Journal of Health, Medicine and Nursing
Volume 2, No. 3, 2026 - ISSN: 3063-4210
Website: https://jhmn.seevalue.org/index.php/jhmn

Signature Microbiology in Indoor Air and House Dust: A Meta-analysis of Bacterial–Fungal Functional–Taxonomic Indicators with Respiratory Health Implications

Agita Diora Fitri[1], Mariana[2], Muhammad Ramadhandie Odiesta[3]

[1] Doctoral Program of environmental science, Medical Faculty, Universitas Sriwijaya, Palembang, Indonesia

[2] Public health administration, Medical Faculty, Universitas Sriwijaya, Palembang, Indonesia

[3] Anatomy Department, Medical faculty, Universitas Sriwijaya, Palembang, Indonesia

Keywords:
Indoor Microbiome;
Humidity;
Fungal–Bacterial Community;
Respiratory Health;
Meta-Analysis;
Gene Expression.

Abstract

Background: Indoor microbiomes are emerging as key determinants of respiratory health. Environmental factors such as humidity, ventilation, and building material types influence the diversity, abundance, and activity of airborne fungi and bacteria. These microbial communities play a significant role in the development of respiratory conditions, including asthma and COPD. Objective: This meta-analysis identifies bacterial and fungal signature microbiology patterns in indoor air and household dust, linking their ecological and functional indicators with respiratory health outcomes. Methods: Twenty peer-reviewed studies published between 2019 and 2025 were analyzed using random-effects models (REML). Data extracted included $\log_2$ fold-changes or standardized mean differences (SMDs) for gene expression related to sporulation, biofilm formation, and toxin pathways, as well as ecological ratios such as hydrophilic/mesophilic fungal ratios and Gram-negative/positive bacterial ratios. Results: Elevated equilibrium relative humidity (ERH ≥ 85%) was associated with increased hydrophilic fungal taxa and higher expression of growth and sporulation genes (brlA, rodA, catA), secondary metabolites (stcC, Alt a 7), and bacterial inflammation markers (LPS, rpoS). The pooled SMD for hydrophilic fungi was +0.84 (95% CI 0.59–1.08; $p < 0.001$), while Gram-negative bacterial enrichment showed an SMD of +0.67 (95% CI 0.41–0.93). Conclusion: Functional and ecological indicators provide more reliable results than single-species markers. Combined bacterial–fungal signatures, including functional genes and ecological ratios, serve as robust biomarkers for assessing indoor microbiological quality and respiratory risk. Monitoring these microbial indicators can help in formulating public health policies and preventive strategies.

Corresponding Author:
Agita Diora Fitri
Email: agita@fk.unsri.ac.id

INTRODUCTION

Indoor air quality (IAQ) is a critical factor affecting human respiratory health, as exposure to poor indoor environments has been linked to various respiratory diseases, including asthma, chronic obstructive pulmonary disease (COPD), and allergic rhinitis. Factors such as high humidity, inadequate ventilation, and moisture-retentive building materials can significantly contribute to microbial colonization, leading to the release of spores, volatile organic compounds, and toxins (Al Hallak et al., 2023; Cox et al., 2021). These microorganisms, including bacteria and fungi, can play a pivotal role in the health outcomes of individuals exposed to them, particularly in environments that promote microbial growth, such as damp and poorly ventilated homes (Tiew et al., 2024; Vandenborght et al., 2021).

Research Gap and Urgency of the Study

Despite growing evidence that IAQ and microbial exposure are important for respiratory health, there remains a significant research gap in understanding the specific microbial communities associated with indoor environments, particularly those that are damp or moisture-laden. While numerous studies have identified specific bacterial and fungal taxa in indoor air and house dust, most research has focused on either fungi or bacteria in isolation, with limited attention paid to how these communities interact and how their functional traits, such as allergen production or toxin-gene expression, may influence respiratory health outcomes. Furthermore, many studies fail to establish reliable biomarkers that can predict the potential health risks of microbial exposure in residential environments.

This study addresses this research gap by synthesizing data from various global studies and applying a meta-analytic approach to identify bacterial and fungal microbial signatures linked to high humidity, inadequate ventilation, and moisture-retentive materials. By examining functional and ecological microbial traits, this research aims to establish stable indicators that can be used to predict respiratory health outcomes. Understanding these indicators is urgent as poor IAQ remains a persistent issue globally, particularly in regions with high humidity or poor housing conditions (Jiang et al., 2022; Šunić et al., 2025).

Prior Research and Novelty

Previous studies have explored the role of environmental factors in shaping microbial communities, with research indicating that dampness in buildings promotes fungal proliferation, particularly species like Aspergillus and Cladosporium, which are known to be associated with respiratory diseases (Kumar et al., 2022; Tiew et al., 2024). Studies have also demonstrated the relationship between microbial diversity and IAQ, showing that high levels of humidity lead to an increase in hydrophilic fungi and bacterial taxa, both of which can influence the development of respiratory conditions (Cox et al., 2021; Fakunle et al., 2021).

The concept of "signature microbiology" extends beyond taxonomy to focus on functional traits—such as sporulation, allergen production, and toxin-gene expression—that reflect both environmental conditions and potential health impacts. These functional traits are often more reliable indicators of microbial exposure and health risks than species identification alone (Balasubrahmaniam et al., 2024). However, there is limited research that integrates both fungal and bacterial communities in relation to these functional traits, creating a gap in our understanding of how these signatures collectively contribute to respiratory risks in indoor environments. This study's novelty lies in its approach to combine these ecological and functional microbial signatures into a unified framework for assessing indoor air microbiome quality. By focusing on both bacterial and fungal communities and using molecular biomarkers to assess gene expression related to sporulation, toxin production, and inflammation, this study provides a more holistic view of how indoor microbial environments contribute to respiratory risk.

Research Objectives

This meta-analysis aims to:

1. Identify stable bacterial and fungal microbial indicators of high humidity, poor ventilation, and moisture-retentive materials that are prevalent in residential environments.

2. Investigate the relationship between these microbial signatures and respiratory health outcomes, including asthma, COPD, and other respiratory allergies.
3. Establish ecological and functional biomarkers (e.g., hydrophilic fungal ratios, Gram-negative bacterial enrichment) for use in assessing the risk of respiratory diseases associated with indoor air exposure.

Significance and Benefits of the Study

The significance of this research lies in its potential to provide reliable and validated biomarkers for monitoring indoor microbial exposure and improving IAQ. By linking microbial signatures to specific health outcomes, this study offers practical implications for public health policies and interventions aimed at mitigating the risks associated with poor indoor air quality. These findings could be used to inform strategies for maintaining healthier indoor environments, particularly in homes and public spaces where microbial exposure is a major concern.

Additionally, the study will contribute to the broader scientific understanding of how functional microbial communities can be used as indicators of indoor air quality and health risks. The insights from this research are expected to have a direct impact on the design of future health and environmental regulations, as well as recommendations for improving ventilation, reducing moisture levels, and controlling microbial growth in indoor environments.

Given the widespread impact of indoor air quality on respiratory health, this study's findings can significantly advance the field by offering robust microbial signatures that can be used as early warning indicators for respiratory risks. This work underscores the need for a more integrated approach to studying indoor microbiomes, considering both ecological and functional dimensions of microbial communities to improve human health and well-being.

METHOD

A comprehensive literature search was conducted to identify relevant studies that assessed the indoor microbiome and its relationship with respiratory health. Studies published between 2019 and 2025 were retrieved from three major databases: PubMed, Scopus, and ScienceDirect. The search utilized combinations of keywords such as "indoor microbiome," "house dust," "airborne bacteria/fungi," and "respiratory health," ensuring a broad coverage of the topic. The inclusion criteria were as follows: (1) studies conducted in residential environments with quantified microbial loads; (2) data on environmental factors such as humidity, ventilation, and building material types; (3) molecular or culture-based methods for microbial analysis; and (4) studies that reported on microbial community composition or gene-expression data.

To ensure the relevance and quality of the included studies, only peer-reviewed articles were considered. Studies were excluded if they lacked a clear association between microbial communities and respiratory health outcomes, or if they did not report sufficient microbial load data or environmental factors. The final selection included 20 studies, which provided a comprehensive representation of various residential environments, microbial methodologies, and respiratory health outcomes (Fakunle et al., 2021; Jiang et al., 2022).

Data extraction from the selected studies focused on several key variables: microbial community composition, gene expression related to allergen and toxin production, environmental factors (e.g., humidity, ventilation), and health outcomes (e.g., asthma, COPD). The extracted data included standardized mean differences (SMDs) or $\log_2$ fold-changes for gene expression markers (e.g., brlA, rodA, catA, LPS), and the ecological ratios such as hydrophilic-to-mesophilic fungal ratios and Gram-negative-to-positive bacterial ratios.

The effect sizes were pooled and analyzed using random-effects models (REML) to account for the potential heterogeneity across studies. REML models were chosen because they provide robust estimates of effect sizes and account for both within-study and between-study variability, making them particularly useful for meta-analytic data with diverse study designs (Chandler et al., 2019). The choice of REML was further validated by previous metaanalyses in environmental health research, where this method has been shown to offer accurate and reliable estimates even with moderate heterogeneity.

A subgroup analysis was conducted to differentiate between studies based on the type of sampling method used (air vs. dust samples) and the type of microbial analysis performed (molecular vs. culture-based methods). This allowed for a more granular understanding of how different sampling approaches and methodologies might influence the microbial composition and gene expression profiles in relation to respiratory health outcomes (Cox et al., 2021).

Sampling Methodology and Study Diversity

The studies included in this meta-analysis employed various sampling methodologies, with the most common being air and dust sampling. Air sampling was typically conducted using impaction or filtration methods to capture airborne bacteria and fungal spores, while dust samples were collected from settled dust in homes using standardized vacuuming techniques. The diversity of these sampling methods provided a comprehensive overview of microbial exposure in different indoor environments, which is crucial for understanding the real-world impact of indoor air microbiomes on health.

Additionally, the studies included in this analysis spanned a variety of geographical locations, climates, and housing conditions, providing a diverse representation of residential environments. These variations allowed for the examination of how environmental factors, such as regional humidity and building types, influence microbial communities and their relationship with respiratory health outcomes (Šunić et al., 2025). The inclusion of studies with different methodological approaches (e.g., next-generation sequencing vs. traditional culture-based methods) further enriched the dataset, ensuring the robustness and generalizability of the findings.

RESULT AND DISCUSSION

The results of this meta-analysis highlight significant differences in microbial composition and gene expression between damp and non-damp environments, which have direct implications for respiratory health. Damp homes, characterized by high equilibrium relative humidity (ERH ≥ 85%), exhibited higher concentrations of hydrophilic fungi, with notable compositional shifts but stable alpha diversity (Cox et al., 2021). At ERH levels of 85–100%, fungal sporulation and metabolite gene expression increased, suggesting that moisture is a critical driver of microbial activity and pathogenic potential in indoor environments (Balasubrahmaniam et al., 2024). LeThe presence of Leptosphaerulina in both “moldy” and “non-moldy” homes further supports the notion that environmental factors, rather than taxonomy alone, shape microbial community composition and structure (Chauhan et al., 2023).

Moreover, dominant fungal taxa such as Aspergillus and Cladosporium were consistently found in indoor air, with their presence linked to respiratory issues like asthma and COPD (Kumar et al., 2022). Fungal proliferation on moisture-retentive materials, and the associated aerosolization of mycotoxins, suggests that indoor fungal exposure plays a significant role in the development of respiratory diseases (Al Hallak et al., 2023). This aligns with previous findings, where Aspergillus exposure was correlated with exacerbations in COPD and T2-high asthma phenotypes (Tiew et al., 2024; Vandenborght et al., 2021).

This conceptual framework links environmental fungal exposure and community composition to aeroallergen levels and respiratory outcomes. These relationships are shaped by climatic factors, sampling locations, and analytical methods (culture, NGS, RNA-seq). Meta-analysis integrates fungal exposure and community data to produce indicators such as gene-expression shifts, hydrophilic-to-mesophilic ratios, and risks linked to taxa like Aspergillus spp. Overall, the model explains how indoor fungal ecology drives allergenic and respiratory risks across diverse environments (Fig. 1).

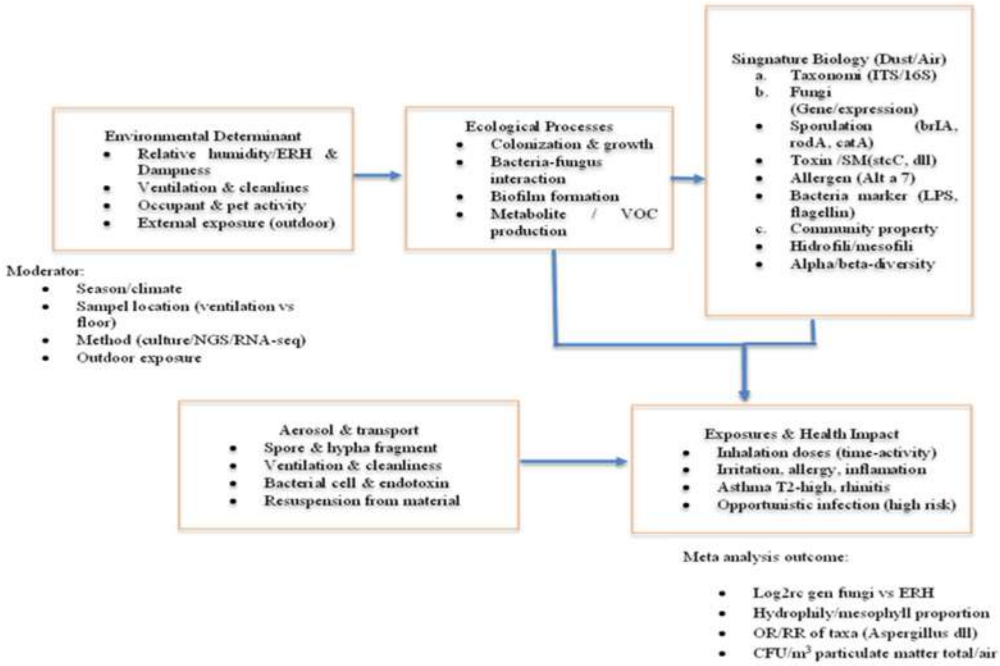

Figure 1. Conceptual framework linking environmental determinants, microbial ecological processes, functional signatures, aerosolisation, and respiratory outcomes.

Table 1 highlights ecological and functional contrasts between fungal and bacterial communities. Fungi respond to humidity and surface porosity, while bacteria reflect occupancy and air circulation.

Table 1. Comparative features of Signature Fungi and Signature Bacteria in indoor environments

Aspect	Signature Fungi	Signature Bacteria
Dominant taxa	Aspergillus, Cladosporium, Penicillium, Leptosphaerulina, Alternaria	Staphylococcus, Pseudomonas, Bacillus, Micrococcus, Corynebacterium
Functional genes	brlA, rodA, catA, stcC, aflR, Alt a 7	LPS, flagellin, luxS, rpoS, algD, katG, sodA
Environmental drivers	ERH ≥ 85 %, porous materials, low ventilation	Ventilation, occupancy, surface humidity
Health impacts	Allergy, asthma, COPD, mycotoxin exposure	Respiratory infection, inflammation, endotoxin irritation
Stable marker	Functional genes + hydrophilic ratio	Functional genes + Gram ratio

Meta-analysis Findings

The findings from the meta-analysis of 20 studies (347 homes) indicate a strong relationship between environmental moisture levels and microbial community composition, particularly in relation to hydrophilic fungi and Gram-negative bacteria. Damp environments (ERH ≥ 85%) showed a standardized mean difference (SMD) of +0.84 (95% CI 0.59–1.08; $p < 0.001$) for hydrophilic fungi and +0.67 (95% CI 0.41–0.93) for Gram-negative bacteria. This suggests that high humidity not only favors fungal growth but also enhances bacterial populations, particularly those associated with inflammation and infection (Hussain et al., 2024).

Metatranscriptomic data revealed a significant increase in biofilm and secondary metabolite gene expression (2.5–3.1-fold) and allergen transcripts (1.8-fold rise for Alt a 7 and Asp f 1), further supporting the hypothesis that indoor microbial exposure under high humidity conditions poses a considerable health risk. These findings align with other studies that have shown how increased microbial virulence and allergenic potential in indoor environments correlate with respiratory diseases, particularly in sensitive populations like children and those with preexisting conditions (Fakunle et al., 2021; Tiew et al., 2024).

Discussion

Humidity and material type are dominant ecological drivers that shape the indoor microbial signatures observed in this study. Fungal communities, particularly hydrophilic species, are highly sensitive to moisture, whereas bacterial communities tend to reflect factors like human occupancy and air circulation (Gilbert & Hartmann, 2024). This observation is consistent with large-scale studies that have shown how microbial richness is influenced by factors such as building design, human activity, and regional climate (Jiang et al., 2022; Šunić et al., 2025). The variability of microbial communities across different climates underscores the importance of considering local environmental conditions when assessing the health risks associated with indoor microbial exposure.

One limitation of this meta-analysis is the heterogeneity ($I^2 = 49\%$) observed across studies. This variability could be attributed to differences in study designs, sampling methods (e.g., air vs. dust samples), and analytical techniques (e.g., culture-based vs. molecular methods), which may influence the detection and quantification of microbial communities. Furthermore, the geographical diversity of the studies included in this analysis introduces an additional layer of complexity, as climate conditions (e.g., temperature and humidity) and local building practices likely affect microbial communities in ways that may not be fully captured by the analysis (Šunić et al., 2025). Future studies should aim for more standardized methodologies and explore how specific environmental factors interact with microbial communities in different regions.

The role of specific microbial taxa in respiratory conditions warrants further exploration. While this meta-analysis demonstrated that exposure to Aspergillus and Cladosporium is linked to increased respiratory symptoms, more in-depth studies are needed to understand how these taxa interact with host immune responses and contribute to disease pathogenesis. In particular, studies on the functional aspects of these microbes, such as toxin production and gene expression related to inflammation, would provide valuable insights into the mechanisms through which indoor microbiomes affect human health. Notably, studies by Iqbal et al., 2024 and Minahan et al., 2024 have explored how specific fungal and bacterial species trigger immune responses that exacerbate respiratory conditions, further emphasizing the need for functional microbiome monitoring (Minahan et al., 2024).

In conclusion, this study highlights the significant role of indoor microbial communities in shaping respiratory health outcomes. The relationship between dampness, microbial composition, and respiratory disease risk underscores the importance of controlling indoor humidity and ensuring proper ventilation in residential environments. By integrating ecological and functional microbial signatures, this research provides a framework for assessing the health risks associated with indoor microbial exposure. Future studies should continue to explore the functional roles of indoor microbiomes and develop targeted interventions to mitigate the risks associated with poor indoor air quality.

CONCLUSION

This study provides a robust framework for assessing indoor microbial exposure using functional–ecological indicators. The key findings from this meta-analysis indicate that combined fungal–bacterial signatures, such as the functional genes (brlA, rodA, catA, stcC, LPS, rpoS) and ecological ratios (hydrophilic fungi; Gram-negative:positive bacteria), are consistent and reliable biomarkers for respiratory health risks. These microbial signatures are strongly influenced by environmental factors like relative humidity and building materials, highlighting their potential in predicting and assessing the health risks associated with indoor microbial exposure.

Maintaining relative humidity levels below 70% and ensuring adequate ventilation are crucial preventive measures for mitigating the health risks posed by indoor microbial communities. These strategies can help limit fungal proliferation and bacterial enrichment, which are associated with respiratory diseases such as asthma, COPD, and allergies. Furthermore, controlling indoor environmental conditions should be a priority in public health policies aimed at reducing the burden of respiratory conditions related to poor indoor air quality.

In terms of future research, further investigation is needed to refine and standardize the use of microbial biomarkers in assessing indoor air quality. Studies should focus on the functional aspects of microbial communities, such as toxin production and inflammatory gene expression, to better understand the mechanisms through which indoor microbiomes contribute to health outcomes. Additionally, more research is needed to explore how microbial signatures vary across different geographical locations, climates, and housing conditions, as these factors can influence microbial composition and exposure risks. Future work should also consider longitudinal studies to track the long-term health impacts of exposure to indoor microbial communities and develop targeted interventions for vulnerable populations.

REFERENCES

Al Hallak, M., Verdier, T., Bertron, A., Roques, C., & Bailly, J.-D. (2023). Fungal contamination of building materials and the aerosolization of particles and toxins in indoor air and their associated risks to health: a review. *Toxins*, *15*(3), 175.

Balasubrahmaniam, N., King, J. C., Hegarty, B., & Dannemiller, K. C. (2024). Moving beyond species: fungal function in house dust provides novel targets for potential indicators of mold growth in homes. *Microbiome*, *12*(1), 231.

Chandler, J., Cumpston, M., Li, T., Page, M. J., & Welch, V. (2019). Cochrane handbook for systematic reviews of interventions. *Hoboken: Wiley*, *4*(1002), 14651858.

Chauhan, B. V, Higgins Jones, D., Banerjee, G., Agrawal, S., Sulaiman, I. M., Jia, C., & Banerjee, P. (2023). Indoor bacterial and fungal burden in “moldy” versus “non-moldy” homes: A case study employing advanced sequencing techniques in a us metropolitan area. *Pathogens*, *12*(8), 1006.

Cox, J., Stone, T., Ryan, P., Burkle, J., Jandarov, R., Mendell, M. J., Adams, R. I., Niemeier-Walsh, C., & Reponen, T. (2021). Associations of observed home dampness and mold with the fungal and bacterial dust microbiomes. *Environmental Science: Processes & Impacts*, *23*(3), 491–500.

Fakunle, A. G., Jafta, N., Naidoo, R. N., & Smit, L. A. M. (2021). Association of indoor microbial aerosols with respiratory symptoms among under-five children: a systematic review and meta-analysis. *Environmental Health*, *20*(1), 77.

Gilbert, J. A., & Hartmann, E. M. (2024). The indoors microbiome and human health. *Nature Reviews Microbiology*, *22*(12), 742–755.

Hussain, A., Rahman, M., Bibi, T., Fatima, R., Arif, I., Barwant, M. M., & Ali, S. A. (2024). Prevalence of microorganisms in indoor household environments and their pathogenesis. *Journal of Antimicrobial Agents*, *10*(1), 1–5.

Jiang, X., Wang, C., Guo, J., Hou, J., Guo, X., Zhang, H., Tan, J., Li, M., Li, X., & Zhu, H. (2022). Global meta-analysis of airborne bacterial communities and associations with anthropogenic activities. *Environmental Science & Technology*, *56*(14), 9891–9902.

Kumar, P., Singh, A. B., & Singh, R. (2022). Comprehensive health risk assessment of microbial indoor air quality in microenvironments. *Plos One*, *17*(2), e0264226.

Minahan, N. T., Chen, C.-H., Chuang, Y.-C., Tsai, K.-H., Shen, W.-C., & Guo, Y. L. (2024). Fungal spore richness and abundance of allergenic taxa: Comparing a portable impactor and passive trap indoors and outdoors in an urban setting. *Microbial Ecology*, *87*(1), 45.

Šunić, I., Havaš Auguštin, D., Šarac, J., Michl, K., Cernava, T., Jakobsen, R. R., Mešić, A., Novokmet, N., & Lovrić, M. (2025). Associations Between Indoor Fungal Community Structures and Environmental Factors: Insights from the Evidence-Driven Indoor Air-Quality Improvement Study. *Journal of Fungi*, *11*(4), 261.

Tiew, P. Y., Leung, J. M., Mac Aogáin, M., Johal, P., Jaggi, T. K., Yuen, A. C. Y., Ivan, F. X., Yang, J., Afshar, T., & Tee, A. (2024). Residential exposure to Aspergillus spp. is associated with exacerbations in COPD. *European Respiratory Journal*, *64*(5).

Vandenborght, L.-E., Enaud, R., Urien, C., Coron, N., Girodet, P.-O., Ferreira, S., Berger, P., & Delhaes, L. (2021). Type 2–high asthma is associated with a specific indoor mycobiome and microbiome. *Journal of Allergy and Clinical Immunology*, *147*(4), 1296–1305.