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Fungi as Indicators of Indoor Air Quality: A Survey of a Building in a University

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Abstract. Indoor air quality (IAQ) significantly impacts human health, with fungal contamination being a major concern. At King Abdulaziz University, 160 samples were collected from 40 rooms, including classrooms, staff offices, microbiology laboratories, and toilets. These samples were cultured on Sabouraud dextrose agar and incubated at 28 °C for 7 days. Initial identification based on morphology was followed by internal transcribed spacer (ITS) rDNA analysis, revealing 11 species across eight genera. The most prevalent fungi included *Aspergillus niger* (183 CFU/m^3), *Penicillium chrysogenum* (139 CFU/ m^3), and *Cladosporium halotolerans* (135 CFU/ m^3), while *Curvularia hawaiiensis* and *A. ustus* were rarely isolated (10 and 19 CFU/ m^3, respectively). Mitigation strategies should emphasize humidity control and proper ventilation. Continuous monitoring and management are essential for reducing fungal contamination, improving air quality, and safeguarding human health from airborne fungi. This study highlights the need for proactive measures to create healthier indoor environments.
Keywords: fungi; indoor air quality; contamination; human health risk.

Introduction

Indoor air quality (IAQ) is a vital determinant of environmental health, as it directly influences human well-being and productivity. Fungal contamination is a key factor influencing indoor air quality, as certain fungi can proliferate in indoor environments and pose various health risks. Common indoor fungi, including *Aspergillus*, *Penicillium*, *Cladosporium*, and *Candida*, are frequently detected in air samples from homes, offices, and hospitals, and even in residential furniture (Sham et al., 2021). These fungi thrive in environments with elevated moisture levels and are often found in areas with poor ventilation or high humidity. Dampness resulting from leaks, inadequate ventilation, or high humidity can create ideal conditions for fungal growth. This is particularly problematic in homes and offices, where these conditions can be exacerbated by the presence of carpets, upholstered furniture, and other materials that can retain moisture and fungal spores (Sánchez Espinosa et al., 2024). The diversity of indoor fungi is primarily driven by outdoor dispersal, with little influence from occupant behavior or room features. These findings emphasize the key role of dispersal limitations in shaping indoor microbial patterns (Adams et al., 2013; Kumar et al., 2022). The fungal diversity in indoor air is typically measured in colony-forming units (CFUs), which indicates the concentration of viable fungal spores present. Studies have shown that CFU concentrations can vary widely, ranging from 20 to over 1300 CFU/m^3 depending on factors such as building maintenance, ventilation, and moisture levels (Sánchez Espinosa et al., 2022). For

instance, high CFU levels of *Aspergillus* and *Penicillium* species are often linked to damp conditions and inadequate ventilation, which can exacerbate respiratory problems and allergic reactions (Tang, 2015). Factors such as temperature, moisture, relative humidity, insulation, air circulation systems, and duct maintenance are key in regulating indoor air quality and influencing the presence of biological contaminants. Indoor environments generally have different bacterial concentrations and types compared to outdoor air, partly due to the lack of ultraviolet light that can kill airborne microorganisms outdoors (Bragoszewska et al., 2018). A concentration of 10^3 microorganisms/m³ is commonly considered a general safety threshold for indoor air quality (WHO, 2020; American Air and Water, 2020).

In medical centers and communities, especially in neonatal units, the presence of fungi is a major concern. The compromised immune systems of patients, coupled with the high humidity and ventilation systems in these critical areas, can lead to an increased risk of fungal infections and complications (Sánchez Espinosa et al., 2022) (Navale et al., 2021; Al Hallak et al., 2023). Commonly isolated fungi in these environments include *Aspergillus niger* and *Penicillium chrysogenum*. These fungi are known to exacerbate respiratory issues and allergies. They produce mycotoxins, such as aflatoxins and ochratoxin A, which can be detrimental to human health even at very low concentrations. Ingestion or inhalation of these toxins can lead to severe health problems.
Fungi in indoor air pose significant human health risks, particularly in environments where moisture levels are high. These microscopic organisms, including molds and yeasts, thrive in damp, warm conditions and can become airborne, leading to indoor air contamination. When inhaled, fungal spores can trigger allergic reactions, asthma, and other respiratory problems, particularly in individuals with weakened immune systems, the elderly, and young children. Some fungi can produce mycotoxins, which are toxic compounds that can lead to more severe health issues, including neurological symptoms and immune suppression (Chawla et al., 2023).
Reducing fungal contamination and enhancing air quality requires a combination of preventive and treatment measures. Effective prevention includes managing moisture levels, improving ventilation, and addressing any leaks or water damage promptly. Regular cleaning is also essential in maintaining a clean and dry indoor environment. When fungal growth is detected, treatments, such as antifungal agents, air purifiers, and fungicidal cleaning products, should be utilized. In more severe cases, professional remediation may be necessary to eliminate the contamination entirely. Evidence suggests that integrating these strategies with ongoing air quality monitoring can lead to significant improvements in health outcomes and reduce the risk of illnesses associated with fungal exposure (Sánchez Espinosa et al., 2022).
This study investigates fungal contamination in a Science Faculty, a setting often overlooked despite its distinct air quality challenges, including frequent laboratory usage and high humidity. The research aims to assess fungal diversity and concentration in indoor air in a University building, identify dominant fungal species, and discuss their implications for health and air quality management. Unique building aspects, such as high moisture levels from laboratory work and specific air circulation patterns, make its fungal load particularly relevant. By combining traditional preventive measures with real-time air quality monitoring, this innovative approach enhances understanding of fungal dynamics and provides valuable insights for managing indoor air quality and health, ultimately influencing policies in similar institutions to mitigate the adverse effects of indoor fungal contamination on human health.

Materials and methods

Sampling Locations

The study conducted in 2023 at the Faculty of Sciences, Microbiology Section, Department of Biological Sciences, King Abdulaziz University, strategically selected 11 a.m. for sample collection to capture a representative snapshot of airborne fungal levels during peak occupancy hours. At this time, classrooms, offices, toilets and laboratories are typically in active use, maximizing the potential for fungal spores to be stirred up and dispersed in the air due to human activity, airflow from ventilation systems, and laboratory processes. Additionally, sampling during mid-morning allows for consistent environmental conditions, as it is less likely to be influenced by extreme temperature fluctuations that can occur earlier or later in the day. This timing provides a clearer picture of indoor air quality and fungal dynamics, crucial for assessing potential health impacts on students and staff.

Sampling Method

Airborne fungi were isolated using the impaction method with a portable air sampler (Spin Air sampler, IUL micro, Spain). The sampler was positioned at a height of approximately 1.5 meters, simulating the breathing zone of occupants. For each location, air samples were collected for 5 minutes at a flow rate of 28.3 liters per minute (L/min) onto 90 mm Petri dishes containing Sabouraud dextrose agar (SDA) supplemented with chloramphenicol (50 µg/mL, QUELAB, USA) to inhibit bacterial growth **(**Tabatabaei et al., 2020). The internal part of the sampler was cleaned with 70% alcohol before each use. A total of 160 air samples were collected from 40 rooms across various areas, including classrooms, staff offices, microbiology laboratories, and toilets, during the summer semester of 2023. For each location, four samples were taken, with the experiment repeated 10 times, resulting in 40 plates per location.

Incubation and Identification

After sampling, the Petri dishes were sealed and transported to the laboratory for incubation. The plates were incubated at 25 °C for 5-7 days in the dark. After incubation, fungal colonies' concentrations were counted and recorded as (CFUs/m^3) of air. Morphologically distinct colonies were sub cultured onto fresh SDA plates to obtain pure cultures.

Microscopic Examination

After isolation, the identification of fungi was based on both macroscopic and microscopic characteristics. This included assessing colony color, texture, size, and the structure of reproductive features such as spores, conidia, and hyphae. For microscopic analysis, a small portion of each fungal colony was placed on a microscope slide, and a drop of lactophenol cotton blue was added. The slide was then covered with a coverslip to create a thin, uniform layer. These prepared slides were examined under a light microscope at magnifications of 400x to 1000x to observe the detailed morphology of the fungal structures. Standard mycological keys and references were employed to compare these features with known fungal species. For accurate and updated fungal identification,

the 2020 edition *Pocket Guide to Mycological Diagnosis* by De Aguiar et al. (2020) was used, providing contemporary methods and diagnostic criteria for reliable classification.

Molecular analysis

Sabouraud Dextrose Agar (SDA) and then transferred into a 100 ml Erlenmeyer flask containing 20 ml of potato dextrose broth (PDB). This was then incubated at 28 °C for 7 days. Following incubation, the broth was filtered through a 0.22µm sterilized nitrocellulose filter paper to collect the mycelia. The collected mycelia were washed several times with deionized sterilized water and stored at -20 °C. The frozen mycelia were then mixed with liquid nitrogen and ground into a fine powder using a sterilized pestle and mortar. This powder was distributed into 1.5 ml Eppendorf centrifuge tubes and stored at -20 °C.

The DNA extraction was performed separately for each fungus isolate. The sample (30 mg) of frozen, ground mycelia was lysed with the lysis buffer from the Gene JET Genomic DNA extraction kit (Thermo Scientific, USA, 10223). The samples were suspended in 500 µl of lysis buffer and incubated in a water bath at 37 °C for 60 minutes. The ITS region of ribosomal DNA (rDNA) was amplified using polymerase chain reaction (PCR). Internal transcribed spacer (ITS) rDNA primers, specifically ITS1 (CTTGGTCATTTAGGGAAGTAA) and ITS4 (TCCTCCGCTTATTGATATGC), were used in a thermal cycler (Esco Healthcare, Swift Max Pro, Malaysia). The 50 µl reaction mixture contained 3 µl of template DNA, 5 µl of each primer, 25 µl of Go Taq® Green Master Mix (Promega, USA), and 50 µl of nuclease-free water. The PCR procedure involved an initial denaturation at 96 °C for 1 minute, followed by 35 amplification cycles at 94 °C for 1 minute, 56 °C for 45 seconds, and 72 °C for 1 minute, concluding with a final extension at 72 °C for 6 minutes. A negative control was prepared by using DNA extract without any additional reagents, while a second negative control was also included that contained no DNA at all. This dual approach ensures the reliability of the results by confirming that any observed reactions are not due to contaminants.

The DNA loading dye was combined with each PCR product, and 20 µl of the mixture was loaded onto a 1.5% agarose gel. The gel was subjected to horizontal electrophoresis (Cleaver Scientific, UK) for 45 minutes at 130 volts and stained with ethidium bromide. A 20 µl DNA marker (100 bp, Invitrogen, USA) was included to help quantify and identify the PCR products. Bands were visualized using UV light (Gel Doc Imager, BioRad, USA). Clear bands were then excised and sent to Macrogen, South Korea, for purification and sequencing. Sequence identities were determined using a basic local alignment search tool (BLAST) against general GenBank databases from the National Center for Biotechnology Information (NCBI). Sequence alignments and neighbor analyses were performed using MEGA-X software.

Data Analysis

Fungal concentrations (CFU/m^3) were analyzed using descriptive statistics and one-way ANOVA to assess differences across locations. Tukey's HSD test was applied for post-hoc pairwise comparisons when significant differences were found.**Results and discussion**

The Concentration and Diversity of Fungal Isolates from Indoor Air

The total count across all of the studied rooms was 971 CFU/m^3, reflecting the presence and distribution of eight fungal genera: *Alternaria*, *Aspergillus*, *Cladosporium*, *Curvularia*, *Fusarium*, *Paecilomyces*, *Penicillium*, and *Trichoderma*, as shown in Table 1. Classrooms exhibited the highest concentration of fungal isolates, with a total of 400 CFU/m^3, which was significantly higher than those in other locations ($p < 0.05$). Staff offices followed, with a significant concentration of 239 CFU/m^3, showing a notable difference from classrooms ($p < 0.05$). Toilets ranked third, with 171 CFU/m^3, significantly lower than classrooms ($p < 0.05$) and staff offices ($p < 0.05$). Microbiology laboratories had the lowest concentration, at 161 CFU/m^3, which was significantly lower than those of classrooms ($p < 0.05$), staff offices ($p < 0.05$), and toilets ($p < 0.05$). The distribution of fungal isolates indicates that classrooms, with the highest human activity and potential dust accumulation, are the most conducive environment for fungal growth, followed by staff offices. Toilets, likely due to higher moisture levels, also support a significant fungal presence. Laboratories, despite being controlled environments, still harbor a notable number of fungi. In addition, classrooms exhibited the greatest fungal diversity, hosting all 11 identified fungal species. The study by Frączek and Bulski (2023) found no significant differences in fungal concentrations across classrooms, with Cladosporium, Penicillium, and Aspergillus being the most common genera. Similarly, our findings confirmed that classrooms showed the highest fungal diversity. The higher fungal concentrations in classrooms may be attributed to several factors, including the frequent presence of students, which can increase moisture levels and introduce organic materials that create an ideal environment for fungal growth. Additionally, limited air circulation and inadequate ventilation in some classrooms may exacerbate fungal accumulation, especially in spaces with high relative humidity. Both studies emphasized the critical role of relative humidity in influencing fungal concentrations, highlighting the need for improved ventilation and humidity control to maintain better indoor air quality. This is particularly important in educational settings, where prolonged exposure to airborne fungi could pose health risks to both students and staff..Staff offices also showed significant diversity, with eight different fungal species. Toilets contained nine fungal species. Microbiology laboratories, despite their controlled environments, harbored nine distinct types of fungi. This highlights that even in regulated settings, fungal diversity can still occur.

In our study, the concentration and diversity of fungal isolates from indoor air have been extensively studied, revealing a wide range of species and varying levels of concentration. *Aspergillus*, *Penicillium*, and *Cladosporium* species were identified as among the most prevalent fungi, found abundantly in various environments. These findings align with studies by Navale et al. (2021) and Belizario et al. (2021). A review of research from 2005 to 2019 highlighted the presence of *Aspergillus*, *Penicillium*, and *Cladosporium* species in the indoor air of critical hospital areas. Furthermore, among the common fungi identified in indoor environments were *Cladosporium halotolerans*, *Paecilomyces variotii*, and *Trichoderma harzianum*, each with its own unique characteristics and implications for indoor air quality. The *Cladosporium* species is often found in indoor environments, particularly in areas with high humidity. Studies have shown that *Cladosporium* species, including *C. halotolerans*, can contribute significantly to indoor air spore concentrations, particularly in damp or water-damaged buildings. This species is known for its tolerance of salt, which allows it to thrive in conditions where other fungi might not survive (Sánchez Espinosa et al., 2022). *Paecilomyces variotii* has been reported as another common indoor fungus. It has been frequently isolated from air samples in various studies. This species is known for its ability to grow in a wide range of environmental conditions, including those with limited

nutrients and varying temperatures (Lu et al., 2021). *Trichoderma harzianum* is a well-known indoor fungus that is often found in soil and decaying organic matter. However, it can also colonize indoor environments, particularly in areas with high moisture levels. *Trichoderma* species are known for their antagonistic properties against other fungi, making them a common contaminant in buildings with water damage or mold issues (Polizzi et al., 2011). A study in Havana, Cuba, collected samples from 44 bedrooms over the years 2018 and 2019. This research aimed to investigate the presence and diversity of fungal species in residential spaces, contributing to the understanding of indoor air quality. The results indicated poor indoor air quality in 18 bedrooms, with concentrations of fungal propagules between 20 and 1330 CFU/m³. The most frequent genera identified were *Cladosporium*, *Aspergillus*, *Penicillium*, and *Curvularia*. Another study using qPCR found *Aspergillus*, *Penicillium*, and *Paecilomyces variotii* among the detected species, highlighting seasonal variations and the presence of fungal fragments in indoor air (Lu et al., 2021; Sánchez Espinosa et al., 2022).

In contrast, *Curvularia* sp appeared to be more restricted in this study, as it was primarily noted in indoor environments but rarely observed. This distribution underscores the adaptability of fungal species and highlights the varied prevalence of fungi in different indoor settings, despite no outdoor sites being sampled.". The *Curvularia* species is associated with plants and soil, and it thrives in outdoor environments. While it can occasionally be detected indoors, it is not typically a dominant mold. Its spores may enter buildings through ventilation systems or open windows, but its lower prevalence indoors minimizes its impact compared to more common indoor fungi such as *Aspergillus* and *Penicillium* species (Tang, 2015). *Aspergillus ustus* is another species that is rarely present in indoor air. It is primarily found in soil and decaying organic matter, making it more common outdoors. Although it can occasionally be detected indoors, its prevalence is significantly lower than that of other *Aspergillus* species. This limited presence indicates that *A. ustus* is not a predominant indoor mold, further emphasizing the variability in fungal species distribution between indoor and outdoor environments (Andersson et al., 2022). Generally, counts below 1,000 CFU/m³ are often considered acceptable in many settings, suggesting that a total of 971 CFU across all studied rooms may fall within an acceptable range. However, it's essential to consider factors like room use and overall health impact.

Table 1. Fungal concentration (CFU/m$^{3)}$ in the air of the studied rooms including classrooms, staff offices, microbiology laboratories and toilets.

No.	Fungal isolates	Classrooms	Staff offices	Microbiology laboratories	Toilets	Total (CFU/m³)
1	*Alternaria* sp.	24	0	12	0	36
2	*Aspergillus flavus*	28	10	22	36	96
3	*A. niger*	80	40	38	25	183
4	*A. ustus*	19	0	0	0	19
5	*Cladosporium* sp.	64	29	20	22	135
6	*Curvularia* sp.	10	0	0	0	10
7	*Fusarium* sp.	0	22	0	3	25
8	*Paecilomyces variotii*	50	41	18	11	120
9	*Penicillium* sp.1	44	50	17	28	139
10	*Penicillium* sp.2	31	11	22	19	83
11	*Trichoderma* sp.	50	36	12	27	125
Total		400*	239*	161*	171*	971

* Significant difference at (p 0.05).

PCR amplifications of DNA extracted from the 11 fungal species were performed using the ITS1/4 universal fungal primer pair. The sequencing data of the fungal strains were then aligned with sequences of closely related strains available in GenBank. Table 2 presents the fungal accession numbers, closest related species, and their similarity percentages based on sequencing data. *Alternaria alternata*, with accession number OR533706.1, shows a 100% similarity to its closest related species. *Aspergillus flavus* (MT635198.1) has an 89.29% similarity, while *A. niger* (JX556221.1) has a 90% similarity. *Aspergillus ustus* (KC800599.1) exhibits an 88.83% similarity, and *C. hawaiiensis* (KY788103.1) has an 87.32% similarity. *Fusarium proliferatum* (MT466521.1) shows a 91.21% similarity, and *P. variotii* (MN547409.1) has an 88.57% similarity. *Penicillium chrysogenum* (OK510242.1) exhibits an 89.69% similarity, while *P. citrinum* (MH990629.1) shows a 91.24% similarity. *Cladosporium halotolerans* (MW412494.1) has a 93.07% similarity, and *T. harzianum* (MF108874.1) exhibits a 91.43% similarity. These data highlight the genetic relationships and diversity among the studied fungal isolates.

Table 2. A list of the accession numbers for the fungal species isolated from the indoor air of the studied rooms, along with the most closely related fungal species and their similarity percentage found in the NCBI website.

Fungal accession numbers	Closest related species	Similarity (%)
Alternaria alternate	OR533706.1	100
Aspergillus flavus	MT635198.1	89.29
A. niger	JX556221.1	90
A. ustus	KC800599.1	88.83
Curvularia hawaiiensis	KY788103.1	87.32
Fusarium proliferatum	MT466521.1	91.21
Paecilomyces variotii	MN547409.1	88.57
Penicillium chrysogenum	OK510242.1	89.69
P. citrinum	MH990629.1	91.24
Cladosporium halotolerans	MW412494.1	93.07
Trichoderma harzianum	MF108874.1	91.43

The phylogenetic tree presented in Figure 1 illustrates the genetic relationships among various fungal isolates, based on sequencing data obtained using ITS primers. *Curvularia hawaiiensis* (KY788103.1) stands out as a distinct outgroup, indicating its unique genetic position. *Alternaria alternata* (OR533706.1) and *C. halotolerans* (MW412494.1) form a close cluster, showing a strong genetic similarity. *Fusarium proliferatum* (MT466521.1) and *T. harzianum* (MF108874.1) also cluster together, indicating a closer genetic relationship. *Paecilomyces variotii* (MN547409.1) is positioned separately, suggesting moderate similarity to the others. *Penicillium* species, including *P. chrysogenum* (OK510242.1) and *P. citrinum* (MH990629.1), show close genetic ties. *Aspergillus* species such as *A. flavus* (MT635198.1), *A. niger* (JX556221.1), and *A. ustus* (KC800599.1) form a tight cluster, highlighting their genetic relatedness. Similar studies have isolated *A. flavus*, *A. niger*, and *A. ustus* from indoor air environments. Internal Transcribed Spacer (ITS) sequencing offers a reliable, rapid method for fungal identification, enabling accurate species-level resolution and enhancing ecological studies (Nafis et al., 2023; Espinosa et al., 2021).

This tree emphasizes the diversity and evolutionary relationships among the studied fungal isolates, providing insights into their genetic affiliations. All 11 fungal species in the current study belong to

the phylum Ascomycota These spores can be pathogenic, thereby causing severe symptoms in immunocompromised individuals or those on long-term antimicrobial treatments. Variations in fungal isolate quantities and identities across studies are influenced by factors such as exposure locations, collection techniques, identification methods (both conventional and molecular), and environmental conditions such as temperature and humidity (Tian et al., 2024).

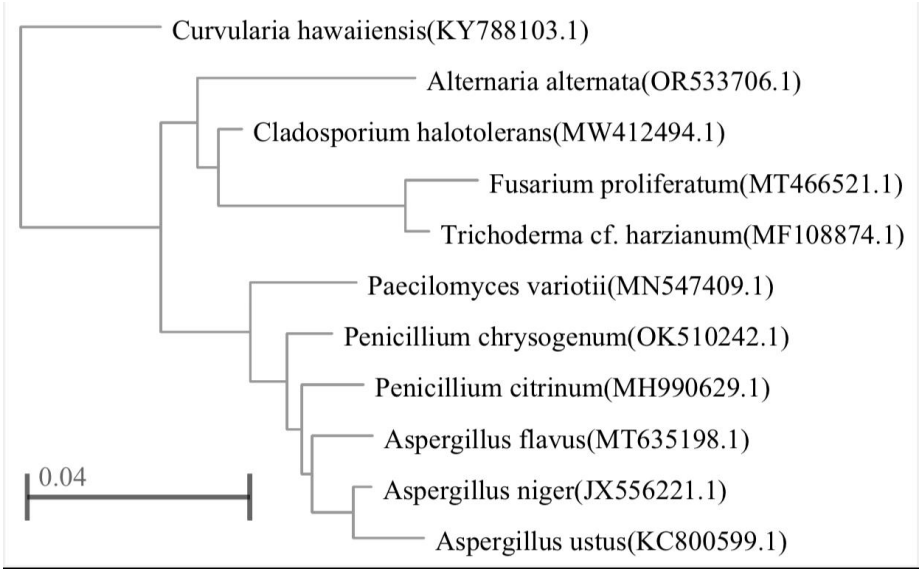

Figure 1. Dendrogram showing phylogenetic analysis based on the ITS region and NCBI GenBank database for 11 fungal species.

The current study on fungi as indicators of indoor air quality at a university building has several limitations that should be acknowledged. First, the sampling was conducted during a limited timeframe, which may not capture seasonal variations in fungal populations that could influence air quality assessments. Future research should consider longitudinal studies across different seasons to provide a more comprehensive understanding of fungal dynamics. Second, the study focused exclusively on specific rooms within the building, potentially overlooking other areas that might harbor significant fungal growth, such as hallways, common areas, or less frequently used spaces. Expanding the sampling to include a broader range of locations within the university could yield a more representative picture of overall indoor air quality. Additionally, the study did not account for the potential impact of external environmental factors, such as outdoor air quality and local climate conditions, which can influence indoor fungal levels. Future investigations should incorporate outdoor sampling and consider the relationship between indoor and outdoor air quality. By addressing these limitations, future research can enhance our understanding of indoor air quality and the role of fungi in academic settings, ultimately leading to improved health outcomes for occupants.

Human Health Risks Associated with Indoor Fungi

Aspergillus species such as *Aspergillus niger* are commonly found in indoor environments and can pose serious health hazards to human health. *Aspergillus niger* is a saprophytic fungus that thrives in damp and poorly ventilated areas, making it a common indoor contaminant. The inhalation of *Aspergillus* spores can cause a variety of respiratory issues, including allergic reactions, asthma exacerbations, and allergic bronchopulmonary aspergillosis (ABPA). For immunocompromised individuals, the risk is significantly higher, as *A. niger* can cause invasive aspergillosis, a severe and potentially fatal infection that can spread from the lungs to other parts of the body. The symptoms of invasive aspergillosis include fever, chest pain, cough, and hemoptysis (coughing up blood), and the infection requires prompt medical treatment (Agarwal et al., 2024). *Penicillium* species, including *Penicillium chrysogenum*, are frequently found in indoor environments, where they can become a significant source of allergens. These fungi thrive in conditions of high humidity and poor ventilation, often contaminating indoor air and surfaces. The spores released by *Penicillium* can contribute to various health issues, particularly for individuals with pre-existing respiratory conditions or compromised immune systems. Exposure to *Penicillium* spores is known to exacerbate asthma and other respiratory conditions. Individuals with asthma may experience increased frequency and severity of symptoms such as coughing, wheezing, and shortness of breath when exposed to these fungal spores. This exacerbation occurs because the allergens from *Penicillium* can trigger inflammatory responses in the airways, leading to heightened asthma symptoms and, potentially, increasingly frequent asthma attacks. In individuals with chronic respiratory conditions or weakened immune systems, prolonged exposure can also lead to more severe health complications (Xing et al., 2022). Moreover, *Penicillium chrysogenum* has been associated with other allergic reactions and respiratory conditions beyond asthma. Studies have shown that inhalation of *Penicillium* spores can induce hypersensitivity pneumonitis, a condition in which the lungs become inflamed due to an allergic reaction to inhaled organic dust, including fungal spores (Al Hallak et al., 2023). *Cladosporium halotolerans* poses significant health risks to humans. Exposure to this fungus can lead to respiratory problems and allergic reactions and can exacerbate conditions such as asthma. *Cladosporium* species, although less common, can cause phaeohyphomycosis, a serious fungal infection, particularly in immunocompromised individuals (Zhou et al., 2023).

Monitoring and Controlling Indoor Air Quality

To manage indoor fungal contamination and maintain a healthy environment, in the sampled Faculty of Science , proper ventilation is effectively maintained through a forced-air ventilation system that promotes airflow and reduces moisture accumulation, complemented by regular maintenance of heating, ventilation, and air conditioning (HVAC) systems, which enhances air quality and prevents mold growth. However, there are notable gaps, such as the lack of air purifiers that could further diminish airborne spores and the absence of ongoing air quality monitoring, highlighting the need for a regular assessment schedule to identify fungal contamination early. To improve air quality, it is crucial to introduce air purifiers, implement routine air quality monitoring protocols, and enhance staff and student education on moisture control practices, as noted by Chen et al. (2023).

Moisture control is another crucial aspect of managing indoor fungal contamination. Leaks, condensation, and high humidity levels create favorable conditions for mold growth. Addressing these issues promptly through repairs and dehumidification can help prevent fungal proliferation. In areas prone to moisture, such as bathrooms and kitchens, the use of exhaust fans and moisture-resistant materials can further reduce the risk of mold growth (Engel et al., 2024).

Regular cleaning and maintenance are essential for minimizing fungal contamination. Dust and organic matter provide a substrate for fungal growth; therefore, routine cleaning of surfaces, carpets, and ventilation systems is necessary to reduce the availability of these materials. Using cleaning agents with antifungal properties can also help eliminate mold spores from surfaces. The diversity and concentration of these and other fungal species in indoor air highlight the complexity of indoor air quality management. Factors such as humidity, ventilation, building materials, and human activity all influence the types and levels of fungi present. These factors include regular inspection and maintenance of HVAC systems, controlling humidity levels, and promptly addressing water damage to prevent the proliferation of fungi such as *Cladosporium halotolerans*, *Paecilomyces variotii*, and *Trichoderma harzianum* (Loukou et al., 2024).

Monitoring indoor air quality is vital for the early detection of fungal contamination. Air sampling and spore counts can provide valuable information about the types and concentrations of fungi present in indoor environments. These data can inform targeted interventions to address specific sources of contamination and improve overall air quality. The use of molecular techniques for pathogen identification has enhanced the accuracy of fungal monitoring, allowing for more precise identification and tracking of fungal species (Tang et al., 2015).

Conclusion

Fungi in indoor air serve as critical indicators of air quality, which has significant implications for human health. Exposure to airborne fungi can lead to respiratory issues, allergies, and more severe conditions in vulnerable populations. Effective management involves regularly monitoring the indoor air quality, controlling moisture, and implementing proper ventilation. Treatment strategies, including antifungal medications and thorough cleaning, are essential for addressing fungal contamination. By maintaining a clean, dry indoor environment and employing targeted interventions, we can significantly reduce the health risks associated with indoor fungal exposure and promote better overall air quality.

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الفطريات كمؤشرات لجودة الهواء الداخلي: دراسة ميدانية في مبنى جامعي

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مستخلص. جودة الهواء الداخلي (IAQ) تؤثر بشكل كبير على صحة الإنسان، حيث تعد التلوث الفطري مصدر قلق رئيسي. وقد تم جمع 160 عينة من 40 غرفة، بما في ذلك الفصول الدراسية، مكاتب الموظفين، مختبرات علم الأحياء الدقيقة، والحمامات، في جامعة الملك عبد العزيز. ومن ثم زراعة هذه العينات على أجار سابورود ديكستروز واحتضانها عند 28 درجة مئوية لمدة 7 أيام. وبذلك تم تحديد الأنواع الأولية بناءً على الشكل الخارجي للفطريات، مع استخدام التحليل الجزيئي للحامض النووي الريبوزي منقوص الأكسجين (ITS) ، مما كشف عن 11 نوعًا مع ثمانية أجناس. كانت الفطريات الأكثر شيوعًا تشمل *Aspergillus niger* (183 من وحدات تكوين المستعمرات لكل متر مكعب)، *Penicillium chrysogenum* (139 من وحدات تكوين المستعمرات لكل متر مكعب)، و *Cladosporium halotolerans* (135 من وحدات تكوين المستعمرات لكل متر مكعب)، في حين من النادر تم عزل *Curvularia hawaiiensis* و *A* (10 و 19 من وحدات تكوين المستعمرات لكل متر مكعب) على التوالي. استراتيجيات الحد من أضرار التلوث الفطري في الهواء تعتمد على التحكم في الرطوبة والتهوية الجيدة. يعد الاستمرار في المراقبة والمكافحة أمران ضروريان للحد من التلوث الفطري، وتحسين جودة الهواء، وحماية صحة الإنسان من الفطريات المحمولة في الهواء. تبرز هذه الدراسة الحاجة إلى اتخاذ تدابير استباقية لإنشاء بيئات داخلية أكثر صحة.

الكلمات المفتاحية :الفطريات؛ جودة الهواء الداخلي؛ التلوث؛ خطرعلى الصحة البشرية.