Public Health Risk Assessment of Bio-aerosols Associated with Soot Pollution in Port Harcourt, Nigeria

*** [1] Asime, O., [2, 5,8,9] Idris, U. H., [3] Barka, J., [4] Jamilu, G., [6] Kwata, V. J. and [7] Hayford, F.**
[1] Independent Researcher, [2]Department of Veterinary Public Health and Preventive Medicine, Faculty of Veterinary Medicine, University of Maiduguri, Borno State, Nigeria, [3] Veterinary Teaching Hospital, Faculty of Veterinary Medicine, University of Maiduguri, Borno State, Nigeria, [4] Independent Researcher, [5] Department of Animal Science, Faculty of Agriculture, Borno State University, Nigeria, [6] Department of Veterinary Pathology, Faculty of Veterinary Medicine, University of Maiduguri, Borno State, Nigeria, [7] Independent Researcher [8] Department of Veterinary Public Health and Preventive Medicine, Faculty of Veterinary Medicine, University of Ilorin, Kwara State, Nigeria, [9] Department of Public Health, Al-ansar University , Maiduguri, Borno State, Nigeria
*Correspondence author: asimejamesoba@gmail.com

Abstract: An assessment of outdoor bio-aerosols and particulate exposure was carried out to study and determine the association of the particulates and the organic matter. This was carried out at Trans Amadi industrial area of Port Harcourt where most outdoor sources of atmospheric particles are emitted, due to industrial activities. Seven locations were established for sampling which consist of Azuabie Market, Abuloma Jetty, Jenny & Jessy Street, Mother Cat, Rivoc Road, Royal Palm Estate, and Slaughter/Coca Cola Axis. The condition of temperature, humidity, cloud cover, wind speed and other air pollutants such as carbon monoxide (CO), nitrogen monoxide (NO), nitrogen dioxide (NO_2), sulphur dioxide (SO_2), ozone (O_3), ammonia (NH_3), and particulate matter (PM 2.5) and (PM 10) were considered. Bio-aerosols were determined by open plate sedimentation technique where a prepared culture media plate was opened for 20 minutes for microbes to settle. The study showed abundance and diversity of microorganisms in the atmosphere of the industrial polluted area. PM 10 was significantly higher than other pollutants with 610.97 at Jenny & Jessy Street and Rivoc Road while PM 2.5 was 498.96 at Jenny & Jessy Street and Rivoc Road, followed by Royal Palm Estate with 386.6. The minimum and maximum temperature values in all sampling sites was between 25-35^oC during the sampling time, while the relative humidity was within 37-72%. Wind speed in all sampled sites was 0.78-1.9 m/s. Cloud cover was 47-76% while ozone (O^3) was higher at 131.1 $\mu g/m^3$ at Jenny & Jessy Street and Rivoc Road followed by Azuabie Market which was 114.4 $\mu g/m^3$. The result revealed isolation of four fungal isolates and nine bacterial isolates including *Aspergillus niger, Aspergillus flavus, Aspergillus fumigatus, Penicillum* sp*,* and *Micrococcus* sp*, Klebsiella* sp*, Streptococcus* sp*, Pseudomonas* sp*, Staphylococcus* sp*, Bacillus* sp*, Shigella* sp*, Enterobacter* sp*, Escherichia coli,* were observed.
This study has presented evidence of biological aerosols in soot deteriorated outdoor ambient air.
Keywords: Bioaerosols, Soot-pollution, $PM_{2.5-10}$ concentration, Public-Health, Bacteria, Fungi.

INTRODUCTION

Port Harcourt, the capital of Rivers State, Nigeria has been experiencing series of air pollutions (The Guardian, 2017; CNN, 2018). This has been attributed to increased formation of soot from the actions of artisanal refining of crude oil and the incomplete combustion of hydrocarbon remains being serious health implication to the peoples (Nrior and Esther, 2018; Nrior and Adiele, 2015).

Bio-aerosols are particulate matter of microbial, plant and animal origin released from terrestrial and marine ecosystem into the atmosphere (Morris *et al.,* 2008; Ambrose *et al.,* 2015). They consist of pathogenic and non-pathogenic live or dead bacteria, fungi, high molecular weight (HMW) allergens, endotoxins, mycotoxins, peptidoglycan β (1-3) – glucans, pollen and plant residue fibres (Frohlich-Nowoisky *et al.,* 2016; Peccia and Hernandez, 2006; Udochukwu *et al.,* 2015).

The study of biological aerosols has advanced because of their ability to transmit microbial pathogens, endotoxin, and allergens in both outdoor and indoor environments associated with wide range of public health effects with adverse health impairment issues which has led to many deaths, contagious infections, respiratory diseases, acute toxic effects, and cancer (Eames *et al.,* 2009; Moretti *et al.,* 2018; Cavalazzi *et al.,* 2018; Clark *et al.,* 2018; Drommond *et al.,* 2019; Hogerwerf et al., 2017; Nrior and Chioma, 2017).

Components of bioaerosols range in size from 0.01 µm to 100 µm in diameter (Wang, Chi-Hsun *et al.,* 2015). Bio-aerosols are highly effective for the distribution of pathogenic organisms, allowing genetic exchange between habitats and increasing geographic shift of biomes which can lead to increase antibiotic resistance in bacteria and the potential effects of airborne transmission of genetically modified organisms (Angevin *et al.,* 2008; Folloni *et al.,* 2012; Kawashima and Hama, 2011; Kabir *et al.,* 2016; Ewa and Izabela, 2019).

Recent studies have shown the emerging threat of bio-aerosol spores to animals, plant and the ecosystem (Fisher *et al.,* 2012; Chmiel *et al.,* 2015). Atmospheric bio-aerosols can also have a direct radioactive coercing because they scatter and absorb solar and infrared radiation in the atmosphere posing as cloud condensation nuclei and ice nucleating particles which promote cloud dewdrop freezing that can modify the formation and precipitation efficiency of liquid water, ice and mixed phase clouds, thereby causing an indirect radiative forcing. The changes in cloud properties can exert a significant effect on the climate (Kanji *et al.,* 2017; Boucher *et al.,* 2013; Amato *et al.,* 2015; Christner *et al.,* 2008; Morris *et al.,* 2004; Bauer *et al.,* 2002; Sattler *et al.,* 2001). Diseases transmitted by etiological agents in the atmospheric air include, bronchitis, pneumonia, rhinitis, pulmonary tuberculosis, diphtheria, whooping cough, sclerosis, lung aspergillosis, lung mucormicosis, lung criptococcosis, bronchial mycosis, lung geotrychosis, fungal pneumonia, pleural mycosis and others (Chmiel *et al.,* 2015; Ebisz *et al.,* 2016).

Several studies have been conducted to investigate the characteristics of airborne microorganisms and their association with anthropogenic activities in Port Harcourt city, especially under soot pollution, to elucidate the microbial diversity and potential effects on public health (Nrior and Chioma, 2017). The public health menace caused by inhalation of various types of biological aerosols and particulate matter can mostly depend mainly on their size, chemical composition, microbiological properties and the place of their deposition in the respiratory system (Balasubramanian *et al.,* 2011). This study was conducted to assess bacterial and fungal communities associated with anthropogenic activities at Trans Amadi, Port Harcourt, Rivers State which is essential for public health benefits.

MATERIALS AND METHODS

Study Area

The present study was carried out in Port Harcourt the capital city of Rivers State Nigeria located in the South-South Niger Delta region. The study area was Trans Amadi industrial area (Latitude: 4.812842 Longitude: 7.063289) with a thousand hectare (2,500 acre), the neighbourhood supports a strong manufacturing sector.

Bacterial and Fungal Isolation

Fungal spores and bacteria were cultured from several locations at Trans Amadi using open plate sedimentation technique at 1-meter height above the ground for 20 minutes at each sample site to avoid contamination from soil degradation, after which the petri dishes were covered and transported to the laboratory for incubation.

The culture media used for isolation of bacteria were selective culture medium of Mannitol Salt agar (MSA) and Standard Plate Count agar (PC) while Potato Dextrose agar was used for fungi isolation from Oxoid. The petri plates exposed at various sampling sites were incubated at 37^0C for bacteria and 25^0C for fungi. Bacterial growth was carried out for 48 hours and fungal growth for 72 hours. Colony counts was expressed as the number of colony forming units and calculated using the formula described by Omeliansky.

$N = 5a \times 10^4 (bt)^{-1}$

Where:

N= microbial CFU/m^3 of outdoor air

a= number of colonies per petri dish

b= surface area of the petri dish (cm^2)

t= exposure time (min) Ambrose *et al.,* (2015).

Identification of Microorganisms

Bacteria isolated were characterised by cultural, morphological and microscopically with several biochemical tests such as Citrate, Catalase, Oxidase, Indole, Urease, Voges Proskaur, Methyl Red, according to Bergeys Manual of Determinative Bacteriology (Bergey & Holt, 2000). Fungal colonies were identified based on macroscopic and microscopic examination of the spore and hyphae as described by (Yeasmin *et al.,* 2018).

Data of Environmental Parameters

Air pollution and meteorological data were determined by (AQI) online application system (https://www.iqair.com/nigeria/rivers/port-harcourt). The data collected correspond at the same temporal interval to when the sampling was carried out in each sampling site. The urban aerosol level corresponds to an industrialized city whose contamination mostly comes from hydrocarbons and manufacturing activities. Environmental parameters monitored include temperature, relative humidity, cloud cover, and wind speed. Types of air pollutants monitored are carbon monoxide (CO), sulfur dioxide (SO_2), nitrogen monoxide (NO), nitrogen dioxide (NO_2), ozone (O_3), Ammonia (NH_3) and particulate matter (PM 2.5) and (PM 10).

RESULTS

This study was carried out to assess bio-aerosol associated with soot pollution and to quantify and identify bacteria and fungi in seven different sites at Trans Amadi Port Harcourt. The studied sites were Azuabie Market, Abuloma Jetty, Jenny & Jessy Street, Mother Cat, Rivoc Road, Royal Palm Estate, and Slaughter/Coca Cola Axis. The minimum and maximum temperature values in the sampling sites was between 25-35^0C during the sampling time, while the relative humidity was within 37-72%. Wind speed in all the sampled sites was 0.78-1.79m/s. cloud cover was 47-76% while ozone (O_3) was higher (131.1 μg/m^3) for Jenny & Jessy Street and Rivoc Road followed by Azuabie Market (114.4 μg/m^3). Shown in Table 6. The account of heterotrophic bacteria, enteric bacteria, and heterotrophic fungi, a colony forming unit (CFU) was used, equivalent to the number of colonies observed on each agar plate. Table 1-3 shows the microbial loads at all sampling sites. Four fungal isolates and ten bacterial isolates including *Aspergillus niger, Aspergillus flavus*, *Aspergillus fumigatus, Penicillum sp,* and *Micrococcus sp, Klebsieella sp, Streptococcus sp, Pseudomonas sp, Staphylococcus sp, Bacillus sp, Shigella sp, Enterobacter sp, Escherichia coli* were identified. The fungal species were stained with lactophenol cotton blue stain and identified macroscopically and microscopically shown in Table 4, while the bacterial species were gram stained with biochemical tests prior to identification shown in Table 5. Environmental parameters such as carbon monoxide (CO), sulfur dioxide (SO_2), nitrogen monoxide (NO), nitrogen dioxide (NO_2), and ammonia which are the contributors of particulate matter (PM) was reported due to the public health risk and the data are presented in Table 6.

Table 1: Total Heterotrophic Bacteria Count at Trans Amadi, Port Harcourt

Sample Location	(CFU/M^3)
Azuabie Market	3.6×10^4
Abuloma Jetty	2.2×10^5
Jenny & Jessy Street	2.9×10^4
Mother-Cat	2.0×10^5
Rivoc Road	1.3×10^5
Royal Palm Estate	2.9×10^4
Slaughter/Coca Cola	1.3×10^5

Table 2: Total Enteric Bacteria Count at Trans Amadi, Port Harcourt

Sample Location	(CFU/M^3)
Azuabie Market	1.7×10^5
Abuloma Jetty	4.2×10^4
Jenny & Jessy Street	5.1×10^4
Mother Cat	8.9×10^4
Rivoc Road	3.6×10^4
Royal Palm Estate	3.1×10^4
Slaughter/Coca Cola	1.6×10^5

Table 3: Total Heterotrophic Fungi Count at Trans Amadi, Port Harcourt

Sample Location	(CFU/M^3)
Azuabie Market	7.6×10^4
Abuloma Jetty	6.7×10^3
Jenny & Jessy Street	4.9×10^4
Mother Cat	6.9×10^4
Rivoc Road	2.2×10^4
Royal Palm Estate	6.7×10^3
Slaughter/Coca Cola	4.0×10^4

Table 4: Macroscopic and microscopic characterization of fungal species

Macroscopic characteristics	Microscopic characteristics	Probable *sp*
Initially white, which quickly turns to black	Smooth colored conidiophores and conida. The conidiophores are protrusions from a septate and haline hyphae. The conidial heads appear radial and they split into columns (biseriate). The conidiophore vesicle produces sterile cells known as metulae which support the phialides on the conidiophores	*Aspergillus niger*
Spreading yellow-green colonies	Vesicles bearing phialides over their entire surface, biseriate or uniseriate, conidiophore stipes are hyaline and coarsely roughened, conida are globose to subglobose and pale green in color	*Aspergillus flavus*
Gray-green with a slight yellow reverse	Hyphae are septate and hyaline. Conidial heads are strongly columnar in an undisturbed culture. Conidiophores are smooth-wallet, uncolored	*Aspergillus fumigatus*
Velvety green colonies, spreading with white margin and yellow bottom	Short conidiophores with chains of single called conidia are produced in besipetal succession specialized conidiogenous cell called a phailide produced singly in groups or branched metulae, giving a brush like appearance	*Penicillum sp*

Table 5: Biochemical test results of nine isolates and their identification

Presumptive organisms	Cat	Oxidase	Ind	Methyl red	Voges proskaur	Citrate	HS	Mot
Micrococcus sp	+ ve	− ve	− ve	− ve	+ ve	− ve	+ ve	− ve
Klebsiella sp	+ ve	− ve	− ve	− ve	+ ve	+ ve	− ve	− ve
Streptococcus sp	− ve	− ve	− ve	+ ve	− ve	− ve	− ve	− ve
Pseudomonas sp	+ ve	+ ve	− ve	− ve	− ve	+ ve	− ve	+ ve
Staphylococcus sp	+ ve	− ve	− ve	+ ve	+ ve	− ve	− ve	− ve
Bacillus sp	+ ve	− ve	− ve	+ ve	− ve	+ ve	− ve	+ ve
Shigella sp	+ ve	− ve		+ ve	− ve	− ve	− ve	− ve
Enterobacter sp	+ ve	− ve	− ve	− ve	+ ve	+ ve	− ve	+ ve
Escherichia coli	+ ve	− ve	+ ve	+ ve	− ve	− ve	− ve	+ ve

KEY: + ve = Positive,−ve = Negative, Cat = Catalase, Ind = Indole Production, HS = Hydrogen sulphide production, Mot = Motility

Table 6: Air pollutant concentration and weather conditions that existed at the time of sampling

Source: https://www.iqair.com/nigeria/rivers/port-harcourt

Sample Location	Min. Temp (^{0}C)	Max Temp (^{0}C)	Relative Humidity (%)	Cloud Cover (%)	Wind Speed (M/S)	CO (µg/m^3)	NO (µg/m^3)	NO_2 (µg/m^3)	SO_2 (µg/m^3)	O_3 (µg/m^3)	NH_3 (µg/m^3)	PM 2.5 (µg/m^3)	PM 10 (µg/m^3)
Azuabie Market	25	35	37	58	0.78	727.6	0.5	4.76	8.11	114.4	23	57.01	126.4
Abuloma Jetty	25	34	43	76	1.2	714.3	0.55	4.5	6.97	92.98	23	50.57	119.2
Jenny& Jessy Street	25	32	63	60	2.3	5874.6	2.35	33.24	12.04	131.1	23	498.96	610.97
Mother Cat	25	34	43	76	1.2	714.3	0.55	4.5	6.97	92.98	23	50.57	119.2
Rivoc Road	25	35	63	60	2.3	5874.6	2.35	33.24	12.04	131.1	23	498.96	610.97
Royal Palm Estate	26	35	72	47	2.28	5554	19.0	58.26	14.19	38.62	23	386.6	488.5
Slaughter/ Coca Cola	25	34	53	70	1.79	867.8	0.64	5.06	6.8	79.39	23	55.94	125.6

DISCUSSION

In this study, the presence of airborne bacterial and fungal spores in the atmosphere of Trans Amadi the City of Port Harcourt was investigated. The study examines the public health risk of atmospheric suspended microbial species redistribution on ecosystem health, and human health due to the deterioration of the ambient air. This research was mainly conducted to determine the levels of microorganisms (mainly bacteria and fungi) in seven selected sites at Trans Amadi industrial layout to characterize them to species level. In addition, the present study tends to determine the relationship of these airborne bacteria and fungi pathogens and the development of respiratory diseases in association to soot pollution. These respiratory diseases in the city were reported in various hospitals. The outcome of the study showed that there was abundance of microbial spores in the air of the city although there were significant dissimilarities in the number of bacteria and fungi among the various sites.

The concentrations of bacteria and fungi are found to be associated to the population, soot pollution, industrial activities as well as anthropogenic activities caused by humans. This was concluded due to the fact that the crowded sites with industrial activities which also include vehicle movement was compared to less industrial site Royal Palm Estate.

Human activities seem to be the highest contributing factor to bio-aerosol concentrations in the ambient air. These occurs through sneezing, coughing talking and shedding of debris from skin. Sneezing is the most effective mechanism by which air borne pathogens are easily circulated in their millions in the air (Krishna, 2004). In addition, the particulate droplet from sneezing can increase bacterial and fungal spores which could result and enhance the survival of these airborne pathogens. Both humans, animals and plant released fragments can contain different microbial species. Human activity can generate up to 5,000 bacteria per minute into the ambient air (Smith, 2006). The highest concentration of heterotrophic bacteria was detected in the atmosphere of Abuloma Jetty with 222222 converted to 2.2×10^5 $CFUm^{-3}$ with the use of Plate Count agar. This area was known for legal and illegal hydrocarbon activities with sailing-boats, rowing-boats, jetty, small-boats, boats, narrowboats and barges. The highest concentration of enteric bacteria was recorded in Azuabie Market with 168888 converted to 1.7×10^5 $CFUm^{-3}$ with the use MacConkey agar and the highest concentration of heterotrophic fungi in the atmosphere was recorded in same Azuabie Market with 75555 converted to 7.6×10^4 $CFUm^{-3}$ using Potato Dextrose agar. These figures may be attributed to the population density in the market and other activities associated with distribution of goods and services. Dong and Yao, (2010) reported a threshold concentration value for culturable air borne bacteria. There suggestion was 5000-10000 $CFUm^{-3}$. The concentrations of bacteria in all the sampled sites in this study exceeded the suggested concentration of Dong and Yao, (2010). However, caution should be taken during the assessment of different studies due to dissimilarities in geographical area, level of environmental deterioration, season and time of sampling, human actions, the media used for cultivation, and meteorological dynamics that can influence the growth of organisms (Abdel Hameed et al., 2009; Dong and Yao, 2010). Nrior and Sampson, 2018 reported several number of bacteria (200-8250 $CFUm^{-3}$ observed in the morning and 2650-11850 $CFUm^{-3}$ observed in the evening in Port Harcourt. The Port Harcourt city environment is considered by being among the highest density and intensity of human activity after Lagos and Kano city. Furthermore, ten bacterial species and four fungal species were isolated from the outdoor air environment of the seven sampled sites at Trans Amadi. The level of culturable fungi was suggested as 5000-10000 $CFUm^{-3}$ by Dong and Yao, (2010). The data of this study revealed that the reported level of fungi in the sampled areas are generally higher than the suggested value limit by Dong and Yao, (2010). Based on our findings, the value of certain physicochemical factors is closely comparable, including the temperature and humidity throughout the whole study. These findings indicated that the concentration of fungi might be due to human population density and activities followed by environmental contamination. The data from this study revealed that *Aspergillus niger, Aspergillus flavus, Aspergillus fumigatus* and *Penicillum sp.,* were the identified fungi species in the atmosphere of these assessed sites. *Aspergillus niger and Aspergillus fumigatus* are usually associated with two respiratory diseases in humans, which are known as allergic and invasive aspergillosis. These species seem to be the most recurrently isolated airborne fungi species in several cities. For example, the most frequent genera of fungi isolated from hospital ambient air in Nigeria were *Aspergillus* and *Penicillum* Agwaranze *et al.,* (2020). Similar *Aspergillus*

and *Penicillum* was reported by Nrior and Chioma, (2017). Study also revealed that the genera *Aspergillus, Penicillum,* and *Candida* were isolated from the outdoor air of Uyo Urban area in Akwa Ibom State, Nigeria by Ambrose *et al.,* (2015). Adeyinka *et al.,* (2020) used open plate sedimentation during their study of microflora of fungi in outdoor ambient air in Lagos State, Nigeria and discovered that *Aspergillus* and *Penicillum* spores are abundant in the atmosphere of Lagos State. Thus, these findings are in agreement with our findings. In addition, these and our findings proposed that the possible source of these fungi species is likely to be related. However, a closer investigation of the aforementioned sites revealed that some of the environmental factors might differ. It is worth mentioning that the concentration and distribution of air borne bacteria and fungi species among the various sampled sites were not even or alike. Various environmental factors can influence microbial presence in the atmosphere. These factors include temperature, humidity, wind speed, cloud cover and human activities and population. The type of media used for cultivation, sampling location and height from which the samples are collected can significantly influence the concentration and distribution of these air borne pathogens. A closer look at these seven assessed sites revealed that there were high similarities regarding the aforementioned factors, with exception of human population, and type of activities as well as the deterioration of the atmosphere. Therefore, the observed concentrations and distribution of these airborne pathogens are more likely due to human population density and activities as well as due to the level of anthropogenic activities in the assessed sites. Based on the findings of this present study, a small number of outdoor airborne bacterial and fungal species were identified in the selected sampled sites by using cultivation-dependent methods. Therefore, it is probable to guess that the exact number of the species of bacteria and fungi in ambient air are likely to be underestimated due to the fact that cultivation method cannot cultivate all the microbial species because there is abundance of microbes that might not grow on agar plates but rather can be identified using metagenomics assessment. Several studies concentrated on aquatic and soil environment for antibiotic resistant genes because these are regarded as essential reservoirs of antibiotics resistant genes due to their direct association with human events. Although airborne antibiotic resistant genes may be linked to a known source, numerous studies proposed that the microbial community in the source might be different from those in atmospheric environment (Lin *et al.,* 2018; Yoo et al., 2020). Several studies also recounted the abundance of aerosolized *Pseudomonas* and *Staphylococcus* in the air that can survive harsh atmospheric environment (Gauthier-Levesque *et al.,* 2016; Perrott *et al.,* 2013). Pathogenic organisms and antibiotic resistant genes in bio-aerosol are believed to intermingle with each other. Research also stated that pathogens such as *Pseudomonas* and *Klebsiella* contain antibiotic resistant genes that can cause meningitis, pneumonia, bacteremia, corneal inflammation, and eye antibiotic resistance. Furthermore, prospective pathogenic organisms such as *E. coli, Pseudomonas* and *Staphylococcus* which are mostly detected in the ambience, and reported in this study can contribute to the airborne distribution of antibiotic resistant genes, and their transmission of antibiotics resistance gene through horizontal gene transfer has also been reported by (Kalwasińska and Burkowska, 2013; Yu *et al.,* 2021; Hsu *et al.,* 2022). Aerosol bacteria are believed to possess multi-drug resistant capabilities (Dijkshoorn *et al.,* 2007), besides their increase in human respiratory diseases is hypothetically connected to the prevalence of biological aerosol and antibiotic resistant genes ascending through horizontal gene transfer (Wang *et al.,* 2014).

Although, substantial data on direct antibiotics resistant gene infection through biological aerosols is limited, but it is continually stated in several studies that inhalation through the respiratory tract is the main route through which antibiotics resistant genes enters the human body (Wei and Li, 2016; Wang *et al.,* 2019; Asadi *et al.,* 2020). The detection of airborne distribution of antibiotic resistant genes usually originate from the direct emission of antibiotics resistant bacteria or their reaerosolization due to natural airstreams and various anthropogenic activities Li *et al.,* (2018). Airborne inhalation of antibiotics resistant genes is usually affected by the particulate matter concentration, antibiotics resistant gene, horizontal gene transfer, and environmental deposition (Jin *et al.,* 2021; Xie *et al.,* 2018; Xie *et al.,* 2019; Xie *et al.,* 2021). Several studies proposed that airborne particulate matter is a unique pathway for the environmental distribution of antibiotics resistant genes, and their results show that multiresistant plasmids of pTAir-3 (containing 26 horizontal gene transfer and 10 antibiotics resistant genes), which promotes horizontal gene transfer, can possibly spread antibiotic resistance through conjugative transfer induced inhalable particulate matter (Ling *et al.,* 2013; Zhou *et al.,* 2021). Furthermore, particulate matter can selectively increase the pathogen levels, through anthropogenic activities like soot pollution and such pathogens are more likely to rapidly spread antibiotic resistance. This study showcases the abundance of microorganisms in deteriorated ambient air. The study recorded diverse bacterial and fungal species adapting to soot pollution which can lead to modification of their structural characteristics which can make them more virulent and pathogenic to human hosts. The bacterial species identified are *Micrococcus sp., Klebsiella sp., Streptococcus sp., Pseudomonas sp., Staphylococcus sp., Bacillus sp., Shigella sp., Enterobacter sp.,* and *Escherichia coli,* while the fungal isolates are *Aspergillus niger, Aspergillus flavus, Aspergillus fumigatus* and *Penicillum sp.* Association between these microbes and pollutants can further escalate the burden upon the Rivers State government and the Nation at large. The rapid response to the 2014-2015 EVD in Nigeria by Government provides a good template for addressing the current environmental menace in Port Harcourt and the entire Niger Delta region. There is need for policy makers to make regulations concerning indoor and outdoor bio-aerosol limit in Nigeria due to public health implications that will pave a way for proper legislative frame work to regulate and implement environmental protection laws with enforcement of prosecuting offenders for public health improvement.

CONCLUSION

In this study, the outdoor bacteria and fungi concentrations at Trans Amadi were determined. The study results can be summarized that the presence of biological aerosols in Port Harcourt and their association with anthropogenic activities and soot pollution can be linked as the cause of various human diseases covering not only infectious/respiratory symptoms but also cancer. Result of this study revealed that ambient air in Port Harcourt is highly deteriorated by biological aerosols of bacterial and fungal spores. Continuous exposure to this biological aerosols and soot in Port Harcourt poses a significant health risk among residents. Future work to examine the factors that predict the cycles of microbial spore abundance in the air may pave way for reliable information to public health agencies.

Consent to Publish

All authors granted consent to publish

Disclosure Statement

The authors declare that they have no conflicting interests.

ORCID
Asime Oba ID https://orcid.org/0000-0002-1769-8383
Dr Idris Umar Hambali ID https://orcid.org/0000-0003-4879-7461
Barka John ID https://orcid.org/0000-0002-2199-4265
Jamilu Garba ID https://orcid.org/0000-0002-7294-3695

REFERENCES

Abdul Hameed A, Khoder MI, Yuosa S, Osman AM and Ghanem S. (2009). Diurnal distribution of airborne bacteria and fungi in the atmosphere of Helman area Egypt. Sci Total Environ, 407: 6217-6222. https://doi.org/10.1016/j.scitotenv.2009.08.028.

Ana G, Sridher MK, Bamgboye, EA. (2009). Environmental risk factors and health outcomes in selected communities of the Niger delta area, Nigeria. Perspect. Public Health. 2009 129 (4), 183-191. doi: 10.1177/1466424008094803. PMID:19650553.

Ambrose, I., Nweke, C. O., Umeh, S. C. I., Braide, W. (2015). Prevalence of bio-aerosols in the outdoor air environment in Uyo Urban, AkwaIbom State, Nigeria. Int. Res. J. Microbial., 6(2): 012-019. http:/dx.doi.org/10.14303/irjm.2015.132.

Asadi S, Bouvier N, Wexler AS, Risten part WD. (2020). The coronavirus pandemic and aerosols: Does Covid-19 transmit via expiration particles? Aerosol Sci Technol 54:6, 635-638, DOI: 10.1080/02786826.2020.1749229.

Balasubramanian, R., Nainar, P., & Rajaseka, A. (2011). Airborne bacteria, fungi, and endotoxin levels in residential microenvironments: a case study. Aerobiologia, 21. https://doi.org/10.1007/s10453-011-9242-.

Bauer, H., Kasper-Giebl, A., Loflund, M., Giebl, H., Hitzenberger, R., Zibuschka, F., (2002). The contribution of bacterial and fungal spore to the organic carbon content of cloud water, precipitation and aerosols. Atmos. Res. 64. 109-119.10.1016/S0169-8095(02)00084-4.

Bergey, D. H. 1., & Holt, J. G. (2000). Bergey's manual of determinative bacteriology 9th ed. Philadelphia: Lippincott Williams & Wilkins.

Deguillaume, L., Leriche, M., Amato, P., Ariya, P. A., Delort, A. M., Poschl, U. (2008). Microbiology and atmospheric processes chemical interactions of Primary Biological Aerosols. Biolgeosci. Discuss. 5, 841-870. 10.5194/bg-5-1073-2008.

D. I. Agwaranze, A. C. Ogodo, C. S. Ezeonu, S. T. C. Brown, C. B. Nwaneri and L. M. Husie, (2020). Microbiological assessment of indoor and outdoor air quality in a general hospital in North-East Nigeria. Res. J. Microbiol., 15: 9-4. DOI:10.3923/jm.2020.9.14.

Dijkshoorne L. Nemec A, Scifert H (2007). An increasing threat in hospitals: multidrug-resistant Acinetobacter baumanii. Nat Rev Microbiol 5(12): 939-951. doi: 10.1038/nrmicro1789. PMID :18007677.

Dong S and Yao M. (2010). Exposure assessment in Beijing, China: biological agents, ultrafine particles, and lead. Environ Monit Assess, 170:331-343. https://doi.org/10.1007/s10661-009-1236-7.

Emuren, K., Ordinioha, B. (2016). Microbiological assessment of indoor air quality at different site of a tertiary hospital in South-South Nigeria. Port Harcourt Med. J., 10(2):79-84. DOI: 10.4103/0795-3038.189459.

Ewa, Bragoszewsky. Izabela Biedron (2019). Air Quality and Potential Health Risk Impacts of Exposure to Bacterial Aerosol in a Waste Sorting Plant

Located in the Mountain Region of Southern Poland, Around Which There Are Numerous Rural Areas. Atmosphere. 10.10.3390/atmos10070360.

Fierer, N., Liu, Z., Rodriguez-Hernandez, M., Knight, R., Henn, M., and Hernandez, M. T., (2008). Short-term temporal variability in airborne bacterial and fungal populations. Appl. Environ. Microbiol., 74(1): 200-207.

Fisher, M., Henk, D., Briggs C. (2012). Emerging fungal threats to animal, plant and ecosystem health. Nature 484, 186-194. https://doi.org/10.1038/nature10947.

Frohlich-Nowoisky, J., Kampf, C.J., Weber, B., Huffman, J. A., Powker, C., Andreae, M. O., Lang-Yona, N., Burrows, S.M., Gunthe, S. S., Elber, W., Su, H., Hoor, P., Thimes, E., Hoffman, T., Despres, V. R., and Poschl, U. (2016). Bioaerosols in the Earth System: Climate, health, and ecosystem interactions. Atmos. Res., 182:346-376.

Gauthier-Levesque L, Bonifait L, Taugeon N, Veillette M, Perrott P, Grenier D, Duchaine C (2016). Impact of serotype and sequence type on the preferential aerosolization of *Streptococcus suis*. BMC Res Notes 9(1): 1-7.

Host, S., Larrieu, S., Pascal, L., Blanchard, M., Declercq, C., Fabre, P. (2007). Short-term Associations Between Fine and Coarse Particles and Hospital Admission for Cardiorespiratory Diseases in Six French Cities. Occup. Environ. Med. 65, 544-551.

Hsu, B.-M.; Chen, J.-S.; Hsu, G.-J.; Koner, S.; Nagarajan, V.; Tsai, H.-C (2022). Role of Bioaerosols on the Short-Distance Transmission of Multidrug-Resistant Methicillin-Resistant *Staphylococcus aureus* (MRSA) in a Chicken Farm Environment. Antibiotics 2022, 11, 81. https://doi.10.3390/antibiotics11010081.

Jaenicke, R., (2005). Abundance of cellular material and proteins in the atmosphere. Science 308, 73.

Jain SK (2005). ''Nosocomial Malaria and Saline Flush''. Emergence Infectious Diseases 11. 7: 1099.

Jin L, Xie J, He T, Wu D, Li X (2021). Airborne transmission as an integral environmental dimension of antimicrobial resistance through the "One Health" lens. Crit. Rev Environ Sci Technol 1-22.

Kabir, M. S., Mridha, F., Islam S., Shorifujjaman M. (2016). Microbiological pollutants in air and antibiotic resistance prophile of some bacterial isolates. Johangimagar University, J. Biol. Sci., 5(1): 47-56.

Kanji, Zamin & Ladino, Luis & Wex, Heike & Boose, Yvonne & Burkert-Kohn, Monika & Cziczo, Daniel & Kramer, Martina (2017). Chapter 1: Overview of Ice Nucleating Particles. Meteorological Monographs. 58.10.1175/AMSMONOGRAPHS-D-16-0006.1.

Kalwasińka A, Burkowska A (2013). Municipal landfill sites as sources of microorganisms potentially pathogenic to humans. Environ Sci Process Impacts 15(5): 1078-1086.

Kawashima, Shigeto & Hama, Takehide. (2011). Pollen Dispersal and Hybridization Model for Risk Assessment of Genetically Modified Crops. 10.1007/978-94-007-1359-8_118.

Krishna V. (2004). Textbook of Pathology, Hyderadad, Orient Longman Private Limited.

Li J, Cao J, Zhu YG, Chen QL, Shen F, Wu Y, Xu S, Fan H, Da G, Huang RJ, Wang J, De Jesus AL, Morawska L, Chan CK, Peccia J, Yao M (2018). Global survey of antibiotic resistance genes in air. Environ Sci Technol 52(19): 10975-10984.

Ling AL, Pace NR, Hernandez MT, Lapara TM (2013). Tetracycline resistance and Class 1 integron genes associated with indoor and outdoor aerosols. Environ Sci Technol 47(9): 4046-4052.

Maron, P., Lejon, D. P. H., Carvalho, E., Bizet, K., Lemanceau, P., Ranjard, L., (2005). Assessing genetic structure and diversity of airborne bacterial communities by DNA Fingerprinting and 16SrDNA Clone Library. Atmos. Environ. 39, 3687-3695.

Moretti, Antonio & Pascale, Michelangelo & Logrieco, Antonio. (2018). Mycotoxin risks under a climate change scenario in Europe. Trends in Food Science & Technology. 84.10.1016/j.tifs.2018.03.008.

Morris, C. E., Sands, D. C., Bardin, M., Jaenicke, R., Vogel, B., Leyronas, C., (2008). Microbial and atmospheric processes: an upcoming era of research on bio-meteorology. Biogeosci. Discuss. 5, 191-212.

Morris, C. E., Geogakopoulos, D. G., and Sands, D. C., (2004). Ice nucleation active bacteria and their potential role in precipitation. J. Phys. IV, 121:87-103.

Naess, Ø., Nafstad, P., Aamodt, G., Claussen, B., Rosland, P. (2007). Relationship Between Concentration of Air Pollution and Cause Specific Mortality: Four-Year Exposure to Nitrogen Dioxide and Particulate Matter Pollutants in 470 Neighborhoods in Oslo, Norway. AM. J. Epedemiol. 165, 435-443.

Nriagu, J., Udofia, E. A., Ekong, I., Ebuk, G., (2016). Health risks associated with oil pollution in the Niger Delta, Nigeria. Int. J. Environ. Res. Publ. Health 13(3),346.

Nrior, Renner & Thompson, Esther. (2018). Black Soot: Percentage Source and Aeromicrobiology. International Journal Science and Research (IJSR). 7.10.21275/ART20183354.

Nrior, Renner & Paul, Sampson. (2018). Sources of Black soot and associated microorganisms in Port Harcourt, Nigeria. 10.13140/RG.2.2.10448.40960.

Nrior, R. R. and Chioma, C. I. (2017). Black Sooth in Port Harcourt: Incidence of Pathogenic Microbes Associated with Black Sooth in Indoor Aerosols of Classrooms in Port Harcourt Nigeria. IOSR Journal of Environmental Science, Toxicology and Food Technology (IOSR-JESTFT). 11(12): 43-49.

Nrior, R. R. and Adiele P. (2015). Microbial Aerosol Contamination in a University Campus in Port Harcourt Nigeria. Journal of International Society of Comparative Education, science and technology (ICEST). 2(1): 105-122.

Odebode, A., Adekunle, A., Stajick, J. (2020). Airborne fungi spores distribution in various locations in Lagos, Nigeria. Environ Monit Assess 192, 87. https://doi.org/10.1007/s10661-019-8038-3.

Olowoporoku, A. O., Longhurst, J. W. S., Barnes, J. H., (2012). Framing air pollution as a major health risk in Lagos, Nigeria. WIT Trans. Ecol. Environ. 157, 472-486.

Omeliansky, V. L. (1940). Manual in microbiology. Moscow: USSR academy sciences.

Passananti, M., Vinatier, V., Delort, A. M., Mailhot, G., and Brigante, M. (2016). Siderophores in cloud waters and potential impact on atmospheric chemistry: photoreactivity of iron complexes under sun-simulated conditions. Environ. Sci. Technol., 50(17): 9324-9332.

Peccia, J., Hernandez, M., (2006). Incorporating polymerase chain reaction-based identification population characterization, and quantification of microorganisms into aerosol science: a review. Atmos. Environ. 40, 3941-3961.

Pell, J. L., Metzger, K. B., Klein, M., Flanders, W. D., Mulholland, J. A., Tolbert, P. E. (2007). Ambient Air Pollution and Cardiovascular Emergency Department Visits in Potentially Sensitive Groups. Am. J. Epidemiol. 165, 625-633. https://doi.org/10.1093/aje/kwk051.

Port Harcourt: Why is this Nigerian city covered in a strange sooth. (2018). https://www.google.com/amp/s/amp.cnn.com/cnn/2018/04/26/africa/nigeria-

portharcourt-soot/index.html Assessed 20th December 2021.

Santl-Temkev, Tina, Finster, K., Hansen, B. M., Pasic, L., and Karlson, U. G (2013). Viable methanotrophic bacteria enriched from air and rain can oxidize methane at cloud-like conditions. Aerobiologia (Bologna)., 29(3): 373-384.

Sattler, B., Puxbaum, H. Psenner, R., (2010). Bacterial growth in super cooled cloud droplets. GeoPhys. Res. Lett. 28, 239-242.

Udochukwu, U., Omeje, F. I., Anulude, O. C., Ogechi, O. K. (2015). Microbiome of enclosed air in selected dormitories in University of Port Harcourt. American. J. Res. Commu., 3(5): 217-224.

Vinatier, V., Wirgot, N., Joly, M., Sancelme, M., Abrantes, M., Deguillaume, L., and Delort, A. M. (2016). Siderophores in cloud waters and potential impact on atmospheric chemistry: production by microorganisms isolated at the Puy de Dome Station. Environ. Sci. Technol., 50(17): 9315-9323

Wang FH, Qiao M, Su JQ, Chen Z, Zhou X, Zhu YG, (2014). High throughput profiling of antibiotic resistance genes in urban park soils with reclaimed water irrigation. Environ. Sci. Technol. 48(16): 9079-9085.

Wang Y, Wang C, Song L. (2019). Distribution of antibiotic resistance genes and bacteria from six atmospheric environments: exposure risk to human. Sci. Total Environ 694: 133750.

Wei J, Li Y. (2016). Airborne spread of infectious agents in the indoor environments. Am J Infect Control 44(9): S102-S108.

Weli, E. V. (2014). Atmospheric Concentration of Particulate Pollutants and its Implications for Respiratory Health Hazard Management in Port Harcourt Metropolis, Nigeria. Civ. Environ. Res. 6(5), 11-17.

Wilson, W. E., Mar, T. F., Koenig, J. Q. (2007). Influence of Exposure Error and Effect Modification by Socioeconomic Status on the Association of Acute Cardiovascular Mortality with Particulate Matter in Phoenix. J. Expo. Sci. Environ. Epidemiol. 17, S11-S19. https://doi.org/10.1038/sj.jes.7500620.

Xie J, Jin L, Luo X, Zhao Z, Li X. (2018). Seasonal Disparities in Airborne Bacteria and Associated Antibiotic Resistance Genes in PM 2.5 between Urban and Rural Sites. Environ Sci Technol Lett 5(2): 74-79.

Xie J, Jin L, He T, Chen B, Luo X, Feng B, Huang W, Li J, Fu P, Li X. (2019). Bacterial and antibiotic resistance genes (ARGs) in PM 2.5 from China: implications for human exposure. Environ Sci Technol 53(2): 963-972.

Xie W, Li Y, Bai W, Hou J, Ma T, Zeng X, Zhang L, An T. (2021). The source and transport of bioaerosols in the air: a review, Front Environ Sci Eng 15(3): 44.

Yeasmin, S., Islam, M. S., Sujon, T., Sultana, R., Alam, M. S., Sikdar, B., Islam, M. A., Khalekuzzaman, M. (2018). Molecular and Microscopic Identification of Fungi in Micropropagation of Nodal and Shoot Tip Culture of Orange, Int. J. Pure App. Biosci. 6(6): 6-19. http://dx.doi.org/10.18782/2320-7081.

Yoo K, Yoo H, Lee J, Choi EJ, Park J. (2020). Exploring the antibiotic resistome in activated sludge and anaerobic digestion sludge in an urban wastewater treatment plant via metagenomics analysis. J. Microbiol 58(2): 123-130.

Yu Y, Liang Z, Liao W. Ye Z, Li G, An T. (2021). Contributions of meat waste decomposition to the abundance and diversity of pathogens and antibiotic-resistance genes in the atmosphere. Sci. Total Environ 784: 147128.