

ORIGINAL ARTICLE

Airborne bacteria and fungi monitoring in a microbiology laboratory

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ABSTRACT

The presence of airborne microorganisms in laboratory environments may increase the risk of microbial exposure among laboratory personnel. Indoor bioaerosols can affect air quality and potentially pose health risks if environmental conditions are not adequately controlled. This study aimed to identify airborne bacteria and fungi present in the office room of the Microbiology Laboratory, Faculty of Medicine, Universitas Jenderal Achmad Yani. Air sampling was performed using the passive settle plate method at three sampling points, with Tryptic Soy Agar (TSA) used for bacterial isolation and Sabouraud Dextrose Agar (SDA) used for fungal isolation. Environmental measurements during sampling recorded a temperature of 25.1°C and a relative humidity of 63%. Bacterial and fungal growth were observed on TSA and SDA plates, respectively, with bacterial colony counts ranging from 0 to 24 colonies. A total of six bacterial isolates were successfully recovered. Bacterial identification was performed based on colony morphology observation, Gram staining, biochemical tests, and molecular analysis using polymerase chain reaction (PCR) and DNA sequencing. Fungal identification was conducted based on macroscopic characteristics and microscopic examination using Lactophenol Cotton Blue staining. Molecular analysis identified the bacterial isolates as *Staphylococcus hominis*, *Staphylococcus epidermidis*, *Mammaliococcus sciuri*, and *Stutzerimonas stutzeri*, whereas fungal isolates were morphologically consistent with *Penicillium* sp. and other suspected hyaline filamentous fungi. The predominance of Gram-positive bacteria and the detection of airborne fungi may be associated with limited ventilation, indoor humidity, and human-related activities within the laboratory environment. These findings demonstrate the diversity of indoor bioaerosols in a laboratory environment and highlight the importance of routine microbiological air monitoring, humidity control, and adequate ventilation to support occupational health and laboratory safety.

Keyword: airborne bacteria, bioaerosols, fungi, indoor air quality, microbiological air contamination, settle plate method

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INTRODUCTION

Indoor air quality is an important factor influencing the health and safety of building occupants. Poor indoor air conditions may lead to the accumulation of particulate matter, chemical contaminants, and biological agents known as bioaerosols, including airborne bacteria and fungi.^{1,2} These microorganisms may originate from human activities, ventilation systems, building materials, and resuspended dust particles within indoor spaces.³ Laboratory environments, particularly microbiology laboratories, represent unique settings where microbial exposure may occur due because of the handling of biological materials and microbial cultures. Previous studies have demonstrated that airborne bacteria and fungi are commonly detected in indoor laboratory environments, and their concentrations may increase under conditions of inadequate ventilation, high occupancy, and poor environmental hygiene.⁴⁻⁶

Exposure to airborne microorganisms has been associated with various adverse health effects, including respiratory infections, allergic reactions, mucosal irritation, and opportunistic infections in immunocompromised individuals.² Several bacterial and fungal genera, such as *Staphylococcus*, *Bacillus*, *Aspergillus*, and *Penicillium*, are frequently detected in indoor environments and may proliferate under humid and poorly ventilated conditions.^{7,8} Therefore, monitoring indoor air quality in laboratory settings is important for preventing occupational health risks and supporting environmental control.⁹ Based on these considerations, this study aimed to identify airborne bacteria and fungi present in the office room of the Microbiology Laboratory, Faculty of Medicine, Universitas Jenderal Achmad Yani, as a preliminary step toward evaluating indoor air quality and supporting environmental control measures.

METHODS AND SUBJECT

This study employed a descriptive observational design to identify airborne bacteria and fungi present in the office room of the Microbiology Laboratory, Faculty of Medicine, Universitas Jenderal Achmad Yani, in 2025. The study object was indoor air collected from the laboratory office environment, which is routinely used by lecturers and laboratory personnel for administrative activities and therefore may be exposed to airborne microorganisms.

Air sampling was performed using the passive settle plate method, a simple and cost-effective technique commonly used for preliminary indoor microbiological air quality monitoring. The office room had an approximate area of ± 60 m² and was equipped with two central air-conditioning units that operated during working hours. The room had limited natural ventilation because no windows could be opened, and air circulation primarily depended on the air-conditioning system. Sampling was conducted in the morning at 07.00 a.m., after routine room cleaning and before daily activities began, while the room was unoccupied.

Sampling was conducted at three different locations representing distinct airflow patterns and activity characteristics: the working desk area in the corner of the room, the area beneath the air-conditioning unit (AC), and the center floor area. At each sampling point, two Tryptic Soy Agar (TSA) plates were used for bacterial isolation, and two Sabouraud Dextrose Agar (SDA) plates were used for fungal isolation, resulting in a total of 12 culture plates (6 TSA and 6 SDA). One unopened TSA plate and one unopened SDA plate served as negative controls. All culture plates were exposed to ambient air for 15 minutes to allow airborne particles containing microorganisms to settle naturally onto the media surface through gravitational deposition.

TSA plates were incubated at 35–37 °C for 24–48 hours, whereas SDA plates were incubated at 25–28 °C for 5–7 days. Bacterial colonies obtained from TSA plates were subsequently subcultured into Tryptic Soy Broth (TSB) for enrichment before further identification procedures. Initial bacterial identification was performed based on colony morphology, Gram staining, and biochemical tests, including Mannitol Salt Agar (MSA), hemolysis patterns on Blood Agar, catalase testing using 3% hydrogen peroxide, and motility testing on semisolid medium.

To confirm bacterial identification, molecular analysis was performed using polymerase chain reaction (PCR) amplification of the 16S rRNA gene, followed by DNA sequencing. The resulting sequences were analyzed and compared with reference sequences available in the National Center for Biotechnology Information (NCBI) GenBank database using the Basic Local Alignment Search Tool (BLAST) to determine bacterial species.

Fungal identification was performed through macroscopic colony observation on SDA plates and microscopic examination using Lactophenol Cotton Blue (LPCB) staining to evaluate fungal hyphae and reproductive structures. Data were analyzed descriptively and presented in narrative and tabular form. This study was conducted after obtaining ethical approval from the Health Research Ethics Committee of the Faculty of Medicine, Universitas Jenderal Achmad Yani (Approval No. 031/UH1.10/2025).

RESULTS AND DISCUSSION

Environmental Conditions and Distribution of Airborne Microorganisms

Air sampling was conducted in the office room of the Microbiology Laboratory, Faculty of Medicine, Universitas Jenderal Achmad Yani, using the passive settle plate method at three sampling points: the working desk, beneath the air-conditioning unit (AC), and the

center of the floor area. Environmental measurements recorded during sampling showed a temperature of 25.1 °C and a relative humidity of 63%. Bacterial growth was observed on Tryptic Soy Agar (TSA) plates, with colony counts ranging from 0 to 24 colonies. The highest colony count was recorded at the working desk sampling point. No bacterial growth was observed on the negative control plates.

Bacterial colonies were detected on TSA plates, whereas fungal colonies were observed on Sabouraud Dextrose Agar (SDA) plates, confirming the presence of microorganisms within the laboratory workspace. Similar findings have been reported in studies investigating microbial contamination in indoor laboratory and public environments, where airborne bacteria and fungi were frequently detected.^{4,10} The higher colony count observed at the working desk may be associated with greater human activity and more frequent surface contact in that area. Human occupancy is recognized as a major contributor to indoor bioaerosol generation through skin shedding, respiratory droplets, and resuspension of settled dust particles.^{2,13}

Environmental conditions may also have contributed to microbial persistence within the room. The relative humidity recorded during sampling slightly exceeded the commonly recommended indoor humidity range of 40–60%, and elevated humidity has been associated with enhanced microbial survival and fungal growth in indoor environments.^{2,13} In addition, ventilation and airflow generated by the air-conditioning system may influence the distribution and deposition of airborne microorganisms within enclosed spaces.⁴ The detection of fungal growth exclusively in samples collected beneath the air-conditioning unit suggests that airflow patterns may have facilitated spore dispersion and accumulation in specific areas of the room. The presence of airborne microorganisms in laboratory workspaces may have implications for indoor air quality and occupational health.

Exposure to airborne bacteria and fungi has been associated with respiratory irritation, allergic reactions, and opportunistic infections, particularly in susceptible individuals.² Therefore, routine microbiological air monitoring, together with appropriate environmental control measures, including ventilation maintenance and humidity regulation, is important to minimize microbial accumulation in laboratory environments.

Bacterial Isolation and Identification

Six bacterial isolates were successfully obtained through the subculturing procedures. Gram staining revealed that all isolates were Gram-positive. Four isolates were cocci arranged in clusters, whereas two isolates were rod-shaped. The microscopic morphology of the isolates is presented in Figure 1A and Figure 1B. Biochemical characteristics, presumptive identification based on phenotypic tests, and molecular identification based on PCR and DNA sequencing are presented in Table 1.

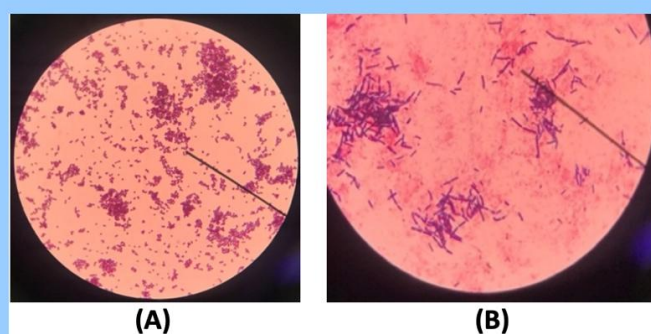


Figure 1. Gram-stained bacterial isolates showing (A) Gram-positive cocci arranged in clusters and (B) Gram-positive rods (1000× magnification).

Table 1. Phenotypic and molecular characterization of airborne bacterial isolates obtained from the laboratory office environment

Isolate	Gram Reaction	Cell Morphology	MSA	Hemolysis Pattern	Catalase	Motility	Presumptive Identification	Molecular Identification
1	Positive	Cocci	Negative	γ	Positive	ND	<i>Staphylococcus</i> sp.	<i>Staphylococcus hominis</i>
2	Positive	Cocci	Positive	γ	Positive	ND	<i>Staphylococcus</i> sp.	Not analyzed
3	Positive	Cocci	Negative	γ	Positive	ND	<i>Staphylococcus</i> sp.	<i>Staphylococcus hominis</i>
4	Positive	Rod	No growth	β	Negative	Positive	<i>Bacillus</i> sp.	<i>Stutzerimonas stutzeri</i>
5	Positive	Cocci	Negative	γ	Positive	ND	<i>Staphylococcus</i> sp.	<i>Staphylococcus epidermidis</i>
6	Positive	Cocci	Positive	γ	Positive	ND	<i>Staphylococcus</i> sp.	<i>Mammaliicoccus sciuri</i>

ND = Not determined.

Biochemical testing provided presumptive identification of the isolates at the genus level, which was subsequently verified by molecular identification using PCR and DNA sequencing. Several cocci isolates demonstrated growth on Mannitol Salt Agar (MSA), with some exhibiting mannitol fermentation, as indicated by a color change from red to yellow. Most

isolates exhibited gamma (γ) hemolysis on Blood Agar, whereas one rod-shaped isolate demonstrated beta (β) hemolysis, characterized by a clear zone surrounding the colony, as shown in Figure 2. The rod-shaped isolate was motile based on motility testing. Molecular identification using PCR and DNA sequencing was subsequently performed to confirm the taxonomic identity of selected isolates.



Figure 2. Beta (β) hemolysis exhibited by a rod-shaped isolate on Blood Agar.
Source: Authors' documentation.

PCR and DNA sequencing identified isolate 1 and isolate 3 as *Staphylococcus hominis*, whereas isolate 5 was identified as *Staphylococcus epidermidis*. Isolate 6 was identified as *Mammaliicoccus sciuri*, a species previously classified within the genus *Staphylococcus*. Isolate 4 was identified as *Stutzerimonas stutzeri*. Molecular analysis was not performed for isolate 2 because of sample limitations.

The predominance of Gram-positive bacteria observed in this study is consistent with previous reports on indoor air microbiology. Gram-positive bacteria possess thick peptidoglycan cell walls that enhance resistance to environmental stressors such as desiccation and ultraviolet radiation, enabling them to persist in airborne conditions.¹¹ Consequently, Gram-positive organisms are commonly reported as the

dominant microorganisms in indoor environments compared with Gram-negative bacteria.¹⁰

The predominance of Gram-positive bacteria identified in this study is also comparable with findings from previous studies conducted in microbiology laboratories and indoor occupational environments, which frequently reported *Staphylococcus spp.* and *Bacillus spp.* as dominant airborne microorganisms.^{6,11} These similarities may reflect the common contribution of human-associated microbiota and environmental dust to indoor microbial contamination. Nevertheless, differences in bacterial diversity and abundance between studies may be influenced by variations in occupancy density, ventilation systems, environmental hygiene, geographic conditions, and sampling methods.^{7,8}

Members of the genus *Staphylococcus*, including *Staphylococcus hominis* and *Staphylococcus epidermidis*, are commonly associated with the human skin and mucosal microbiota and are therefore frequently detected in indoor environments with human occupancy.¹¹ Human activities such as movement, talking, and contact with surfaces may contribute to the dispersal of these microorganisms into the surrounding air through skin particles and respiratory droplets.¹³ Previous studies have also reported *Staphylococcus* species as one of the dominant airborne bacteria in indoor environments.⁹

Another isolate was identified as *Mammaliococcus sciuri*, a Gram-positive coccus belonging to the family *Staphylococcaceae*. This species was previously classified as *Staphylococcus sciuri* but was later reclassified into the genus *Mammaliococcus* based on phylogenomic analysis.¹⁴ *M. sciuri* has been detected in animals, environmental sources, and occasionally in human-associated environments.¹⁴

One isolate was identified as *Stutzerimonas stutzeri*, an environmental Gram-negative bacterium previously classified within the genus *Pseudomonas*. This species is widely distributed in soil, water, and various environmental habitats

and exhibits diverse metabolic capabilities, including denitrification processes.¹⁵ In the present study, the isolate phenotypically resembled Gram-positive rod bacteria and was initially presumed to belong to the genus *Bacillus*. However, molecular identification using 16S rRNA gene sequencing revealed that the isolate corresponded to *S. stutzeri*. This discrepancy highlights the limitations of relying solely on phenotypic identification. Morphological observations and basic biochemical tests provide preliminary classification, whereas molecular approaches offer greater specificity and accuracy for bacterial identification at the species level. The presence of *S. stutzeri* in indoor air may be associated with environmental sources, such as dust particles or microorganisms introduced through the ventilation systems.¹⁵

Fungal Identification

Fungal growth was observed on SDA plates placed beneath the air-conditioning unit. Two morphologically distinct colonies were identified. Microscopic examination using Lactophenol Cotton Blue (LPCB) staining revealed septate hyphae and brush-like conidiophores with clustered conidia, consistent with the morphology of *Penicillium* sp., as shown in Figure 3.

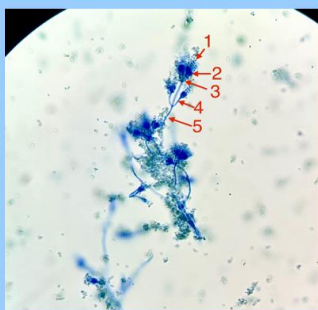


Figure 3. Microscopic morphology of *Penicillium* sp. stained with Lactophenol Cotton Blue (LPCB). (1) Conidia; (2) Phialide; (3) Metula; (4) Conidiophore; (5) Septate hyphae.

Another fungal isolate demonstrated thin, elongated hyaline hyphae without clearly visible reproductive structures. Due to the absence of definitive conidia or conidiophores, further identification was not possible. The isolate was therefore classified as a suspected hyaline filamentous fungus.

Penicillium species are commonly reported as airborne fungi in indoor environments.¹² These fungi are filamentous organisms typically identified through microscopic morphology using staining techniques such as Lactophenol Cotton Blue.¹⁶ Members of this genus belong to the phylum *Ascomycota*, which is widely distributed in both natural and indoor environments.¹⁷ Fungal organisms may persist in enclosed environments because of their structural adaptability and ecological diversity.¹⁸ Accurate identification of filamentous fungi may require the integration of morphological and molecular approaches to improve taxonomic resolution.¹⁹

The spores produced by *Penicillium* are lightweight and easily dispersed through the air, enabling the fungus to colonize indoor spaces.¹² The fungal cell wall structure also contributes to environmental resilience and survival under various environmental conditions.²⁰ Environmental measurements recorded during sampling showed a temperature of 25.1 °C and a relative humidity of 63%, which slightly exceeded the commonly recommended indoor humidity range of 40–60%. Elevated humidity has been associated with enhanced microbial persistence and fungal survival, potentially contributing to increased concentrations of airborne microorganisms.¹³

The identification of *Penicillium* sp. in the present study is consistent with previous reports describing this genus as one of the most common airborne fungi detected in educational buildings, laboratories, and office environments.^{10,12} Similar findings suggest that *Penicillium* species readily colonize indoor air because their spores can disperse efficiently through airflow and

ventilation systems.^{10,12} However, differences in fungal distribution and abundance across studies may be attributed to variations in environmental humidity, air circulation, building conditions, occupancy, and seasonal factors.¹²

The presence of airborne fungi in laboratory environments may have important implications for indoor air quality and occupational health. Airborne fungal spores may act as allergens and contribute to respiratory irritation, hypersensitivity reactions, and opportunistic infections, particularly among susceptible individuals.² These findings emphasize the importance of maintaining adequate ventilation, environmental sanitation, and humidity control to minimize fungal proliferation in enclosed laboratory spaces.

Study Limitations

This study has several limitations. The settle plate method used in this study is a passive air sampling technique that primarily detects microorganisms settling by gravitational deposition. Consequently, this method may underestimate the actual concentration of airborne microorganisms compared with active air sampling techniques. Additionally, fungal identification relied solely on macroscopic and microscopic morphological characteristics without molecular confirmation, which may have limited the accuracy of species-level identification.

Despite these limitations, the study provides preliminary data on the presence of airborne microorganisms in a laboratory office environment. The findings underscore the importance of maintaining environmental hygiene, proper ventilation systems, and routine monitoring of indoor air quality to minimize microbial exposure risks in laboratory settings. Future studies should incorporate active air sampling techniques together with molecular identification of fungal isolates to obtain more accurate quantification and identification of airborne microorganisms in indoor environments.

CONCLUSION

This study demonstrated that the office room of the Microbiology Laboratory, Faculty of Medicine, Universitas Jenderal Achmad Yani, contained diverse airborne bacterial and fungal bioaerosols associated with indoor environmental conditions and human activity. The predominance of Gram-positive bacteria and the detection of environmental fungi are consistent with previous reports describing indoor laboratories as potential reservoirs of airborne microorganisms.

The use of molecular identification through PCR and DNA sequencing improved the accuracy of bacterial identification beyond conventional phenotypic methods and revealed the presence of bacterial species that may not be reliably distinguished using morphology and biochemical tests alone. The discrepancy observed between phenotypic and molecular identification in one isolate further highlights the value of molecular approaches in environmental microbiology studies.

These findings contribute to a better understanding of indoor bioaerosol composition in laboratory environments and emphasize the importance of routine microbiological air monitoring, adequate ventilation, humidity control, and environmental sanitation to support occupational health and indoor air quality management. Further studies incorporating quantitative air sampling and comprehensive molecular analyses are recommended to better evaluate microbial exposure risks in indoor laboratory settings.

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DECLARATION OF INTERESTS

The authors declare that they have no conflicts of interest related to the publication of this paper.

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