Dextrose agar

Dumpsite	Time	5 Meters(cfu/m <sup>3</sup> )	10 Meters(cfu/m <sup>3</sup> )
DUA	5 MINS	34166.67±47500.98 <sup>a</sup>	5166.67±1724.34 <sup>a</sup>
	10 MINS	7000.00±264.58 <sup>a</sup>	4700.00±300.00 <sup>a</sup>
DUB	5 MINS	21333.33±2081.58 a	11666.67±1527.53 <sup>b</sup>
	10 MINS	24000.00±9539.39 <sup>a</sup>	14000.00±1000.00 <sup>b</sup>
DUC	5 MINS	6833.33±3074.62 <sup>a</sup>	1866.67±665.83 <sup>a</sup>
	10 MINS	5633.33±57.74 <sup>a</sup>	23666.67±3785.94°

Different alphabetical superscripts in the same column means there is a significant difference at  $P \le 0.05$  between treatments according to Duncan test while same alphabetical superscripts in the same column means no significant difference at  $P \le 0.05$  between treatments according to Duncan test.

# **Microbial Load** (cfu/m<sup>3</sup>) at 26°c for Potato Dextrose agar

From the below table, for distance 5 meters, in DUC in 10mins is seen with the lowest microbial load count value of  $11000.00\pm1000.00$  (cfu/m<sup>3</sup>) while DUB in 5mins had the highest microbial load count of 24666.67±2081.67 (cfu/m<sup>3</sup>). There is no significant difference at P≤0.05 confidence interval between DUA in 5min, DUA in 10mins, DUC in 5mins and DUC in 10mins. This is also applicable to DUB in 5mins and DUB in 10mins with respective microbial load value of 3966.67±115.47 (cfu/m<sup>3</sup>) while DUB in 5mins had the highest microbial load of 59000.00±40037.48 (cfu/m<sup>3</sup>). No significant difference is seen at P≤0.05 in DUA in 5mins, DUA in 10min and DUB in 10mins. This is also applicable to DUC in 5mins and DUC in 5mins.

# Table 4: Microbial Load (cfu/m<sup>3</sup>) at 26°c for Potato Dextrose agar

Dumpsite	Time	5 Meters( $cfu/m^3$ )	10 Meters(cfu/m <sup>3</sup> )
DUA	5 MINS	12000.00±1000.00 <sup>a</sup>	4600.00±1178.98 <sup>a</sup>
	10 MINS	11433.33±3370.95 <sup>a</sup>	3966.67±115.47 <sup>a</sup>
DUB	5 MINS	24666.67±3370.95 <sup>b</sup>	59000.00±40037.48 <sup>c</sup>
	10 MINS	24000.00±6557.44 <sup>b</sup>	11333.33±577.35 <sup>a</sup>
DUC	5 MINS	8833.33±1106.04 <sup>a</sup>	41333.33±7371.11 ab
	10 MINS	11000.00±1000.00 <sup>a</sup>	27900.00±38201.18 <sup>ab</sup>

Different alphabetical superscripts in the same column means there is a significant difference at  $P \le 0.05$  between treatments according to Duncan test while same alphabetical superscripts in the same column means no significant difference at  $P \le 0.05$  between treatments according to Duncan test.

#### **Bacterial Isolates from Air Samples**

Isolates	Α	В	С	d	e	f
CULTURAL CHARACTERISTIC	Cream flat & smooth colonies	Cream, rough or slightly yellow	Dark yellow smooth edge	Creamy converse colonies with smooth edge	Creamy- white with rough edges	Light brown with smooth edges
MICROSCOPY	Gram positive rods in long and short chains	Gram positive rods in short chains	Gram positive rods in twos	Gram positive cocci appearing in bunches	Gram positive cocci in chains	Gram positive cocci appearing in single bunches
GRAM STAIN	+	+	+	+	+	+
CATALASE TEST	-	+	+	+	-	+
INDOLE TEST ORGANISM IDENTIFIED	- Bacillus sp	- Bacillus subtilis	- Bacillus cereus	- Staphylococcus sp	- Streptococcus sp	- Micrococcus Sp

#### Table 6: Identification and characterization of bacteria from air samples

# Table 7: Distribution of airborne bacterial isolates

ORGANISM	DUG	DUC	DUN	
Bacillus sp	+++	++	++	
Bacillus subtilis	-	+	-	
Bacillus cereus	-	+	-	
Streptococcus sp	+	-	+	
Staphylococcus sp	+	++	++	
Micrococcus sp	+	-	-	

Key: -Absent, +Rare, ++Intermediate, +++ large in number

#### British Journal of Environmental Sciences

Vol.8, No.3, pp. 1-12, October 2020

#### Published by ECRTD-UK

ISSN 2054-6351 (print), ISSN 2054-636X (online)

isolates	Α	b	С	d
COLONIAL	Blue-green with	Black on the	Gray-green at	White cottony
CHARACTERISTIC	a suede-like surface	surface and white underneath	the center and white at the periphery, flat, filamentous with a wooly surface	colonies with the aerial mycelia becoming tinged in purple, underneath is purple
MICROSCOPIC APPEARANCE	Conidial heads are strongly columnar. Conidiophores are smooth- walled and colourless	Conidia are brown to black, very rough, globose. Conidiophores are long and smooth	Conidia are round to ovoid, pigmented, rough walled, in chains Conidiophores are branched	Conidiophores are short with a slight bulge in the middle, they appear singly
ORGANISM IDENTIFIED	Aspergillus fumigatus	Aspergillus niger	Penicillium notatum	Fusarium sp

### **Fungal Isolates from Air Samples**

 Table 8: Identification and characteristics of fungal isolates from air sample

#### Table 9: Distribution of airborne fungal isolates

ORGANISM	DUG	DUC	DUN
Aspergillus niger	++	+	-
Aspergillus fumigatus	++	-	+
Penicillium notatum	-	+	+
Fusarium sp	-	++	-
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Key: -Absent, +Rare, ++Intermediate, +++ large in number

#### DISCUSSION

The airborne bacteria and fungi in the present study showed variations ranged between  $10^3$ - $10^4$  (cfu/m<sup>3</sup>). The microbial loads of the air samples taken from the dumpsites were higher than the normal atmospheric concentration of the microorganisms as the reported average level of the microbes in the ambient air is 3.0 log10 cfu/ml (Panthi and Shrestha, 2008). This is an indication of the extent of microbial pollution caused by the waste dump sites in the study area. From the study, it was observed that the bacterial load for the air samples showed that the bacterial counts decreased with distance from the dumpsite. This could be seen in table 2, as the mean values decreased as the sampling distance increased from 5meters to 10meters. The decreasing bacterial counts with distance away from the dumpsite could be due to increased microbial activity in the

# ISSN 2054-6351 (print), ISSN 2054-636X (online)

dumpsite as a result of putrefaction and increased decomposition of organic matter in the vicinity of the dumpsite. DUA and DUB in particular are seen to have higher bacterial load because they are located around the hostels and as a result of that the waste there is composed mainly of household, cabbage and sanitary wastes which are acted upon by putrefying bacteria as well as contaminants generated naturally that were propelled through the air, such as particles of dust and soil microbial spores in the air within the dumpsites. These results agree with the report of (McCarthy, 2001), who listed these amongst others as possible sources of air contaminants. This study was carried out in October which is rainy season therefore the observed increased trend in the bacterial counts could be as a result of increased rainfall. These results agree with the reports of Obire *et al.*, 2002 who stated that seasonal variations favour physiological types.

Temperature is widely recognized as an important controlling factor in influencing microbial growth. It is clear from the results obtained in this study that bacterial load and fungal load increased at a favorable temperature; a greater increase is seen in microbial load when organisms were incubated at  $37^{\circ}$ c than  $26^{\circ}$ c. This is seen in the difference between bacterial load of DUA in 5mins incubated at  $37^{\circ}$ c as seen in Table 2 and DUA in 5 mins incubated at  $26^{\circ}$ c with respective values of  $15666.67\pm4932.88$  (cfu/m<sup>3</sup>) and  $8400.00\pm556.78$  (cfu/m<sup>3</sup>) as seen in Table 3.

Fungal load for the air samples showed that the fungal counts decreased with distance from the dumpsite. The decreasing fungal count with distance away from the dumpsite could be due to same reasons propounded for bacterial counts above. These results agreed with the report of McCarthy 2001, who reported similar suggestions. It is also observed from the study that bacterial load is higher than fungal load as seen in the difference between Table 2 and Table 4. This could be because bacteria thrive better in rainy seasons whereas fungi thrive better in dry season. Bacteria thrive in wet seasons possibly due to the atmospheric particles to which the microbes are attached, which are being deposited by the process of rainfall. The increased water activity therein provides favourable conditions for bacteria to thrive and multiply.

The bacterial and fungal genera encountered in this study had been reported by previous studies (Ayanru, 1981; Ryan *et al.*, 2004; Kirk *et al.*, 2004) as the possible microbial isolates from the air. The bacteria genera isolated in this study as seen in Table 6 are *Bacillus sp*, *B. subtilis*, *B. cereus*, *Staphylococcus sp*, *Streptococcus sp and Micrococcus sp*. *Bacillus sp* and *Staphylococcus sp* were more abundant in the air sample as seen in Table 7. The presence and prevalence of some of these species of bacteria in the dumpsite could be as a result of the presence of damp organic materials, materials impregnated with water, food and food products and spores of microorganisms propelled through the air. These results agree with the report of Osha (1999) and Sola (2000), who reported these as possible sources of air microflora. These bacteria can cause different forms of bacterial pneumonia, influenza and gastrointestinal diseases (Douwes *et al.*, 2003).*Bacillus cereus and Bacillus subtilis* are associated with endocarditis, meningitis and infections of wounds, ears, eyes, respiratory tract, urinary tract and gastrointestinal tract diseases (Turnbull, 1996). The endotoxin of bacterial bio-aerosols has been recognized also as an important factor in the aetiology of occupational lung diseases including (non-allergic) asthma (Douwes *et al.*, 1997).

ISSN 2054-6351 (print), ISSN 2054-636X (online)

The fungal genera isolated from air sample as seen in Table 8 are *Aspergillus fumigatus*, *Aspergillus niger*, *Penicillium notatum and Fusarium sp*. From the study *Aspergillus fumigatus* and *Aspergillus niger* were the fungi specie observed to be predominant in the air sample which is shown in Table 9. These results agree with the report of Prescott *et al.*, 2005 who listed these amongst the most common allergenic moulds associated with man and live stocks. Obire *et al.*, 2002 also identified *Aspergillus sp* as one of the most common fungi.

Aspergillus is not harmful for people with healthy immune systems, however for people who have weakened immune systems, breathing in *Aspergillus* spores can cause infection in the lungs or sinuses which can spread to other parts of the body. According to Dennig, *et al.*, 2003 *Aspergillus* can cause lung disease and can kill after as little as 10-14 days. Fungi are known to cause allergies and they are of particular concern to immune compromised patients in health-care facilities (Lee, 2011).

# CONCLUSION

Study on the distribution of airborne micro-organisms is an essential tool in evaluating the quality of air present around dump sites and the effects dump sites have on man and the environment. The result shows that the microbial loads of the air samples taken from the dumpsites were higher than the normal atmospheric concentration of microorganisms as the reported average level of the microbes in the ambient air is 3.0 log10 cfu/ml which is an indication of the extent of microbial pollution of waste dump sites in the study area. This microbial pollution is a source of various diseases which can lead to the death of man. Bacteria and fungi were the microorganisms prevalent in the study area. The species of these microorganisms predominant in the study area have been found to be harmful to the health of man. Therefore, it is ideal that dumpsites should not be located around residential areas.

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British Journal of Environmental Sciences

Vol.8, No.3, pp. 1-12, October 2020

Published by ECRTD-UK

ISSN 2054-6351 (print), ISSN 2054-636X (online)

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