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Interaction Between Building Design and Indoor Airborne Microbial Load in Nigeria

[1]S.A. Wemedo, [2]P.N. Ede and [2]A. Chuku

[1]Department of Applied and Environmental Biology, [2]Institute of Geosciences and Space Technology, Rivers State University of Science and Technology, Nkpolu-Oroworukwo, P.M.B. 5080, Port Harcourt, Nigeria

Corresponding Author: S.A. Wemedo, Department of Applied and Environmental Biology, Rivers State University of Science and Technology, Nkpolu-Oroworukwo, P.M.B. 5080, Port Harcourt, Nigeria

ABSTRACT

Studies on building design and microbial load in buildings in Port Harcourt metropolis was done in wet and dry seasons and during the day and at night periods. Different microbiological media were used to determine the level of microbial populations and physiological types in the sampling sites. Microbial counts ranged from 1.16×10^2-4.0×10^2 CFU 30 min^{-1} exposure to air (wet season) and 8.6×10^2 to 2.93×10^3 CFU 30 min^{-1} exposure to air (dry season). Microbial populations were more in dry season than in wet season. Mean microbial counts were 1.05×10^3 CFU 30 min^{-1} and 9.7×10^2 CFU 30 min^{-1} exposure to air during the day and night periods, respectively. Microbial counts were higher during the day than at night. Seven organisms isolated in all the sites include: *Bacillus* sp., *Enterobacter* sp. and *Staphylococcus* sp. (bacteria) and *Cladosporium* sp., *Mucor* sp., *Penicilium* sp. *and Rhizopus* sp. (fungi). Some genera occurred in all sites and were more prevalent while others did not occur in all the sites and were less prevalent. Generally, more bacterial genera were isolated during the dry season than during the wet season, whereas the reverse was the case for fungi.

Key words: Airbone, seasons, sampling, populations, physiological, microbial load

INTRODUCTION

Indoor environments are fundamental environmental factors capable of impacting health (Cobanglu and Kiper, 2006; Gocgeldi *et al*., 2011). Air quality of indoor environments is one of the main factors affecting the health, well-being and productivity of people (Gocgeldi *et al*., 2011). The effect on health rises as exposure to and density of air pollution increases (Hoskins, 2007; Li *et al*., 2007). The problem of indoor air quality is caused by microorganisms present in the air which include bacteria, moulds and viruses (Dawes and Sutherland, 1991; Riberon *et al*., 2002; Toflum, 2004; Fanger, 2006; Chen *et al*., 2006; Gocgeldi *et al*., 2011). These biological contaminants, carried by particles suspended in air, enter human body through breathing and usually cause diseases of the respiratory system (PEOSH, 1997; Smith *et al*., 2000). Biological particles such as animal and insects allergens, viruses, bacteria and fungi can cause allergic reactions or infectious diseases (USEPA, 2003; Shukla and Shukla, 2011).

Studies carried out by Mayo Clinic (2002) concluded that microorganisms can get indoors through heating, ventilation and air conditioning systems, doors, windows, cracks in walls, water system, or shoes and clothes of people working or visiting the building. An indoor environment with

excess moisture will enhance the growth of moulds and other biological contaminants (Ede *et al.*, 2008; Al-Sheikh, 2008). Fungal spores have long been known as one of the important environmental bio-particles causing dermatitis, respiratory and cardiac diseases along with allergic manifestation in human beings (Singh, 2001; Shukla and Shukla, 2011). Air-borne microbial load in a building can be regarded as significant when identified as causes of illness and discomforts; and insignificant, when their presence makes no impact on the health or general well-being of the building occupants (Burge, 1990; AIHA, 2003).

Microbial presence indoors constitutes biological air pollutants especially when their numbers increase due to favourable conditions (Gocgeldi *et al.*, 2011). Thus indoor air quality depends on the level of the biological contaminants and the factors which enhance their growth and multiplication in the indoor atmosphere. Other factors which determine air quality indoors include building structure and location, poor design and ventilation system as well as interior redesign (Kreiss, 1990; Gocgeldi *et al.*, 2011). Also, numbers and types of fungal spores in air depend on the time of day, weather, season and geographical location (Wadhwani, 1994; Shukla and Shukla, 2011).

Provision of adequate housing has been a problem in developing countries like Nigeria. Shortage of decent accommodation particularly in cities has resulted in individuals occupying bungalows or rooms above specified capacity. More so, in the quest to provide for themselves with urgent accommodation, people have resorted to building houses outside required specifications and/or at indecent locations. Despite this problem, there is no available information on the indoor microbial air quality of living homes in Port Harcourt metropolis. It is therefore on this basis that this study was designed to assess the effect of building design (structure and site of location) on the indoor microbiological air quality.

MATERIALS AND METHODS

Study area: The study area was Port Harcourt metropolis in Rivers State, Southern Nigeria. The area is located in the low coastal region of Niger Delta and it records high rainfall in most months of the year. It is characterized by high humid atmosphere particularly during the wet season. The sampling area was divided into three main zones namely: zone A (Rivers State University of Science and Technology) zone B (Creek road Waterfront area) and zone C (Orazi area). The sampling area was designated into seven sites with zone A housing 5 sites namely:

Site 1: Main library hall
Site 2: Science Faculty Lecture theatre
Site 3: Applied and environmental biology department
Site 4: Postgraduate hostel room
Site 5: Block 'C' female undergraduate hostel room
Site 6: Zones B and C housed site 6 a room
Site 7: Two-bedroom apartment

These sites represent different physiographic locations as regards the factors that may influence microbial growth in the atmosphere. The sampling design was purposive in that the researchers had to decide that certain building environment (based on structure and site) are likely to harbor more microorganisms than others. This led to choice of the different sampling sites.

Building design of sampling sites: Each sampling site had its peculiar building design in relations to size, interior decorations, ventilation and number of persons occupying it at a time. Physical conditions of the sampled rooms in terms of building layout, construction materials and ventilation were observed and considered. Site 1 is a large hall with very low head-roof made of hollow pot floor slabs; German-floored having rows of windows at two parallel sites of the walls. The hall is crammed with wooden chairs, tables, bookshelves with books and cubicles for reading. It lacked fans and had no functional air conditioners. Average of 100 persons uses this hall for at least 2 h at a time. Site 2 is a large lecture theatre with high head-roof of suspended gypsum board it had no windows, no ceiling and no fans. There are two outlets at opposite ends and provision for central writing desk built in stepwise plan. Average of 80 persons occupy this lecture theatre for at least 3 h at a time. Site 3 is a classroom with formica covered tables round the walls and only one entrance door on the wall separating the room and corridor. It has one ceiling fan and average of 30 persons occupy the room for at least 3 h at a time; the dimension is 7.0 m^2. Site 4 is 3.0 m^2 with head-roof of 2.8 m a single entrance door and windows on the opposite walls. The floor is cemented and the room fitted with one ceiling fan. Two persons occupy the room. Site 5 is 4.0-5.0 m, it has a head-roof of 3.1 m high; a single entrance door with windows on opposite walls. The floor is cemented and covered with nylon carpet and fitted with a ceiling fan. Eight persons occupy the room originally designed to accommodate 2 persons. Site 6 is a room covered with zinc sheet and the head-roof is 3 m with a thick-cemented floor. It has only one entrance door, a window each on opposite plywood walls and adjoining rooms on both ends. Average of 8 persons occupy the room as living room. Site 7 is a two bedroom apartment with two windows on adjacent walls of rooms 1 and one window on outward wall of room 2. The sitting room adjoined to the dinning room, has four windows on each side of the walls and the head roof is 3.0 m. Bedrooms and sitting room each has a ceiling fan with nylon carpet and average of four persons occupy this flat.

Media used for analysis: Media used for isolation and enumeration of microorganisms include nutrient agar, blood agar, chocolate agar and McConkey agar for bacteria; Sabouraud's Dextrose agar for fungi. The media were prepared in accordance with the manufacturer's specifications. The wide choice of media was to give fair chance for different physiological types of microorganisms present in the atmosphere to grow and thus be isolated.

Microbiological analysis of air: Microbiological analysis of indoor air was carried out using sedimentation method called culture settling plate technique one of the methods proposed by APHA (Vanderzant and Slittstoeser, 1992; Salustiano *et al*., 2003). This method is a simple, easy and cheap, air sampling method employed for the purpose of enumeration and isolation of microorganisms from indoor atmosphere in this study. This method was adopted in this study due to non availability of other microbiological air sampling equipment in our locality; more so, to enable us provide baseline information on the level of microbial populations and types in different category of living homes of the study area.

In this method, petri dishes (in duplicate) containing freshly prepared sterile agar media were exposed to the sites and left to stand open for 30 min. In this way, microorganisms were allowed to impinge on the agar surfaces. After the period of exposure, the agar plates were closed and incubated at 37°C for 24-48 h. After incubation, colonies that developed were counted and recorded and taken as the total number of microorganisms enumerated in colony forming units per 30 min (CFU 30 min^{-1}) exposure to air. Colonies were also observed for their cultural characteristics namely: size of colony, color/pigmentation, texture, outline, elevation, edge, translucency, odor and surface appearance.

Sub-culturing of discrete colonies of different cultural types purified all bacterial and fungal isolates and used for characterization procedures. Pure bacterial isolates were characterized using the following standard tests: Gram stain, motility test and biochemical reactions which include catalase, coagulase, oxidase, methyl-red, indole, Voges-proskauer, citrate utilization, starch hydrolysis and sugar fermentation tests. The characterized bacteria were identified on the basis of their cultural, morphological and physiological characteristics, as described by Buchanan (1994), Cowan and Steel (1974) and Winn *et al*. (2006).

Standard tests performed to characterize fungal isolates included macroscopy to observe colony morphology-size, shape, color, texture, surface appearance, microscopy by needle mount method (Harrigan and McCance, 1990) to observe sexual and asexual reproductive structures like sporangia, conidial head, arthrospores and vegetative mycelium. Sugar fermentation tests were also carried out for fungal classification. The characterized isolates were identified to Burnett (1976), Haley and Collaway (1978), Olds (1983) and Winn *et al*. (2006). The sampling period lasted for two seasons, wet season (April-October, 2005) and dry season (November, 2005-March, 2006). Sampling was carried out twice a month throughout the sampling period, both at day and night hours.

Analysis of variance was employed to test for significant difference between the day and night microbial count and as well as between dry and wet season counts.

RESULTS

Results of microbiological analysis of air in the various sites are shown in Tables 1 and 2. Daytime counts ranged from 6.2×10^1 CFU 30 min^{-1} exposure to air in sites 4 and 7 (lowest counts) to 2.22×10^2 CFU 30 min^{-1} exposure to air in site 5 (highest counts). During the night period, the microbial counts ranged from 5.2×10^1 CFU 30 min^{-1} in site 7 (lowest counts) to 1.75×10^2 CFU 30 min^{-1} in site 5 (highest counts) during the wet season. The mean microbial counts were 1.40×10^2 CFU 30 min^{-1} during the day and 1.16×10^2 CFU 30 min^{-1} during the night. During the dry season, microbial counts in the day ranged from 4.4×10^2 CFU 30 min^{-1} exposure to air in site 4 (lowest counts) to 1.49×10^3 CFU 30 min^{-1} exposure to air in site 5 (highest counts). In the night, the microbial counts ranged from 4.1×10^2 CFU 30 min^{-1} exposure to air in site 7 (lowest counts) to 1.44×10^3 CFU.

Table 1: Diurnal and seasonal microbial populations of the sampling sites

	Microbial populations			
	Dry season ($\times10^3$ CFU 30 min^{-1})		Wet season ($\times10^2$ CFU 30 min^{-1})	
Sampling sites	Day	Night	Day	Night
1	1.25	1.18	1.62	1.42
2	1.41	1.22	1.78	1.29
3	0.76	0.72	1.21	1.05
4	0.44	0.43	0.62	0.58
5	1.49	1.44	2.22	1.75
6	1.40	1.39	1.76	1.55
7	0.59	0.41	0.62	0.52
Mean	1.05	0.92	1.40	1.16

Table 2: Mean seasonal microbial populations of the sampling sites

	Microbial populations	
Sampling sites	Dry season ($\times10^3$ CFU 30 min^{-1})	Wet season ($\times10^2$ CFU 30 min^{-1})
1	2.43	3.00
2	2.53	3.10
3	1.48	2.26
4	0.86	1.20
5	2.93	4.00
6	2.79	3.30
7	0.99	1.16
Mean	2.00	2.57

Table 3: Microbial types isolated from the different sampling sites

	No. of organisms isolated							
Type of organisms	Site 1	Site 2	Site 3	Site 4	Site 5	Site 6	Site 7	Total
Bacteria								
Staphylococcus sp.	125	13	72	25	154	141	45	696
Bacillus sp.	12	7	13	18	8	13	9	80
Enterobacter sp.	0	0	0	1	2	1	1	5
Fungi								
Cladosporium sp.	2	2	2	0	9	3	0	48
Mucor sp.	3	5	1	4	14	11	5	43
Rhizopus sp.	5	6	4	6	12	7	8	26
Penicillium sp.	0	4	3	0	11	4	4	18

30 min^{-1} exposure to air in site 5 (highest counts). Mean microbial counts during the day were 1.05×10^3 CFU 30 min^{-1} exposure to air and during the night, microbial counts were 9.7×10^2 CFU min^{-1} exposure to air.

Total microbial counts during the wet season ranged from 1.16×10^2 to 4.0×10^2 CFU 30 min^{-1} exposure to air and from 8.6×10^2 to 2.93×10^3 CFU 30 min^{-1} exposure to air in the dry season. Site 7 had the lowest total microbial counts of 1.16×10^2 CFU 30 min^{-1} and site 5 had the highest microbial counts of 4.0×10^2 CFU 30 min^{-1} during the wet season; site 4 had the lowest counts of 8.6×10^2 CFU 30 min^{-1} while site 5 had the highest microbial counts of 2.93×10^3 CFU 30 min^{-1} during the dry season. The mean microbial counts for the wet and dry seasons were 2.57×10^2 and 2.00×10^3 CFU 30 min^{-1}, respectively. Microbial counts were generally higher in all sites during the dry season than during the wet season. Site 5, which is crowded with the greatest number of occupants per space, recorded the highest microbial counts of 3.32×10^3 CFU 30 min^{-1} followed by site 6 with microbial counts of 3.11×10^3CFU 30 min^{-1} exposure to air. The count of microorganisms for site 1 was 2.74×10^3 CFU 30 min^{-1} while those of site 2 were 2.83×10^3 CFU 30 min^{-1}. Microbial populations of site 3 and 7 were 1.71×10^3 CFU 30 min^{-1} and 1.11×10^3 CFU 30 min^{-1}, respectively. The least number of microorganisms were isolated from site 4 with counts of 8.5×10^2 CFU 30 min^{-1} exposure to air, though as had been noted previously this is a hostel room of about the same capacity as site 5, it is however occupied by two persons.

The varieties of microorganisms isolated in this study are shown in Table 3. The bacterial genera included *Bacillus* sp. *Enterobacter* sp. and *Staphylococcus* sp. while the fungal genera were *Cladosporum* s.p., *Mucor* sp., *Penicillium* sp. and *Rhizopus* sp. Results showed that some genera were isolated from all the sites and were more prevalent while others did not occur in all

Table 4: Seasonal distribution of organisms

Type of organisms	Seasonal frequency of the isolates	
	Dry season	Wet season
Bacteria		
Staphylococcus sp.	628	67
Bacillus sp.	64	16
Enterobacter sp.	2	3
Total	694	86
Fungi		
Cladosporium sp.	20	30
Mucor sp.	13	28
Rhizopus sp.	9	17
Penicillium sp.	6	12
Total	48	87

the sites and were less prevalent. Seasonal distribution of organisms isolated during this study are shown in Table 4. Generally, more bacterial genera were isolated during the dry season than during the wet season whereas the reverse was the case for fungi.

DISCUSSION

Every organism that is capable of causing air pollution must be airborne. This means that the environmental conditions of the sites as related to building design must be conducive for the microorganisms to be airborne and cause pollution. The environmental conditions most favourable for airborne microorganisms are dry, hot and airy. The study revealed that micrbial counts were higher during the day than at night period. The reason may be that there is increased activities in the indoor environments during the day than at night. Also, dry season had higher microbial load in the study sites compared to the wet season which had lower microbial load. Statistical analysis showed significant different ($p<0.05$) between the day and night microbial counts and between dry and wet season counts. Site 5 recorded the highest microbial load because of very poor ventilation due to overcrowding caused by eight people occupying a room originally designed to house two people and their luggage in the same room. The room trapped dust and because of frequent movement of too many occupants in and out of the room for various activities, more opportunity was created for microorganisms to be introduced into the room through clothing, shoes and other materials. This condition was made unbearable in the wet season because the environment was stuffy, damp and practically airless inside. In contrast, site 4 had lower microbial numbers than site 5 because the room was well ventilated and spacious enough to allow the free flow of air. Only two people occupy this room just as it was designed to be, thereby reducing the chances of microorganisms being introduced into the room. Proper ventilation and reduced degree of activity resulted in low microbial number for this particular site. This agreed with the study of Gocgeldi *et al.* (2011), who reported that the total organism count in homes of adequately ventilated rooms was lower than inadequately ventilated rooms.

The environment of site 6 encouraged the presence of microorganisms due to poor ventilation, permanent closure of the windows and large number of people occupying the room. These created suitable conditions that supported growth and activities of microorganisms and hence high microbial loads were recorded in the site. Also, site 1 which has low head-roof, is poorly ventilated

and stuffy most times; many people also occupy the place at a time. These situations created a condition that encouraged and supported high microbial load. In site 2, the room lacked windows, fans or air conditioners and was constantly occupied by many people at a time. The environmental conditions resulted in dust and other particles being blown up due to frequent movement of persons and because of poor circulation of air, the dust settles and remains, thereby increasing the microbial load of the room in dry season. Similar situation was observed by other researchers in thier findings that as the number of people living in a house rises, so does the count of organisms in the air (Gocgeldi *et al*., 2011). The building conditions of site 3 and 7 were generally the same. They are well ventilated and housed a few people at a given time. During the dry season, the sites remain airy because the windows were properly situated which resulted in good circulation of air coupled with fans installed in the rooms, hence there was reduced number of microorganisms particularly in the wet season.

Three genera of bacteria and four fungal genera were isolated and characterized during this study. These microbial species were also isolated by other researchers during their study on indoor environments (Salustiano *et al*., 2003; Al-Sheikh, 2008; Shukla and Shukla, 2011). *Staphylococcus* sp., *Bacillus* sp., *Mucor* sp. and *Cladosporium* sp. occurred in all the sites, *Penicillium* sp. and *Rhizopus* sp occurred in five sites out of the seven sites (Table 3). *Penicillium* sp. occurred in sites 1, 2, 3, 5 and 6 not in sites 4 and 7, whereas, *Rhizopus sp.* was isolated from sites 2, 3, 5, 6 and 7 not in sites 1 and 4. *Enterobacter* sp., did not occur in sites 1, 2 and 3 but were isolated from sites 4, 5, 6 and 7. *Staphylococcus* sp., were more prevalent in the sites that had more occupants, because they were regularly shed from human skin and mucus membrane. *Bacillus sp.* were the next prevalent in all the sites while *Enterobacter* sp. was the least prevalent. The most prevalent fungal genera were *Cladosporium* sp., followed by *Mucor* sp and *Rhizopus* sp., respectively. *Penicillium* sp.was the least prevalent. Al-Sheikh (2008) and Shukla and Shukla (2011) reported that *Cladosporium* sp., *Penicillium* sp. and *Aspergillus* sp. were most common during their studies. The only contradiction was *Penicillium* sp. which was found to be least prevalent in the present study. Generally, more bacterial organisms were isolated during the dry season than wet season while the reverse was the case for fungi which occurred more in wet season than in dry season (Table 4). The reason may be that during dry season the weather conditions (elevated temperature) activated the growth of bacteria better than that of fungi. More so, the dampness of the materials during wet season provided good substrate for the mycelial growth of the fungi.

In conclusion, building design determined the microbial quality of the various sites. Sites whose building design did not include vents, proper situation of windows and doors, as well as low head-roof gave high microbial numbers and types. Sampling sites that were occupied beyond the original capacity even with adequate vents, well positioned windows and doors also yielded high microbial counts. Also, sites whose building design failed to take into consideration the effect of the surrounding yielded high microbial load. This study therefore recommends that adequate ventilation be provided for buildings used as living homes and for other purposes in addition to proper and regular cleaning of the room environment. More so, use of rooms and buildings should follow the designed capacity and where possible, multiple uses for houses should be avoided.

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