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Microbiological Analysis of Air Microflora of Unilorin Microbiology Department

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ABSTRACT Air is considered one of the least hospitable environments for microbes because it has fewer nutrients and supports relatively fewer organisms. Exposure to bioaerosols containing airborne pathogenic microorganisms and their by-products can cause respiratory disorders and air-borne diseases. The objective of this research was to determine the air microflora present at the Department of Microbiology of University of Ilorin, Kwara state, Nigeria and with particular emphasis on pathogenic microorganism. In this study microbiological samples were collected through settling plate method using Nutrient Agar and Potato Dextrose Agar from four sampling sites which were in pair at Unilorin Microbiological Department. All numeric data were subjected to T-test at 95% confidence level. Bacteria characterization was made based on colonial morphology, cellular characters through staining techniques and biochemical reaction tests while the fungal isolates were characterized based on their macroscopic and microscopic characteristics. The bacterial load ranged from 9.3 ± 1.92 cfum^{-3} to 15.5 ± 5.39 cfum^{-3} while the fungal load ranged from 4.9 ± 1.24 cfum^{-3} to 7.8 ± 2.11 cfum^{-3}and there were no significant difference within each pair of sampling site. The result shows that the Department falls below suggested recommended limit of microorganisms' concentration of outdoor air by National Institute of Occupational Safety and Health and World Health Organization and may therefore constitute no risk to the staff and students of the Department. Regular study of this kind is recommended at various places to forestall dangers to health due to air microorganisms.

KEYWORDS: Microorganisms, Microflora, Species, Pathogenic.

I. INTRODUCTION

Air serves as means of transportation or dispersal medium for microorganisms. Air microflora occurrence is relatively small in number compared to soil and water (Oden, 2021). Air was considered one of the least hospitable environments for microbes because it has fewer nutrients and supports relatively fewer organisms (Habiba, 2020). Although air as a medium is not suitable for the survival and multiplication of microorganisms, the concentration of fungi spore in outdoor air (e.g., polluted farming area) can reach up to 3×109 spores/m^3 (National academic press, 2020). Aeromicrobiology is the study of living microbes which are suspended in the air. These microbes are referred to as bioaerosols. The main components of the bioaerosol include bacteria, viruses and unicellular organisms, fungi, algae, mites, insect debris/animal epithelia, and their byproducts (WHO 1988; Moldoveanu 2015; EPA 2020). The origin of these bioaerosol are pets (such as dogs, birds and cat), building materials, plants (e.g pollen, allergens, odors), and their effects can be aggravated by the heating modes (temperature, humidity), the degree of ventilation, carpets, and tissues (mites). Institutions are public places occupied by numerous students, lecturers and other staff almost every day and there are high levels of activities that can cause higher levels of airborne fungi and bacteria. The quantity of the air microflora of indoor and outdoor air of institutions is very important because it has a direct impact on the state of health of the students and staff of the institutions (Naruka and Gaur; 2013).

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Microbes that are found in the air get there accidently by being introduced from another source unlike soil microbes that can be regarded as native to their environment. Indeed, certain human activities, such as waste disposal, waste treatment, agriculture and industry, have the potential to release microbes into the air. Soil is a major source of bioaerosols as one gram of soil can hold millions (or even more!) bacterial and fungal cells, some of which exist in their spore form, making it easier for them to survive the harsh conditions of the atmosphere when they do become suspended (Habiba; 2020). Air microflora can be studied from indoor air or outdoor air. Chirca (2019) reported that bio-contaminants are present everywhere in indoor and outdoor air, even in highly controlled environments (e.g., the operating rooms of modern hospitals). It was reported that People spent most of the time (90% or above) in indoor areas, e.g., houses, schools, university rooms, colonial buildings like shops, cars, planes, and workplaces (Moldoveanu, 2015). Chirca (2019) observed that indoor air has microorganisms/spores at all time, and in fact in clean rooms there is present of around 25 spores/m3 microorganisms/spores. The major sources of spread and transportation of microorganisms in indoor environments are fans, humidifiers, coolers, etc which are usually colonized by fungi (e.g.,*Aspergillus, Penicillium, Phialophora, and Geotrichium*), bacteria and yeast (Dubey and Maheshwari, 2014). The indoor and outdoor environments are interlinked together as a result, microorganisms spread randomly within them. Roshan et al. (2019) stated that the indoor to outdoor ratio (I/O) of bio-contaminants is very important in the estimation of their sources. Roshan et al. (2019) observed that the (I/O) of < 1 of sampling sites supports the fact that, the outdoor air might serve as the origin of indoor air bio-contaminants.

Commonly found microorganisms in indoor/outdoor air are fungi and bacteria; the prevalent genera of fungi are *penicillium* and *aspergillus* while bacillus and clostridium are most common genera of bacteria found in indoor air. However, in outdoor air the commonest genera of fungi are clostridium and *sporobolomyces.* Apart from these two genera *Aspergillus*, *Aternaria*, *Pytophthora* and *Erysiphe*; some forms of yeasts like basidiospores, arcospores are also found. The fragments of mycelium and conidia molds along with bacterial flora like B*acillus, Clostridium, Sarnia, Micrococcus, Corynebacterium* and A*chromobacter* are widely found (Oden, 2021). The impact of microorganisms such as bacteria and fungi in pollution of outdoor and indoor air quality is enormous. Awad et al (2018) and Nevalainen et al. (2015) reported that bacteria, fungi and viruses contributed approximately 5–34% pollutant towards total indoor air pollution. It is important to know that the concentration of these pollutants serve as an indicator in assessment of microbial air quality (Yassin and Almouqatea, 2010). If the concentration of these microorganisms exceeded the recommended limit or there is long-term exposure to infectious bioaerosols, these can lead to various health problems such as asthma (Reboux et al., 2019), respiratory diseases (Wu et al., 2019), allergic issues (Stark et al., 2005), Sick building syndrome (SBS) (Laumbach and Kipen, 2005), hypersensitivity (Yassin and Almouqatea, 2010), headache, rhinitis and other nosocomial infections (Flannigan et al., 2003; Mendell et al., 2011; Śmiełowska et al., 2017).

II. METHODOLOGY

Air samples were collected from the Department of Microbiology, University of Ilorin, Ilorin, Kwara state, from four sampling site at the department because the site serves as entrances and sources of outdoor air in the department. These four sampling sites were down floor upper stair case (DSUSC), down floor lower stair case (DSLSC), first floor upper stair case (FFUSC) and first floor lower stair case (FFLSC). The air samples were taken with two duplicate plates in each of the sites, first plate was represented with ‘a’ while it duplicates was represented with ‘b’. Duplicate plates of the prepared petri dishes containing potato dextrose agar (used for fungal culture) and nutrient agar (for bacteria culture) were exposed for a period of 10 minutes. The samples were collected once weekly for 10 weeks during rainy season (in the month of July to September)

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A. Purification of Bacterial Isolates

Distinct representative colonies were selected using colonial and morphological characteristics. They were purified by sub-culturing onto a sterile nutrient agar plate using streaking method. Pure cultures obtained were then transferred onto separate nutrient agar slant in MacCartney bottles and were incubated at 37^0C for 24 hours. After growth has been observed the agar slants were stored in the refrigerator at 4^0C as stock culture.

B. Purification of Fungal Isolates

Distinct representative colonies were selected and purified by sub-culturing onto a sterile PDA plate using streaking method for non–filamentous fungi but for the mycelia fungi little portion of their hyphae was picked with the aid of sterile inoculating needle onto the surface of set plate of PDA and incubated at 25^0C for 3-4 days. The process of sub-culturing was repeated until pure culture was obtained. The pure isolates obtained were transferred into sterile set plate of PDA slant in macCartney bottles and incubated at 25^0C for 3-4 days. This agar slants obtained were kept in the refrigerator at 4-8^0C until required for use (Fawole and Oso, 2004).

C. Identification of Bacterial Isolates

Bacteria characterization was made based on colonial morphology, cellular characters through staining techniques and biochemical reaction tests. The colonial morphology used were shape, elevation, edge of colony, optical characteristics, consistency, colonial surface and pigmentation of the colony. Cellular characters used include Gram Staining where Gram positive organisms stained purple while gram negative stained red (Aneja, 2003). The researcher also did Spore Staining,of the bacterial isolates, the vegetative cells stained red while the spores stained green (Fawole and Oso, 2004). Biochemical tests of all the bacteria test were done for reliable identification. All biochemical tests done were motility test, catalase test, coagulase test, methyl red test, Voges-Proskauer test, indole production test, citrate utilization test, oxidase test, urease test, starch hydrolysis test, oxidative and fermentative utilization of sugars, carbohydrate fermentation tests and triple sugar iron test. After all the tests, reference was then made to Bergey's manual of Determinative Bacteriology to get the names of the bacterial isolates.

D. Identification of Fungal Isolates

The colonial morphology of the pure culture of each fungus was examine and recorded. Microscopic examination of each pure fungal culture was also made in both vegetative and sporulating stages for the microscopic examination. A portion of mycelium was picked from the colony and tested out carefully on a glass slide containing a drop of methylene blue and then covered with cover slip. The slides were examined under the x10 objective lens and x40 objective lens. The fungal isolates were characterized based on their macroscopic and microscopic characteristics (Fawole and Oso, 2004). They were then identified using standard mycological texts (Onions *et al.,* 1981; Samson and Van Reenen-Hoekstra, 1988)

E. Statistical Analysis

The statistical analysis employed were mean, standard deviation, standard mean of error and T-test using IBM SPSS statistics 21 package.

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III. RESULTS AND DISCUSSION

A. Bacterial Isolates from Outdoor Air of Unilorin Microbiology Department

A total of eleven species were isolated. They were *Nesseria sicca, Serratia fonticola, Bacillus alvei, Staphylococcus aureus, Klebsiela pneumoniae, Acetobacter calcoaceticus, Bacillus polymyxa, Listeria monocytogenes, Corynebacterium xerosis, Bacillus coagulans* and *Staphylococcus epidermis.*

B. Colonial Counts of Bacterial Isolates

The bacterial count throughout the period of research was presented in Table 1.

Table 1: Colonial Counts of Bacterial Isolates

Study Area	Week									
	1	2	3	4	5	6	7	8	9	10
DSUSC[a]	10	13	0	20	20	5	5	26	20	28
DSUSC[b]	9	59	5	7	22	9	1	24	4	15
DSLSC[a]	24	17	5	8	17	18	10	14	17	11
DSLSC[b]	20	26	11	13	13	8	8	18	6	7
FFUSC[a]	16	17	6	6	8	5	3	23	10	3
FFUSC[b]	19	2	3	13	13	13	5	1	12	12
FFLSC[a]	32	15	0	9	3	5	24	20	15	20
FFLSC[b]	38	13	5	5	11	2	20	21	17	18

Key: Superscript 'a' means first plate while 'b' signifies the duplicate

The highest count was in week two from site DSUSC[b] where there were 59 colonial counts, the least count was in third week at site DSUSC[a] and FFLSC[a] there were no colony count.

C. Colonial Morphology of the Isolated Bacteria and their Biochemical Characteristics

Most of the isolates were gram positive rods and they were *Bacillus alvei, Bacillus polymyxa, Listeria monocytogenes, Corynebacterium xerosis and Bacillus coagulans. Staphylococcus aureus* and *Staphylococcus epidermis* were gram positive cocci. The gram negative cocci were *Nesseria sicca* and *Acetobacter calcoaceticus* while *Serratia fonticola* and *Klebsiella pneumoniae* are gram negative rod. All the bacterial isolates were indole negative and none of them produce hydrogen sulphide. All of them were glucose and fructose fermenter. All of them also have catalase enzyme. All the isolates except *Serratia fonticola* ferment sucrose. *Nesseria sicca, Bacillus alvei, Staphylococcus aureus, Listeria monocytogenes, Bacillus coagulans* and *Staphylococcus epidermis* are urease positive while others are urease negative. The citrate positive isolates are *Serratia fonticola, Nesseria sicca, Staphylococcus aureus, Listeria monocytogenes, Corynebacterium xerosis, Bacillus coagulans* and *Staphylococcus epidermis.*

D. Bacterial Concentration of the Air

The concentrations of the bacteria in the four sites are presented in Table 2.

Table 2: Bacterial Concentration of the Air

Study area	Range	Mean ±SEM (n=10) (Cfum^{-3})
DSUSC[a]	0-28	14.7 ± 3.01
DSUSC[b]	1-59	15.5± 5.39
DSLSC[a]	5-24	14.1± 1.78
DSLSC[b]	6-26	13.0± 2.01
FFUSC[a]	3-23	9.7± 2.14
FFUSC[b]	1-19	9.3± 1.92
FFLSC[a]	0-32	14.3± 3.20
FFLSC[b]	5-38	14.4± 3.31

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The air concentrations of bacteria of DSUSC[a] was 14.7 ± 3.01 cfum^{-3}, DSUSC[b] was 15.5 ± 5.39 cfum^{-3}, DSLSC[a] was 14.1 ± 1.78 cfum^{-3}, DSLSC[b] was 13.0 ± 2.06 cfum^{-3}, FFUSC[a] was 9.7 ± 2.14 cfum^{-3}, FFUSC[b] 9.3 ± 1.92 cfum^{-3}, FFLSC[a] was 14.3 ± 3.20 cfum^{-3} and FFLSC[b] was 14.4 ± 3.31 cfum^{-3}. The concentration was presented in mean ± SEM (Standard Error of Mean). The highest bacterial concentration was found in DSUSC where DSUSC[a] was 14.7 ± 3.01 cfum^{-3} and DSUSC[b] was15.5 ± 5.39 cfum^{-3} while the least concentration found in FFUSC where FFUSC[a] was 9.7 ± 2.14 cfum^{-3} and FFUSC[b] 9.3 ± 1.92 cfum^{-3}. The overall concentration of bacteria of the down stair samples was found to be more than that of the first floor where DSUSC was more concentrated than DSLSC while FFLSC was more concentrated than FFUSC.

E. Statistical Analysis of the Bacterial Isolates

The results of the colonial counts were subjected to paired T-test. Each duplicate plate from closely the same site was also compared with T-test and this was presented in Table 3.

Table 3: T-test of Bacterial Colonial Count

S/No	Sampling Site	Paired Samples Statistics				Paired Samples Correlation		Paired Samples Test							
		mean	N	Std. Deviation	Std. Error Mean	Correlation	Sig.	Paired Differences					T	df	Sig. (2-tailed)
								mean	Std. Deviation	Std. Error Mean	95% CID				
											Lower	Upper			
1	DSUSC[a]	14.70	10	9.53	3.01	0.23	0.53	-0.80	17.54	5.55	-13.34	11.75	-0.14	9	0.89
	DSUSC[b]	15.50	10	17.05	5.39										
2	DSLSC[a]	14.10	10	5.62	1.78	0.38	0.28	1.10	6.82	2.15	-3.78	5.98	0.51	9	0.62
	DSLSC[b]	13.00	10	6.51	2.06										
3	FFUSC[a]	9.70	10	6.77	2.13	-0.29	0.43	0.40	10.29	3.25	-6.96	7.76	0.12	9	0.91
	FFUSC[b]	9.30	10	6.06	1.91										
4	FFLSC[a]	14.30	10	10.11	3.20	0.88	0.001	-0.10	5.15	1.63	-3.79	3.59	-0.06	9	0.95
	FFLSC[b]	14.40	10	10.48	3.31										

P = 0.05 T-Table = 2.101 CID = Confidence Interval of the Difference

The table above shows paired T-test of the results of the colonial counts. Each duplicate plate from closely the same site was compared with paired T-test and these shows that the null hypothesis that there is no different in the concentration of the pair was correct because the calculated t does not exceed the tabulated t at p = 0.05.

F. Fungal Isolates from the Outdoor Air of Unilorin Microbiology Department

A total of ten fungi were isolated. They were *Aspergllus fumigatus, Penicillium spinulosum, Aspergillus niger, Cladosporium herbarium, Saccharomyces cerevisiae, Motierella ramanniana, Rhizopus stolonifer, Mucor racemosus, Paecilomyces fumosorosus* and *Mucor plumbeus.*

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G. Colonial Counts of Fungal Isolates

As presented in Table 4, the highest colonial count was found in fifth week with a total count of 30 colonies at site DSUSC[a]. The least count was found in first week at site DSUSC[a], DSUSC[b], and FFUSC[b] with only one colonial count, second week at site FFLSC[a], third week at site FFUSC[a] and FFLSC[b], week four at site FFUSC[a], week six at site DSLSC[a] and also in the ninth week at site DSUSC[a] and DSLSC[b]. However, site FFLSC[a] has no colonial count in the third week.

Table 4: Colonial Counts of Fungal Isolates

Study Area	Week									
	1	2	3	4	5	6	7	8	9	10
DSUSC[a]	1	6	7	5	30	4	12	2	1	5
DSUSC[b]	1	4	4	3	19	6	13	4	19	5
DSLSC[a]	2	2	3	6	14	1	5	2	8	6
DSLSC[b]	2	6	5	4	12	4	6	10	1	5
FFUSC[a]	3	2	1	3	13	4	13	11	5	4
FFUSC[b]	1	4	4	1	12	12	15	10	3	7
FFLSC[a]	2	1	0	2	8	11	11	6	7	4
FFLSC[b]	2	3	1	7	9	8	7	7	2	8

H. Concentration of Fungal Isolates

As presented in Table 5, the fungal concentration of Site DSUSC[a] was 7.3 ± 2.72, DSUSC[b] was 7.8 ± 2.11 $cfum^{-3}$, DSLSC[a] was 4.9 ± 1.24 $cfum^{-3}$, DSLSC[b] was 5.5 ± 1.06 $cfum^{-3}$, FFUSC[a] was 5.9 ± 1.46 $cfum^{-3}$, FFUSC[b] was 6.9 ± 1.59 $cfum^{-3}$, FFLSC[a] was 5.2 ± 1.27 $cfum^{-3}$ and FFLSC[b] was 5.4 ± 0.96 $cfum^{-3}$. The highest concentration was found in DSUSC where site DSUSC[a] was 7.3 ± 2.72 $cfum^{-3}$ and site DSUSC[b] was 7.8 ± 2.11 $cfum^{-3}$ while the least concentration was found in DSLSC where DSLSC[a] was 4.9 ± 1.24 $cfum^{-3}$ and DSLSC[b] was 5.5 ± 1.27 $cfum^{-3}$. The overall concentration of the down stair was found to be more than the overall concentration of the first floor.

Table 5: Fungal Concentration of the Air

Study Area	Range	Mean ± SEM (n=10) ($cfum^{-3}$)
DSUSC[a]	1-30	7.3 ± 2.72
DSUSC[b]	1-19	7.8 ± 2.11
DSLSC[a]	1-14	4.9 ± 1.24
DSLSC[b]	1-12	5.5 ± 1.06
FFUSC[a]	1-13	5.9 ± 1.46,
FFUSC[b]	1-15	6.9 ± 1.59
FFLSC[a]	0-11	5.2 ± 1.27
FFLSC[b]	1-9	5.4 ± 0.96

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I. Statistical Analysis of Fungal Isolates

The result of the colonial counts of fungal isolates was subjected to paired T-test. Each duplicate plate from closely the same site were also compared and this was presented in Table 6

Table 6: Statistical Analysis of Fungal Isolates

S/NO	Sampling site	Paired samples statistics				Paired samples correlation		Paired samples test							
		mean	N	Std. deviation	Std. error mean	correlation	Sig.	Paired differences					t	df	Sig. (2-tailed)
								mean	Std. deviation	Std. Error Mean	95% CID				
											lower	upper			
1	DSUSC[a]	7.30	10	8.62	2.72	0.58	0.08	-0.50	7.21	2.28	-5.66	4.66	-0.22	9	0.83
	DSUSC[b]	7.80	10	6.68	2.11										
2	DSLSC[a]	4.90	10	3.93	1.24	0.38	0.27	-0.60	4.06	1.28	-3.50	2.30	-0.48	9	0.65
	DSLSC[b]	5.50	10	3.34	1.06										
3	FFUSC[a]	5.90	10	4.61	1.46	0.78	0.01	-1.00	3.23	1.02	-3.31	1.31	-0.98	9	0.35
	FFUSC[b]	6.90	10	5.04	1.59										
4	FFLSC[a]	5.20	10	4.02	1.27	0.60	0.07	-0.20	3.29	1.04	-2.56	2.15	-2.56	9	0.85
	FFLSC[b]	5.40	10	3.02	0.96										

P = 0.05 T-table = 2.101 CID = confidence interval of the difference

Table 6 shows the statistical analysis of fungal isolates. The result of the colonial counts was subjected to paired T-test and each duplicate plate from closely the same site were compared. The result of these samples shows that the null hypothesis that there is no different in the concentration of the pair was correct because the calculated t does not exceed the tabulated t at p = 0.05.

In this study of air microflora of Unilorin Microbiology Department eleven species of bacteria were isolated which were *Nesseria sicca, Serratia fonticola, Bacillus alvei, Staphylococcus aureus, Klebsiela pneumonia, Acetobacter calcoaceticus, Bacillus polymyxa, Listeria monocytogenes, Corynebacterium xerosis, Bacillus coagulans and Staphylococcus epidemis.* The bacterial isolates in this study which include S*taphylococcus aureus, Bacillus sp,* and *Corynebacterium sp,* were also isolated in the work of Umana et al (2018) where eight species were isolated which were: *Bacillus* spp, *Staphylococcus aureus, Escherichia coli, Salmonella* spp, *Micrococcus* spp, *Citrobacter* spp, *Proteus* spp and *Corynebacterium* spp while there is diversity in the other bacteria isolates in both researches and this is likely due to variation in geographical locations, seasons of the research and areas cover by the researchers.

Ten species of fungi were isolated in this study and they were: *Aspergillus fumigates, Penicillium spinulosum, Aspergillus niger, Cladosporium herbarium, Saccharomyces cerevisiae, Motierella ramanniana, Rhizopus stolonifer, Mucor racemosus, Paecilomyces fumosoroseus and Mucor plumbeus.* In research done by Raisa et al (2023) done at different indoor and outdoor sites on a college campus in Bengaluru isolated twelve fungi species which were *Clasdosporium sp, Aspergillus niger, Penicillim sp, Rhizopus sp, Fusarium sp, Mucor sp, Alternaria sp, Nigrospora sp, Trichoderma sp, Aspergillus flavus, Neurospora sp and Aspergillus fumigates.* The fungi species isolated by these researchers were similar to species isolated from this study except *Fusarium sp, Alternaria sp, Nigrospora sp, Trichoderma sp* and *Neurospora sp* that were not isolated while in this present study *Saccharomyces sp, Motierella sp* and *Paecilomyces sp* were not isolated by aforementioned researchers.

The concentration of bacterial isolates in this study was more than fungi isolates and this was in agreement with what was obtained by Raisa et al., (2023) and Yassin and Amougatea, (2010). This can be because bacteria can be dispersed through droplets during coughing, sneezing or skin peeling and can be maintained in aerial suspension (Soto et al., 2009).

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In this study, the most frequently isolated bacterial was *Staphylococcus aureus* and this is not in accordance with research work of Ana et al., (2021) that frequently isolates *Micrococcus species*. Mathew et al., (2023) reported that pathogenic *S. aureus* is the most frequently isolated pathogen in skin and soft tissue infections. They further stated that the infectious ability varies from superficial infections with local symptoms to monomicrobial necrotizing fasciitis, and that these infections can lead to gradual manifestation to serious complication and even death of the infected person.

In this study *Aspergillus niger* was the most frequently isolated fungal isolate. Ahmad et al, (2021) performed research on indoor and outdoor microbiological air quality in naturally and mechanically ventilated university libraries where they discovered that *Clasdosporium spp* and *Aspergillus spp* were the most dominant fungi isolated. This might however be because of higher scope of their studies. Environmental surveillance of filamentous fungi in three tertiary care hospital in Greece indicated that *Aspergillus flavus* and *Aspergillus niger* were the most prevalent species (Panagopoulou et al., 2002) but in this sudy *A. flavus* was not isolated this might be because the type of microorganism present in the air varied with different places and time of sampling.

It is important to note that Aspergillus sp may be tolerable for healthy individuals, it may however be dangerous for high-risk patients. The spores readily invade the airways and could lead to aspergillosis in immune-compromised host (Bowers et al. 2009). *Aspergillus flavus and Aspergillus niger* were reported by Ana et al (2022) to contaminate dried figs after and before harvest which consequently produce aflatoxins (AFs) and achratoxin A (OTA). In order to minimize growth of these filamentous fungi synthetic fungicides are used which have negative impact on the health of human.

The bacterial concentration in this study ranges from 0.93×10^1 to 1.55×10^2 cfu/m^3 while the fungal concentration ranges from 0.49×10^1 to 0.78×10^1 cfu/m^3. The suggested recommended limit of bacterial concentration of outdoor air by National Institute of Occupational Safety and Health (NIOSH) was given as 10^3 cfu/m^3, the American Conference of Government Industrial Hygienists (ACGIH) suggested the limit as 500 cfu/m^3 for culturable bacteria (Kalogerakis *et al.,* 2005) while Gorny and Dutkiewiez (2002) earlier presented to WHO expert in Berlin, proposed residential limit values of 250 cfu/m^3 for bacterial concentration. The research of Makut *et al.* (2014) exceeded the above recommended limits of bacterial concentration of outdoor air but this study did not exceed the limits and this shows that microflora of the outdoor air of the Microbiology Department of University of Ilorin is alright at the period of this study.

It was discovered that DSUSC has the highest concentration for both bacteria and fungi and this can be because it is the busiest of the four sites. In relation to this discovery Soto et al (2009) also discovered in their research that minimum bacterial concentration occurred where there is no activities of human being while maximum concentration were found in busiest area. They however stated that fungal concentration was not affected by present or absent of human being because fungi present in the air were not human-borne.

IV. CONCLUSION

In conclusion, it is important to note that our environment is full of millions of microorganisms some of which might be detriment to our wellbeing if their populations reach the infectious dose. As it was realized in this study and some other studies that population of microorganisms varied with time. It is very essential to evaluate the quality of air which human breathe whether indoor or outdoor. The number and type of airborne microorganisms can be used to determine the degree of air cleanliness as a means of determining the source of human discomfort and certain airborne microbial infection. It was discovered that the microbial load of DSUSC was the highest of all the sampling sites. It is however essential to note that in this study the microbial load of the outdoor microflora of the Microbiology Department of the University of Ilorin did not suggest any risk to the staff and students of the Department at the period of this study because the concentration of the air microflora is below the recommended limits.

I recommended that this type of study should be performed regularly so as to create awareness of the likely microorganisms in the aerosols at different period and place. This will help in realizing the probable risk that those living at that particular place might face and also the control measures that can be provided to

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prevent infections that the pathogenic microorganism can cause. The pathogenic bacteria can be avoided to some extent by ensuring cleanliness of our environment which can serve as source or carrier of these microorganisms. In addition, an environment that is heavily loaded with microorganisms can be cleaned using any of the following methods:

(a). Gaseous chemicals like hypochlorus acid (kills S*treptococci* and *Staphylococci*), quarternary (kills *Salmonella*) and glycols (kills nearly all the microorganism in a litre of heavily contaminated air within 15 seconds);

(b). Suppressing the emergence or distribution of dust such as applying oil emulsion to floors, will produce an effective control over dust and dust borne bacteria;

(c). Electrostatic precipitation where dust particles containing microorganisms are subjected to electric field when the dust containing air is passed through as the dust particles through collector which contains both negative and positive electrode; and

(d). Heat sterilization by passing air through a heated pipe to produce sterile air.

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