



Isolation and Comparative Analysis of Airborne Microorganisms in Different Location within Biology Department, Ibrahim Badamasi Babangida University Lapai, Niger State

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Abstract

Airborne microorganisms, also known as bioaerosols, are key determinants of indoor air quality and human health, particularly in densely populated environments such as universities. This study investigated the diversity and distribution of airborne bacteria and fungi across classrooms, laboratories, libraries, and toilets within the Department of Biology, Ibrahim Badamasi Babangida University, Lapai, Niger State, Nigeria. Air samples were collected using settle plates and an Anderson air sampler, followed by culture-based isolation and characterization. Bacterial isolates were identified using colony morphology, Gram staining, and a series of biochemical tests. Fungal isolates were characterized based on microscopic features and colony morphology. Results revealed six bacterial species: *Staphylococcus aureus*, *Bacillus anthracis*, *Streptococcus pneumoniae*, *Pseudomonas aeruginosa*, *Corynebacterium diphtheriae*, and *Micrococcus* sp., and four fungal species: *Aspergillus* sp., *Mucor* sp., *Candida* sp., and *Fusarium* sp. The highest microbial loads were detected in laboratories and toilets, indicating these areas as hotspots for airborne contamination. *Staphylococcus aureus* and *Aspergillus* sp. were the most prevalent across all locations, suggesting that human activity, environmental dust, and poor ventilation are major contributors to microbial dissemination. These findings suggested the need for routine monitoring, improved ventilation, and enhanced hygiene practices to mitigate airborne microbial exposure, thereby safeguarding the health of students and staff in educational settings.

Keywords: Bacteria, Fungi, Airborne, diseases, Biology

Introduction

Airborne microorganisms, or bioaerosols, comprising bacteria, fungi, viruses, and spores, are key determinants of indoor air quality and human health (Ghosh, 2015; Jabeen et al., 2023). Prolonged exposure to these microorganisms can cause respiratory infections, allergies, and other health issues, particularly among children and young adults. University environments, where students, staff, and faculty spend extended periods in classrooms, laboratories, hostels, and dining areas, present complex microenvironments for microbial accumulation and transmission (Sadigh et al., 2021). Factors such as human activity, occupancy density, ventilation, and hygiene practices strongly influence the concentration and diversity of airborne microorganisms across these spaces (Song et al., 2024). Indoor air quality in educational institutions has emerged as a significant public health concern. Poor ventilation, high occupancy, and environmental conditions such as temperature and humidity can enhance microbial proliferation and dispersal (Sadigh et al., 2021; Wang et al., 2022; Jabeen et al., 2023). Children and young adults are especially susceptible, highlighting the need for systematic monitoring of bioaerosols in learning environments. Comparative analyses of microbial loads across different university spaces provide critical insights into exposure risks and factors influencing microbial distribution.

Isolation and characterization of airborne microorganisms enable the identification of both culturable and non-culturable species, providing comprehensive data on microbial diversity and distribution. Culture-based approaches, including plate exposure and air impaction, coupled with molecular techniques such as 16S rRNA and ITS sequencing, facilitate detailed profiling of bacterial and fungal communities (Akinyemi et al., 2021). Such analyses can reveal spatial variations in microbial load associated with human activity, sanitation practices, and building design, highlighting high-risk areas and informing strategies for air quality management (Ghosh, 2015; Jabeen et al., 2023).

In many Nigerian universities, including Ibrahim Badamasi Babangida University, Lapai, inadequate ventilation, poor maintenance, and overcrowding can lead to elevated airborne microbial concentrations. These microorganisms, originating from human occupants, building materials, and outdoor air, pose potential health risks, including infections, allergies, and illness-related absenteeism, which may negatively impact academic performance (Jabeen et al., 2023; Sadigh et al., 2021). Despite these risks, there is limited data on the diversity and distribution of airborne microorganisms across different university environments in Nigeria, leaving exposure patterns under-assessed (Song et al., 2024; WHO, 2017).

This study, therefore, aims to isolate and comparatively analyze airborne microorganisms—including bacteria and fungi across diverse environments within Ibrahim Badamasi Babangida University, Lapai. By identifying areas of high microbial load and characterizing microbial communities, the research seeks to generate evidence-based insights to guide targeted interventions, such as improved ventilation, routine cleaning, and building maintenance. These measures are critical for safeguarding the health of students and staff and for ensuring university environments remain safe, hygienic, and conducive to learning and academic productivity.

Materials and Methods

Study area

The study was carried out within the Biology Department of Ibrahim Badamasi Babangida University, Lapai, Niger State, Nigeria.

Sample Collection

Air samples were collected from classrooms, laboratories, the library, and toilets using both the settle plate technique and an Andersen air sampler. Nutrient agar plates were exposed at approximately 1 m above ground level for 1 hour to simulate the human breathing zone.

Preparation of media

All culture media were prepared according to manufacturers' specifications and sterilized by autoclaving at 121°C for 15 minutes. Glassware and work surfaces were sterilized using standard laboratory procedures.

Nutrient Agar

Twenty-eight (28) grams of Nutrient agar was weighed and dispensed in a 1000ml capacity conical flask, and 1000ml distilled water was added gradually and gently shaken to have a homogeneous mixture. Cotton and aluminum foil were used as a cover (stopper). It was then autoclaved at 121°C for 15 minutes. The media was allowed to cool at 45 °C, and 15 to 20ml aliquot were dispense in to the sterile petri dishes in the presence of flame and allowed to solidify.

Isolation and identification of bacteria

Distinct bacterial colonies were sub-cultured to obtain pure isolates. Identification was based on colony morphology, Gram staining, and biochemical tests including catalase, coagulase, oxidase, indole, citrate, urease, methyl red–Voges Proskauer, and carbohydrate fermentation assays, following standard microbiological protocols (Cheesbrough, 2000; 2006).

Isolation and Identification of Fungi

Fungal isolates were purified on potato dextrose agar. Microscopic identification was performed using lactophenol cotton blue staining, and species were identified based on hyphal structure, spore morphology, and colony characteristics using standard fungal identification keys (Samson et al., 1984).

Results

Bacteria Morphology

The morphological and biochemical characterization revealed six distinct bacterial isolates from airborne samples in different locations. These include *Staphylococcus aureus*, *Bacillus anthracis*, *Streptococcus pneumoniae*, *Pseudomonas aeruginosa*, *Corynebacterium diphtheriae*, and *Micrococcus sp.*

TABLE 1: Morphological, Biochemical and Cultural Profiles of Airborne Bacterial Isolates

Morphological Physical Appearance		Cell shape	Gram reaction	Catalase	Oxidase	Coagulase	Citrate	Urease	Indole	Methyl/Red	Motility	Spore	Lactose	Glucose	Maltose	Sucrose	Manni	Probable organisms
Golden smooth	Yellow	Cocci	+	+	-	+	-	-	-	-	-	-	+	-	-	+	+	<i>Staphylococcus aureus</i>
Distinctive tailed edge	curly,	Rod	+	+	-	-	+	+	+	+	-	+	-	-	+	+	-	<i>Bacillus anthracis</i>
Small translucent	white	Diplo Cocci	+	-	-	-	-	-	-	-	-	-	+	+	+	+	-	<i>Streptococcus pneumonia</i>
Slightly curved		Rod	-	+	+	-	+	+	-	-	+	-	-	-	-	-	-	<i>Pseudomonas aeruginosa</i>
Small circular grey	smooth	Rod	+	+	-	-	-	-	-	-	-	-	-	+	+	-	-	<i>Corynebacterium diphtheriae</i>
Creamy circular	white	Cocci	+	+	+	-	-	-	-	-	-	-	+	+	+	-	+	<i>Micrococcus sp.</i>

Key = +; Positive, -; Negative

Distribution of Bacteria

The bacterial distribution across locations showed *Staphylococcus aureus* was present in all areas, indicating its wide airborne spread and adaptability. *Bacillus anthracis* appeared mainly in the laboratory and toilet, while *Pseudomonas aeruginosa* was found in multiple sites. *Micrococcus sp.* and *Corynebacterium diphtheriae* were notably present in classrooms and laboratories, suggesting human and environmental sources of contamination.

Table 2: Distribution of Bacteria Isolated from Different Location

Sampling Area	Detected Bacterial Species
Laboratory	<i>S. aureus</i> , <i>B. anthracis</i> , <i>S. pneumoniae</i> , <i>P. aeruginosa</i> , <i>Micrococcus</i> spp.
Toilet	<i>S. aureus</i> , <i>B. anthracis</i> , <i>P. aeruginosa</i> , <i>C. diphtheriae</i>
Classroom	<i>S. aureus</i> , <i>C. diphtheriae</i> , <i>Micrococcus</i> spp.
Library	<i>S. aureus</i> , <i>S. pneumoniae</i>

Fungi isolate

The fungal isolates exhibited distinct morphological features that enabled their identification. The isolates included *Aspergillus sp.*, *Mucor sp.*, *Candida sp.*, and *Fusarium sp.* These fungi displayed variations in hyphae structure, spore types, and colony color, which are characteristic of airborne fungal contaminants typically associated with indoor environments.

Table 3 Morphological Features of Fungi Isolates

Colony morphology	Hyphae	Rhizoid	Conidia	Conidiospore	Probable fungi species
Moderately rapid growing colonies that appeared white	Septate	Present	Conidia	Conidiospore	<i>Aspergillus sp.</i>
Yeast growing that fill up the petridish colonies are floccose white and cottony but change to grey with abundant woody aerial mycellum	Non septate	Absent	Sporangia	Sporangiospore	<i>Mucor sp.</i>

Colonies appear light due to green with moderate growth	Septate	Absent	Conidia	Conidiospore	<i>Candida sp.</i>
Fast growing, pale or bright colour cottony aerial mycelium	Septate	Absent	Conidia	Conidiospore	<i>Fusarium sp.</i>

Distribution of Fungi

The distribution of fungal isolates across different locations showed *Aspergillus sp.* was the most prevalent, especially in laboratory and toilet areas. *Mucor sp.* was also detected in both locations, while *Fusarium sp.* appeared only in the classroom. *Candida sp.* was primarily found in the laboratory, suggesting that environmental and human activity levels influence fungal presence and diversity.

Table 4: Distribution of Fungi Isolated from Different Location

Location	Dominant Fungal Genera Recovered
Laboratory	<i>Aspergillus, Mucor, Candida</i>
Toilet	<i>Aspergillus, Mucor</i>
Classroom	<i>Fusarium</i>
Library	<i>Aspergillus</i>

Discussion

The present study on the *isolation and comparative analysis of airborne microorganisms in different environments within a school* revealed a diverse range of bacterial and fungal species, suggesting that indoor air serves as a major reservoir for microbial contaminants. The bacterial isolates identified included *Staphylococcus aureus*, *Bacillus anthracis*, *Streptococcus pneumoniae*, *Pseudomonas aeruginosa*, *Corynebacterium diphtheriae*, and *Micrococcus sp.*, while the fungal isolates were *Aspergillus sp.*, *Mucor sp.*, *Candida sp.*, and *Fusarium sp.* These microorganisms are known to be part of the normal environmental flora but can also act as opportunistic pathogens under favorable conditions (Li et al., 2021; Adebayo et al., 2022).

The predominance of *Staphylococcus aureus* in all sampled locations indicates its high prevalence in the indoor air of the school environment. This organism is commonly associated with human skin and mucosal surfaces, suggesting that human activities such as talking, sneezing, and movement contribute significantly to its dispersion in air (Ekhaise&Ogboghodo, 2011). Similar findings by Ghosh et al. (2020) reported that *S. aureus* was frequently isolated from classrooms and laboratories due to high human traffic and inadequate ventilation. The presence of *Bacillus anthracis* and *Micrococcus sp.* further indicates the influence of environmental dust and spore-forming bacteria, which are known to survive in air for prolonged periods (Madigan et al., 2022).

In contrast, *Pseudomonas aeruginosa* and *Corynebacterium diphtheriae* were detected mainly in laboratory and toilet areas. These bacteria are often associated with moisture and organic residues, suggesting that humidity and sanitation levels may affect bacterial diversity in those areas (Nevalainen et al., 2015). The detection of *Streptococcus pneumoniae* in the laboratory and library could indicate occasional respiratory contamination from infected individuals, as the bacterium is a known respiratory pathogen (WHO, 2022).

The fungal isolates *Aspergillus sp.*, *Mucor sp.*, *Candida sp.*, and *Fusarium sp.* reflect the typical composition of airborne mycoflora in indoor environments. *Aspergillus sp.* was the most dominant, found in the laboratory, toilet, and library. This genus is widely distributed in air due to its efficient spore dispersal mechanism and ability to thrive on dust particles (Nielsen et al., 2020). *Mucor sp.* and *Fusarium sp.* were present in the toilet and classroom, respectively, indicating their preference for damp or nutrient-rich environments (Samson et al., 2019). *Candida sp.*, a yeast-like fungus, was primarily isolated from the laboratory, suggesting possible human origin since *Candida* species are part of the normal skin and mucosal flora (Cheesbrough, 2016).

The distribution patterns indicate that microbial contamination is influenced by human presence, ventilation, cleanliness, and humidity levels within the school environment. The laboratory and toilet showed the highest microbial diversity, consistent with findings from previous studies that associated such environments with higher microbial load due to frequent use and inadequate air circulation (Kumar & Kalpana, 2020). This highlights the need for improved hygiene practices, regular disinfection, and proper ventilation to reduce airborne microbial concentration in schools, thereby minimizing the risk of infections among students and staff.

Conclusion

This study concludes that school environments contain a variety of airborne bacteria and fungi, with the highest prevalence in frequently used and poorly ventilated areas. The predominance of *Staphylococcus aureus* and *Aspergillus sp.* suggests that human activity and environmental factors play major roles in microbial distribution. Continuous exposure to these airborne microorganisms may increase the risk of infections, especially in immunocompromised individuals. Hence, monitoring and control of indoor microbial load are essential for safeguarding public health within educational environment.

Recommendations

The following recommendations are proposed to reduce airborne microbial contamination and improve indoor air quality within the Biology Department and similar educational environments:

1. Provision of adequate natural and mechanical ventilation in classrooms, laboratories, libraries, and toilets to reduce the accumulation and spread of airborne microorganisms.
2. Implement regular monitoring of airborne bacteria and fungi to enable early detection of high microbial loads and prompt corrective actions.
3. Enforce consistent and thorough cleaning, especially in laboratories and toilets, using appropriate disinfectants to minimize microbial contamination.
4. Encourage good personal hygiene practices and reduce overcrowding in classrooms and laboratories to limit human-related microbial dissemination.
5. Address water leaks, poor drainage, and high humidity levels to prevent fungal growth and reduce the prevalence of moulds such as *Aspergillus* and *Mucor* species.

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