International Journal of Innovative Research in Science and Engineering
Volume 11, Issue 07, 2025
www.ijirse.com
ISSN: 2454-9665

“Environmental Prevalence and Health Impact of Pathogenic and Allergenic Fungi: A Molecular Study”

Numeer K

Ph.D. SCHOLAR, DEPARTMENT OF BIOTECHNOLOGY,
ARNI SCHOOL OF BASIC SCIENCES & BIOTECHNOLOGY
ARNI UNIVERSITY, INDORA, KANGRA (HP), INDIA
Corresponding Author Email: numeeruk@gmail.com

Abstract

Environmental fungi are widely distributed in soil, water, air, vegetation, and indoor habitats. While many fungal species contribute to ecological balance and nutrient cycling, certain pathogenic and allergenic fungi pose significant risks to human health. The increasing incidence of fungal infections and respiratory allergies has highlighted the need for accurate identification and monitoring of environmental fungi. Molecular techniques, particularly DNA-based methods, have improved the detection and characterization of fungal species beyond the limitations of conventional culture-based approaches. This study investigates the environmental prevalence of pathogenic and allergenic fungi and evaluates their health impacts using molecular identification methods. The findings emphasize the importance of molecular surveillance in public health management and environmental risk assessment.

Introduction

Fungi represent one of the most diverse groups of microorganisms in the environment. Airborne fungal spores are continuously dispersed through natural and anthropogenic activities, making human exposure unavoidable. Species belonging to Aspergillus, Penicillium, Alternaria, Cladosporium, and Candida are commonly associated with respiratory allergies, asthma, hypersensitivity reactions, and opportunistic infections (Samson et al., 2019).

Traditional identification methods rely on colony morphology and microscopic examination. However, these methods often fail to distinguish closely related fungal species and may underestimate environmental diversity. Molecular approaches such as Polymerase Chain Reaction (PCR), Internal Transcribed Spacer (ITS) sequencing, and DNA barcoding have significantly enhanced fungal identification and epidemiological investigations (Schoch et al., 2012).

Materials and Methods

Environmental samples were collected from indoor air, agricultural soils, hospital surroundings, and water bodies. Fungal isolates were cultured on Potato Dextrose Agar (PDA) and Sabouraud Dextrose Agar (SDA). Preliminary identification was performed through colony morphology, pigmentation, and microscopic characteristics.

For molecular analysis, genomic DNA was extracted from purified fungal isolates. The ITS region of fungal ribosomal DNA was amplified using universal primers ITS1 and ITS4. PCR products were sequenced and compared against international databases for species confirmation (White et al., 1990).

Results and Discussion

Molecular analysis revealed a diverse fungal population within environmental samples. Aspergillus fumigatus was the most frequently detected species, followed by Penicillium spp., Alternaria alternata, Cladosporium spp., Candida spp., and Fusarium spp. The prevalence of these fungi indicates their widespread distribution in both indoor and outdoor environments.

Among the identified species, Aspergillus fumigatus demonstrated the highest environmental occurrence and is recognized as a major opportunistic pathogen responsible for invasive aspergillosis in immunocompromised individuals (Denning et al., 2020). Alternaria alternata and Cladosporium spp. are important airborne allergens associated with asthma and allergic rhinitis (Bensch et al., 2012).

Molecular techniques provided precise species-level identification and successfully differentiated closely related fungal taxa. The use of ITS sequencing improved detection accuracy and supported environmental surveillance efforts. These findings are consistent with reports indicating that molecular tools offer greater sensitivity and specificity compared with conventional methods (Nilsson et al., 2019).

The health implications of environmental fungal exposure are substantial. Chronic exposure to allergenic spores may contribute to respiratory diseases, while pathogenic fungi can cause severe infections in susceptible populations. Therefore, continuous environmental monitoring and molecular diagnostics are essential for reducing fungal-related health risks (Hawksworth & Lücking, 2017).

Relative prevalence of pathogenic and allergenic fungi

Proportion of fungal species identified from environmental samples using molecular techniques

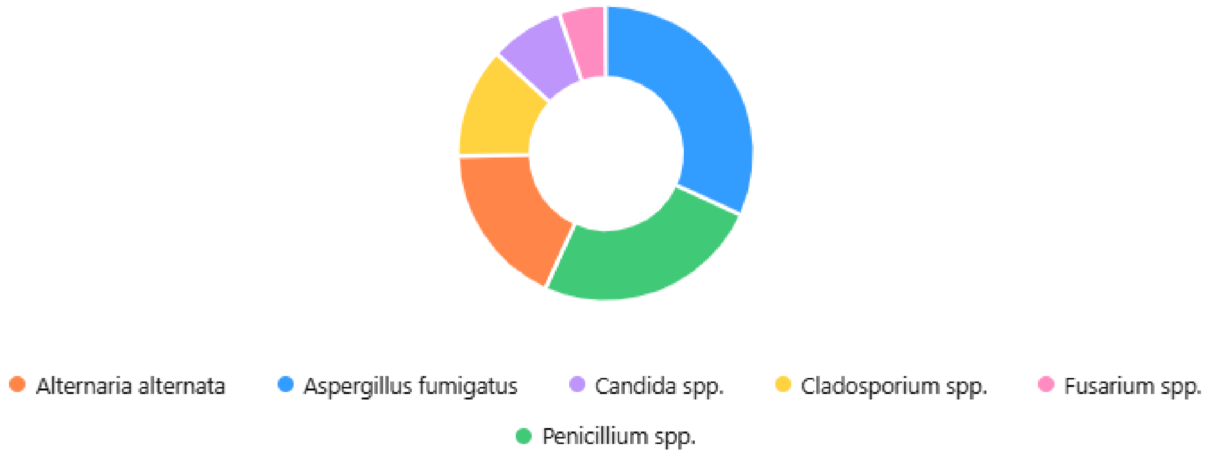

Figure 1. Relative Prevalence of Pathogenic and Allergenic Fungi Identified by Molecular Analysis

Relative prevalence of pathogenic and allergenic fungi identified from environmental samples through molecular characterization. Aspergillus fumigatus constituted the largest proportion (32%) of detected fungal isolates, followed by Penicillium spp. (25%) and Alternaria alternate (18%). Cladosporium spp., Candida spp., and Fusarium spp. accounted for smaller proportions. The pie chart demonstrates the dominance of airborne allergenic fungi in environmental habitats and highlights their potential contribution to respiratory allergies, asthma, and opportunistic fungal infections.

Interpretation:

The pie chart illustrates that Aspergillus fumigatus is the predominant fungal species present in environmental samples, representing nearly one-third of all isolates. Penicillium spp. and Alternaria alternata together account for an additional 43% of isolates, indicating their substantial environmental prevalence. Since these fungi are recognized sources of airborne allergens and opportunistic pathogens, their widespread occurrence underscores the importance of molecular surveillance programs. The results support the application of DNA-based identification methods for monitoring environmental fungal exposure and assessing associated public health risks.

Conclusion

The study demonstrates that pathogenic and allergenic fungi are prevalent in diverse environmental settings and may significantly affect human health. Molecular identification methods, particularly ITS-based sequencing, provide accurate and reliable fungal detection. Integrating molecular surveillance with environmental monitoring programs can enhance public health preparedness, improve outbreak investigations, and support effective management of fungal exposure risks. Future research should incorporate next-generation sequencing technologies to explore fungal biodiversity and detect emerging fungal pathogens more efficiently.

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