International Journal of Scientific Research and Engineering Development-– Volume 9 Issue 3, May-June 2026
Available at www.ijsred.com

RESEARCH ARTICLE OPEN ACCESS

Prevalence and Distribution of Fungal Contamination Across Indoor Microenvironments in Tropical Residential Settings: A Cross-Sectional Study in Bangkok, Thailand

Phuwit Kanjanarujee*, Nunnaphat Wongsuwan**, Arunrat Suwanvoradit***, Napinprapa Angkanavisan****, Chawanakorn Klumwilai*****, Sarunrak Wiwatwongsakul******, Ratnapee Mornchan*******, Thanunchanok Tosomsakul********* and Khwanchai Pramoonsap**********

* (Suankularb Wittayalai School, Bangkok, Thailand
Email: jeen0553@gmail.com)
** (Anglo Singapore International School, Bangkok, Thailand
Email: cutemayah2017@gmail.com)
*** (Singapore International School of Bangkok, Bangkok, Thailand
Email: meiji.arunrat@gmail.com)
**** (Benchamaracharungsarit School, Chachoengsao, Thailand
Email: napinprapaairi@gmail.com)
***** (Potisarnpittayakorn School, Bangkok, Thailand
Email: thanawinpoch@gmail.com)
****** (Sarasas Ektra School, Bangkok, Thailand
Email: sarunrak21@gmail.com)
******* (Triam Udom Suksa School, Bangkok, Thailand
Email: morncanghotmail@gmail.com)
******** (Patumwan Demonstration School, Srinakharinwirot University, Bangkok, Thailand
Email: thanunchanok.to@gmail.com)
********* (Patumwan Demonstration School, Srinakharinwirot University, Bangkok, Thailand
Email: cutemayah2017@gmail.com)
********** (Independent Researcher, Bangkok 10400, Thailand
Email: Khwananight@gmail.com)

\-************************\-

Abstract:

Indoor fungal contamination poses a recognized public health risk in tropical climates; however, surface-level fungal data from residential settings in Southeast Asia remain limited. This study aimed to quantify surface fungal loads, characterize yeast-to-mold distributions, and identify principal contamination hotspots across eight indoor room types in Bangkok households. A cross-sectional study was conducted in multiple residential units in Bangkok and its surrounding areas, Thailand, from October to December 2025. A total of 139 surface samples were collected from bedrooms, living rooms, bathrooms, kitchens, dining rooms, laundry areas, storage rooms, and pet rooms using sterile swabs and adhesive tape-lift methods. Samples were cultured on Potato Dextrose Agar supplemented with chloramphenicol and incubated at 28°C for 14 days. Fungal colonies were counted as colony-forming units per milliliter (CFU/ml) and provisionally classified as yeast, mold, or mixed types based on macroscopic morphology confirmed by Lactophenol Cotton Blue microscopy for representative isolates. All 139 samples tested positive (prevalence = 100%), with an overall mean load of 8.92×10^2 CFU/ml. The highest mean loads were recorded in bathrooms (1.49×10^3 CFU/ml), kitchens (1.34×10^3 CFU/ml), and laundry areas (1.04×10^3 CFU/ml), reflecting the influence of moisture, organic matter accumulation, and limited ventilation. The most contaminated surfaces were shower areas, curtains, and washing machines. Yeasts predominated on fabric and human-contact surfaces, while molds were more frequent in high-moisture zones. These findings support targeted control measures to reduce fungal exposure in tropical households, including maintaining indoor relative humidity below 60%, routine textile laundering at ≥60°C, and regular cleaning of air-conditioning filters.

Keywords — **Indoor fungi, Household contamination, Yeast and mold, Tropical environment, Surface sampling**

* * *

I. INTRODUCTION

Among indoor microorganisms, fungi are of particular public health concern. Prolonged exposure to fungal allergens is associated with increased airway hyperreactivity, dysregulated IgE-mediated immunity, and worsening respiratory symptoms, with odds ratios for asthma onset of 1.5–2.0 in mold-exposed cohorts [3,4]. Environmental conditions such as sustained high humidity (>70% RH), inadequate ventilation (<0.35 air changes/hour), and persistent dampness have been associated with enhanced fungal growth and increased release of allergenic proteins [5]. Understanding fungi's contribution to allergic disease is therefore important for developing evidence-based prevention strategies [6,7].

In residential settings, indoor microbial communities reflect a combination of endogenous sources, such as household dust and biofilms, and exogenous inputs from the outdoor environment, creating exposure gradients that vary by climate and building design [2]. Microorganisms originate from natural reservoirs such as soil, plant debris, and decaying organic matter, as well as anthropogenic activities including wastewater treatment, construction, and human respiration [1].

Previous studies have documented recurring patterns of indoor fungal contamination. Cladosporium spp. have been identified as a dominant genus across diverse indoor environments, including hospital ventilation systems (comprising 25–40% of airborne isolates) and reusable face masks (10^2–10^3 CFU/cm^2) [8,9]. Indoor fungal concentrations in university residences have been reported to exceed outdoor levels by 1.5–3-fold [10,11]. In urban tropical settings, seasonal surges in airborne spore counts—reaching 2,000–5,000 spores/m^3 during monsoon periods—reflect the combined effects of high humidity (80–95% RH) and elevated temperatures (>30°C) on fungal proliferation [12].

Xerophilic genera such as Aspergillus, Penicillium, and Cladosporium thrive in humid, poorly ventilated homes, and have been linked to increased rates of atopy and asthmatic episodes [2,13]. High-moisture areas such as bathrooms and kitchens are recognized contamination hotspots, with longitudinal data associating chronic fungal exposure with 15–30% higher rates of respiratory symptom recurrence [14,15]. However, most existing studies have focused on airborne spore sampling rather than surface contamination.

Despite these known risks, surface-level fungal surveys in Thai and broader Southeast Asian residential settings are conspicuously absent from the literature. This gap precludes the development of region-specific control thresholds and targeted decontamination guidelines.

This study therefore aimed to: (i) assess fungal prevalence and load across different room types and surface categories in Thai residential households; (ii) compare yeast and mold distribution by room type and surface material; and (iii) identify surface types and specific sampling locations associated with the highest fungal loads.

II. MATERIAL AND METHOD

A. Study Design

A cross-sectional observational study was conducted to investigate the prevalence and distribution of fungal contamination on surfaces and appliances within residential indoor environments. Surface sampling was performed in multiple residential units in the Bangkok Metropolitan Region from October to December 2025. The study focused on common indoor areas and appliances that may serve as fungal reservoirs, including air conditioners, fans, windows, pillows, bedsheets, walls, and sinks. The primary outcomes were fungal load (CFU/ml), morphological classification of isolates as yeast or mold, and identification of major contamination hotspots.

Written informed consent was obtained from all household owners prior to sampling. No identifiable personal data were collected during this study.

B. Sample Size Calculation

The sample size was calculated based on the mean prevalence reported in three previous studies: Ghazanfari et al. (2022) (P_1 = 0.771), Ghodsi et al. (2025) (P_2 = 0.803), and Kamali & Taheri Sarvtin (2024) (P_3 = 0.45), yielding a pooled arithmetic mean prevalence (P) of 0.675. The lower prevalence reported by Kamali & Taheri Sarvtin (2024) (P_3 = 0.45) may reflect a different sampling substrate or arid climatic context; the arithmetic mean was nonetheless used to generate a conservative sample size estimate. The following formula was applied:

$$n = Z^2\alpha/2 \times P(1-P) / e^2$$

where n = required sample size; P = mean prevalence; Z = 1.96 (95% confidence level); and e = 0.10 (10% margin of error). This calculation yielded a minimum of 85 sampling points. To allow for subgroup analysis across surface types and room categories, a total of 139 samples were collected.

C. Study Site Selection

Seven room types commonly found in residential homes were selected: bedroom, bathroom, living room, kitchen, laundry area, storage room, and pet room. Sampling sites within each room were chosen based on a systematic multistage sampling approach in which primary sampling units (room types) were selected based on their prevalence in urban Thai households, and secondary units (specific surfaces) were selected to represent the full range of surface materials and moisture microenvironments present in each room. Surfaces were categorized into three types: (i) hard surfaces (metal/plastic), including fans, air-conditioner casings, window frames, door knobs, and sinks; (ii) airborne-related equipment, including air purifiers, air-conditioner vents, dehumidifier filters, and exhaust fans; and (iii) fabric/soft surfaces, including pillows, curtains, bedsheets, sofa covers, and mattresses.

D. Sampling Procedure

1) Surface Sampling

Sterile cotton swabs moistened with 0.85% sterile saline were used to swab a standardized 2 cm × 2 cm (4 cm^2) area from each selected hard or semi-hard surface, including air-conditioner vents, window frames, walls, and sinks. For delicate or porous materials such as fabrics and plastics, adhesive tape-lift methods were applied over an equivalent 4 cm^2 area for direct surface imprinting. All samples were transported to the laboratory within 24 hours of collection.

2) Culture and Identification Methods

Each swab was suspended in 1 mL of 0.85% sterile saline and vortexed for 30 seconds at maximum speed on a standard benchtop vortex mixer to dislodge adherent fungal material. From each 1 mL suspension, a 100 µL aliquot was spread-plated onto Potato Dextrose Agar (PDA) supplemented with chloramphenicol (50 µg/mL) using a flame-sterilized glass spreader. Because only 100 µL (0.1 mL) of the 1 mL suspension was plated, colony counts were multiplied by a factor of 10 to back-calculate CFU/ml of the original suspension, yielding a minimum detection threshold of 10 CFU/ml.

Plates were incubated in an inverted position to prevent condensation contamination. Early growth was monitored at 25°C for 48–96 hours, with inspections at 24, 48, 72, and 96 hours to document colony emergence and characteristics. Incubation then continued aerobically at 28°C up to day 14 to allow slower-growing taxa to develop. Colony-forming units (CFU) were counted manually using a colony counter under ambient light and stereomicroscopy.

All fungal classifications reported in this study are provisional and based on macroscopic morphological criteria. Isolates were classified as yeast or mold based on colony color, surface texture, margin characteristics, and the presence or absence of aerial hyphae. Representative isolates from each morphotype were subcultured to purity and confirmed microscopically using Lactophenol Cotton Blue staining, documenting budding cells and pseudohyphae in yeasts, and hyphal septation and conidiogenous structures in filamentous molds. Genus- or species-level identification was not performed; all classifications represent morphological phenotypes rather than confirmed taxonomic assignments.

E. Statistical Analysis

Descriptive statistics were used to characterize fungal contamination across samples. Prevalence was defined as the proportion of samples yielding $\geqslant 1$ CFU/ml and was calculated for each room type and surface category. Fungal load was summarized as the arithmetic mean, standard deviation (SD), and range (minimum–maximum) for each category. Samples in which colonies were too numerous to count accurately (TNTC; >300 CFU/plate, equivalent to $>3 \times 10^3$ CFU/ml in the original suspension) were assigned a censored value of 3×10^3 CFU/ml for computational purposes, to avoid overestimation bias; 14 samples (10.1%) met this criterion.

Fungal composition (yeast, mold, or mixed) was reported as proportions within each room and surface category. Given the non-normal distribution of fungal load data and the unequal, limited sample sizes within several room categories, formal inferential comparisons across room types were not performed. Data were organized and analyzed using Microsoft Excel and SPSS version 26.

III. RESULTS AND DISCUSSION

F. Distribution of Sampling Sites

A total of 139 samples were collected from eight room types. Bedrooms contributed the largest proportion of samples (n = 53; 38.1%), followed by living rooms (n = 37; 26.6%), bathrooms (n = 23; 16.2%), kitchens (n = 10; 7.2%), dining rooms (n = 6; 4.3%), laundry areas (n = 5; 3.6%), storage rooms (n = 3; 2.2%), and pet rooms (n = 2; 1.4%). This distribution reflects the relative frequency with which these room types are found in typical urban Thai households, where bedrooms, living rooms, and bathrooms are nearly universal, while specialized rooms such as pet rooms and storage rooms are less common (Fig. 1).

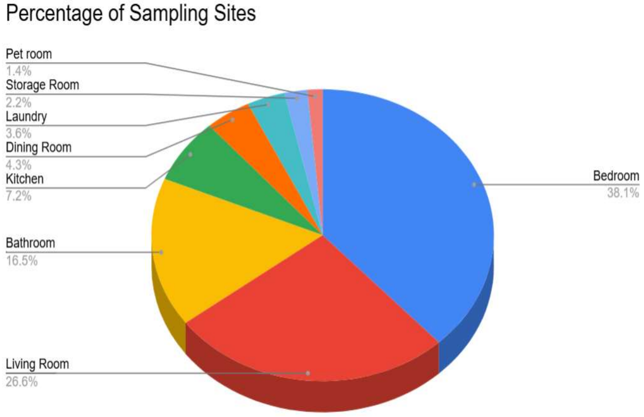

Fig. 1 Percentage distribution of sampling sites across eight room types (n = 139).

G. Fungal Contamination by Room Type

All 139 samples tested positive, representing a prevalence of 100% across all room types (Table 1). Mean fungal loads varied markedly by room, ranging from 2.00×10^1 CFU/ml in pet rooms to $>3 \times 10^3$ CFU/ml in kitchens. The overall mean fungal load was 8.92×10^2 CFU/ml.

Bathrooms recorded the highest corrected mean load ($1.49 \pm 1.41 \times 10^3$ CFU/ml), consistent with their persistent dampness and limited ventilation. Kitchens ($1.34 \pm 1.43 \times 10^3$ CFU/ml) and laundry areas ($1.04 \pm 1.18 \times 10^3$ CFU/ml) also showed high mean loads, reflecting the combined effects of moisture, organic residue accumulation, and heat. Bedrooms ($9.48 \pm 12.8 \times 10^2$ CFU/ml) and living rooms ($7.80 \pm 12.0 \times 10^2$ CFU/ml) showed similar intermediate loads, likely attributable to comparable humidity levels, frequent human activity, and similar ventilation patterns. Pet rooms and dining rooms recorded the lowest mean loads; however, given the very small sample sizes for these room types (n = 2 and n = 6, respectively), definitive conclusions about these categories cannot be drawn.

These findings are consistent with prior studies documenting elevated indoor fungal loads in humid tropical environments. Tabatabaei et al.

reported mean surface fungal loads of 10^2–10^3 CFU/ml in high-moisture indoor environments in hot, humid climates [20], a range comparable to the bathroom and kitchen loads observed in the present study. Similarly, Jabeen et al. documented indoor surface contamination levels of 10^2–10^3 CFU/m³ in subtropical educational settings, further supporting the role of humidity and limited ventilation as primary drivers of fungal accumulation [21]. When the surface-derived loads from the present study are extrapolated to airborne equivalents using a theoretical surface-to-air resuspension transfer efficiency of 10–20% [26], estimated airborne concentrations would approximate 10^2–10^3 CFU/m³; however, this calculation carries substantial uncertainty and should not be interpreted as measured airborne data. This estimated range nonetheless exceeds reported temperate indoor air baselines of 78–788 CFU/m³ [20,21], a disparity that may reflect tropical amplification, where elevated temperatures (>25°C) favor thermotolerant species such as Aspergillus spp. [19].

TABLE 1. FUNGAL CONTAMINATION BY ROOM TYPE (N = 139).

Room/Area	No. of Sampling Sites	Positive Samples (n)	Prevalence (%)	Range of CFU/ml	Mean ± SD CFU/ml
Bedroom	53	53	100	2×10^1 – >3×10^3	$(9.48 \pm 12.8)\times10^2$
Living Room	37	37	100	1×10^1 – >3×10^3	$(7.80 \pm 12.0)\times10^2$
Bathroom	23	23	100	1×10^1 – >3×10^3	$(1.49 \pm 1.41)\times10^3$
Kitchen	10	10	100	1×10^2 – >3×10^3	$(1.34 \pm 1.43)\times10^3$
Dining Room	6	6	100	1.3×10^2 – 1.9×10^2	$(9.0 \pm 6.3)\times10^1$
Laundry	5	5	100	6×10^2 – >3×10^3	$(1.04 \pm 1.18)\times10^3$
Storage Room	3	3	100	1×10^2 – 1.5×10^2	$(1.30 \pm 0.58)\times10^2$
Pet Room	2	2	100	1×10^1 – 3×10^1	$(2.00 \pm 1.41)\times10^1$

H. Yeast and Mold Distribution by Room Type

Mixed fungal contamination (combined yeast and mold) predominated overall, accounting for 33.8% of all samples (Table 2). Bedrooms showed the highest proportion of yeast-positive samples (45.3%), which may be explained by organic skin residues on bedding providing substrates for yeast growth. Kitchens and laundry areas showed a higher proportion of mold-positive samples (40.0% and 60.0%, respectively), consistent with their acidic, detergent-rich microenvironments. Bathrooms were predominantly mixed (39.1%), reflecting diverse moisture-dependent fungal niches. These patterns align with studies reporting yeast enrichment in human-proximate zones [22,23], and contrast with mold-dominant bathroom patterns observed in temperate climates, suggesting that tropical warmth may alter competitive dynamics among fungal taxa.

TABLE 2. DISTRIBUTION OF YEAST, MOLD, AND MIXED CONTAMINATION BY ROOM TYPE.

Room	No. of Sampling Points	No. of Positive Samples	Yeast-Positive Samples (n, %)	Mold-Positive Samples (n, %)	Mixed Yeast + Mold (n, %)	Predominant Fungal Type
Bedroom	53	53 (100%)	24 (45.3%)	12 (22.6%)	17 (32.1%)	Mixed
Living Room	37	37 (100%)	13 (35.1%)	11 (29.7%)	13 (35.1%)	Mixed
Bathroom	23	23 (100%)	6 (26.1%)	8 (34.8%)	9 (39.1%)	Mixed
Kitchen	10	10 (100%)	3 (30.0%)	4 (40.0%)	3 (30.0%)	Mold
Dining Room	6	6 (100%)	4 (66.7%)	1 (16.7%)	1 (16.7%)	Yeast
Laundry	5	5 (100%)	1 (20.0%)	3 (60.0%)	1 (20.0%)	Mold
Storage Room	3	3 (100%)	1 (33.3%)	0 (0.0%)	2 (66.7%)	Mixed
Pet Room	2	2 (100%)	0 (0.0%)	1 (50.0%)	1 (50.0%)	Mixed
Total	**139**	**139 (100%)**	**52 (37.4%)**	**40 (28.8%)**	**47 (33.8%)**	—

I. Fungal Contamination by Surface Type

Surface-specific contamination data are presented in Table 3. Among individual surface types, shower areas (>3×10^3 CFU/ml), refrigerators (>3×10^3 CFU/ml), and curtains (1.28×10^3 CFU/ml) recorded the highest fungal loads, followed by washing machines (1.27×10^3 CFU/ml) and air conditioners (1.12×10^3 CFU/ml). Air conditioners and washing machines displayed predominantly mixed fungal communities, consistent with condensate-driven biofilm formation in these appliances [6,13]. Hard surfaces such as door knobs (4.35×10^2 CFU/ml), mirrors (3.85×10^2 CFU/ml), and tables (1.90×10^2 CFU/ml) showed comparatively lower loads, likely because smooth, non-porous surfaces retain less moisture and organic debris.

When grouped by surface category, fabric/soft surfaces showed the highest mean fungal load ($9.35 \times 10^2 \pm 3.88 \times 10^2$ CFU/ml), followed by airborne-related equipment ($8.62 \times 10^2 \pm 3.16 \times 10^2$ CFU/ml) and hard surfaces ($7.85 \times 10^2 \pm 3.42 \times 10^2$ CFU/ml) (Figure 2). Fabric surfaces also showed the highest positivity rate (96.2%), highlighting their role as persistent fungal reservoirs due to their porous structure and resistance to routine cleaning [24].

TABLE 3. SUMMARY OF FUNGAL CONTAMINATION BY SURFACE TYPE.

Surface Type / Sampling Area	No. of Samples (n)	Samples (n, %) in 139	Mean Fungal Load (CFU/ml ± SD)	Range (CFU/ml)	Dominant Fungal Type
Air-conditioner	23	16.5%	$1.12 \times 10^3 \pm 2.65 \times 10^2$	$7.8 \times 10^2 – >3 \times 10^3$	Mixed
Fan	12	8.6%	$9.85 \times 10^2 \pm 1.88 \times 10^2$	$6.8 \times 10^2 – >3 \times 10^3$	Mold
Window frame	5	3.6%	$7.45 \times 10^2 \pm 2.04 \times 10^2$	$3.2 \times 10^2 – >3 \times 10^3$	Mixed
Pillow/Side pillow	7	5.0%	$1.05 \times 10^3 \pm 2.12 \times 10^2$	$8.2 \times 10^2 – >3 \times 10^3$	Yeast
Curtain	3	2.2%	$1.28 \times 10^3 \pm 2.15 \times 10^2$	$9.5 \times 10^2 – 1.45 \times 10^3$	Mixed
Bedsheet/Mattress/Bed area	10	7.2%	$9.60 \times 10^2 \pm 1.92 \times 10^2$	$6.8 \times 10^2 – >3 \times 10^3$	Yeast
Wall surface	5	3.6%	$6.25 \times 10^2 \pm 1.46 \times 10^2$	$3.1 \times 10^2 – 8.6 \times 10^2$	Mixed
Sink / Basin area	8	5.8%	$8.85 \times 10^2 \pm 2.01 \times 10^2$	$5.5 \times 10^2 – >3 \times 10^3$	Mixed
Washing Machine (surface and drum)	4	2.9%	$1.27 \times 10^3 \pm 2.21 \times 10^2$	$9.0 \times 10^2 – >3 \times 10^3$	Mixed
Toilet seat	3	2.2%	$8.40 \times 10^2 \pm 1.58 \times 10^2$	$6.2 \times 10^2 – >3 \times 10^3$	Yeast
Floor tile/Stairs	5	3.6%	$5.75 \times 10^2 \pm 1.35 \times 10^2$	$3.5 \times 10^2 – >3 \times 10^3$	Mold
Dehumidifier / Air purifier	10	7.2%	$8.62 \times 10^2 \pm 1.97 \times 10^2$	$5.9 \times 10^2 – >3 \times 10^3$	Mixed
Door knob / Handle	4	2.9%	$4.35 \times 10^2 \pm 1.04 \times 10^2$	$2.7 \times 10^2 – 5.8 \times 10^2$	Yeast
Mirror / Glass surface	3	2.2%	$3.85 \times 10^2 \pm 1.08 \times 10^2$	$2.5 \times 10^2 – 5.3 \times 10^2$	Mold
Closet/Closet area	5	3.6%	$5.20 \times 10^2 \pm 3.45 \times 10^2$	$1.4 \times 10^2 – >3 \times 10^3$	Yeast
Sofa	2	1.4%	$1.02 \times 10^3 \pm 4.12 \times 10^2$	$1.3 \times 10^2 – >3 \times 10^3$	Mold
TV	2	1.4%	$6.75 \times 10^2 \pm 2.12 \times 10^2$	$5.0 \times 10^1 – 1.9 \times 10^2$	Mixed
Printer	1	0.7%	$1.00 \times 10^2 \pm 0.00$	1.0×10^2	Mixed
Table/Table area	3	2.2%	$1.90 \times 10^2 \pm 1.23 \times 10^2$	$1.4 \times 10^2 – 2.1 \times 10^2$	Mixed
Refrigerator/Refrigerator area	3	2.2%	$>3 \times 10^3 \pm 0.00$	$>3 \times 10^3$	Mold
Shower area	2	1.4%	$2.39 \times 10^3 \pm 8.63 \times 10^2$	$1.78 \times 10^3 – >3 \times 10^3$	Mixed
Shelf	3	2.2%	$6.80 \times 10^2 \pm 2.34 \times 10^2$	$3.0 \times 10^1 – 1.28 \times 10^3$	Mixed
CPU	1	0.7%	$8.00 \times 10^1 \pm 0.00$	8.0×10^1	Yeast
Furniture/Home decor	15	10.8%	$7.25 \times 10^2 \pm 1.89 \times 10^2$	$1.0 \times 10^1 – >3 \times 10^3$	Mixed
Average / Overall	139	100%	$8.92 \times 10^2 \pm 2.14 \times 10^2$	$1.0 \times 10^1 – >3 \times 10^3$	—

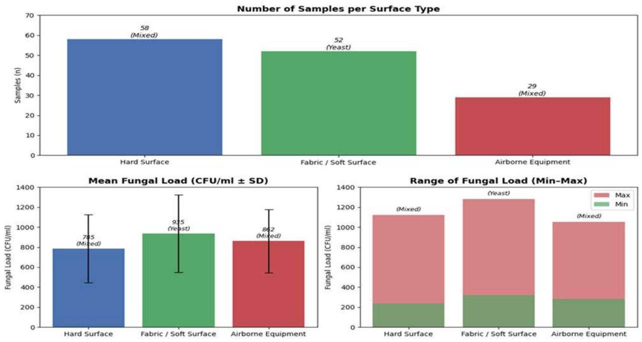

Fig. 2 Summary of fungal contamination across three surface categories. (2A) Number of samples; (2B) Mean fungal load (CFU/ml ± SD); (2C) Range and dominant fungal type.

J. Top 10 Most Contaminated Sampling Points

Table 4 presents the ten sampling points with the highest fungal loads. Bathroom showers ranked first (>3 × 10^3 CFU/ml; mixed), consistent with persistent biofilm formation driven by high humidity and organic residues from soap and skin shedding. This exceeds surface measurements reported in comparable bathroom environments of 43.7 ± 30.2 CFU/cm³ and implies extrapolated airborne equivalents of approximately 300–450 CFU/m³, approaching the WHO's suggested indoor threshold of 500 CFU/m³ [28,29].

Bedroom curtains (Rank 2; 1.28 × 10^3 CFU/ml) and the area behind the washing machine (Rank 3; 1.27 × 10^3 CFU/ml) also showed high contamination, reflecting moisture-trapping properties of porous fabrics and stagnant condensate in poorly ventilated laundry spaces [30].

Air-conditioning units in both living rooms (Rank 4; 1.12 × 10^3 CFU/ml) and bedrooms (Rank 5; 1.05 × 10^3 CFU/ml) were consistent contamination vectors, attributed to dust accumulation on coils and periodic condensate formation that facilitates spore dissemination through cooled airstreams [6].

Bathroom toilet seats (Rank 6; 8.40 × 10^2 CFU/ml; yeast) and bedroom pillows (Ranks 7–8; 6.50 × 10^2 and 6.10 × 10^2 CFU/ml; yeast) showed moderate contamination driven by human-derived organic substrates and nocturnal humidity, respectively [31,32]. The predominance of mixed fungal communities at 70% of the highest-load sites is consistent with the possibility that yeast activity may precondition surfaces for subsequent mold colonization through acidification and substrate modification, though this mechanistic explanation remains speculative and warrants direct investigation in future studies.

Extrapolated airborne fungal loads at high-exposure sites frequently exceeded recommended residential limits of <150 CFU/m³ [33], and in some cases, the WHO guideline of <500 CFU/m³ [29], particularly in humid tropical conditions where elevated vapor pressure accelerates spore germination. These extrapolations are theoretical and should be interpreted with caution pending direct airborne sampling.

TABLE 4. TOP 10 MOST CONTAMINATED SAMPLING POINTS, RANKED BY FUNGAL LOAD.

Rank	Room / Location	Specific Sampling Area	Dominant Fungal Type	CFU/ml	Interpretation
1	Bathroom	Shower	Mixed	>3×10^3	Highest proliferation; persistent humidity and biofilms amplify spore release.
2	Bedroom	Curtain	Mixed	1.28×10^3	Fabric traps dust/moisture, fostering mixed growth akin to neglected textiles.
3	Laundry	Behind washing machine	Mixed	1.27×10^3	Poor ventilation and condensate create anaerobic niches for resilient molds.
4	Living Room	Air conditioner	Mixed	1.12×10^3	Condensate/dust accumulation in HVAC systems promotes aerosolized dissemination.
5	Bedroom	Air conditioner	Mixed	1.05×10^3	Cooled, humid airstreams select for psychrotolerant fungi.
6	Bathroom	Toilet seat	Yeast	8.40×10^2	High-touch organic residues favor yeast in intermittent wet conditions.
7	Bedroom	Pillow	Yeast	6.50×10^2	Skin-derived nutrients and nightly humidity sustain yeast colonization.

Rank	Room / Location	Specific Sampling Area	Dominant Fungal Type	CFU/ml	Interpretation
8	Bedroom	Pillow	Yeast	6.10×10^2	Repeated exposure to body oils exacerbates soft-surface contamination.
9	Living Room	Fan	Mold	6.00×10^2	Circulating dust-laden air deposits spores on blades, aiding dispersal.
10	Kitchen	Washing machine	Mixed	4.80×10^2	Detergent residues and warmth synergize with moisture for diverse growth.

K. Practical Implications

Based on the contamination patterns identified, targeted dehumidification to maintain indoor relative humidity below 60% is recommended as a primary intervention, particularly in bathrooms and laundry areas [5]. Routine disinfection of high-load surfaces—including shower areas, air-conditioner coils, and washing machine drums—using antifungal agents such as sodium hypochlorite (1,000 ppm) or ethanol-based disinfectants is advisable. HEPA filtration in HVAC systems may reduce aerosolized spore dissemination by up to 70%, as reported in meta-analytic studies [23]. For fabric surfaces, weekly laundering at temperatures exceeding 60°C and periodic UV exposure of bedding and curtains are recommended to disrupt yeast-dominated reservoirs.

IV. CONCLUSIONS

This study provides evidence of widespread fungal colonization across indoor residential microenvironments in a humid tropical setting, with 100% prevalence among 139 samples collected in the Bangkok Metropolitan Region. Mean fungal loads ranged from 2.00×10^1 CFU/ml in pet rooms to $>3 \times 10^3$ CFU/ml in kitchens, with an overall mean of 8.92×10^2 CFU/ml. High-moisture areas, particularly bathrooms (1.49×10^3 CFU/ml), kitchens (1.34×10^3 CFU/ml), and laundry areas (1.04×10^3 CFU/ml), showed the greatest fungal burdens. Among surfaces, shower areas, curtains, washing machines, and air conditioners were identified as principal contamination hotspots, collectively accounting for a substantial proportion of high-load ($>10^3$ CFU/ml) samples.

The predominance of mixed yeast–mold communities (33.8% of all samples) indicates that multiple fungal taxa coexist across residential microenvironments, a pattern with implications for both allergen diversity and occupant exposure risk. Yeasts were more prevalent on human-contact surfaces, while molds predominated in persistently damp areas. These findings are consistent with established principles of indoor mycology and underscore the role of moisture, organic substrates, and limited ventilation in driving fungal proliferation in tropical households.

LIMITATIONS

This study has several important limitations. First, the unequal distribution of samples across room types, particularly the very small numbers in pet rooms (n = 2) and storage rooms (n = 3), limits the generalizability of findings for those categories. Second, fungal classification relied on morphological criteria rather than molecular identification, so genus- and species-level conclusions cannot be drawn. Third, the cross-sectional design precludes assessment of temporal variation in fungal load across seasons. Finally, the absence of concurrent airborne sampling means that extrapolated airborne estimates carry substantial uncertainty and should be treated as theoretical approximations.

Prioritizing dehumidification, HVAC filtration, and fabric maintenance represents the most practical public health strategy for reducing fungal exposure and mitigating the associated risks of allergic sensitization and mycotoxin-mediated illness among residents. Future research should incorporate longitudinal designs, molecular identification methods such as ITS rRNA amplicon sequencing, and controlled intervention trials across diverse socioeconomic settings. These approaches would help refine evidence-based guidelines for indoor fungal management in tropical urban environments.

REFERENCES

[1] Stockwell RE, Rinehart AR, Smith DL. Microbial volatile organic compounds in indoor environments: a review. Microbiome. 2019;7(1):144.
[2] Nevalainen A, Täubel M, Hyvärinen A, Rintala H, Laitinen S. Control of exposure to airborne fungal spores. Indoor Air. 2015;25(Suppl 1):10–19.
[3] Kettleson EM, Adhikari A, Vesper S, Coombs K, Schaffer C, Reponen T. Applying quantitative bias analysis to epidemiologic data to improve risk assessments of residential indoor exposure to fungal allergen. Sci Total Environ. 2015;527–528:262–270.
[4] Bush RK, Prochnau JJ. Fungal allergens. J Allergy Clin Immunol Pract. 2017;5(2):282–286.
[5] Fisk WJ, Lei-Gomez Q, Mendell MJ. Meta-analyses of the associations of respiratory health effects with dampness and mold in homes. Indoor Air. 2010;17(4):284–296.
[6] Zhang Z, Lv X, Zhao Z. Indoor fungal exposure and respiratory health: a systematic review. Environ Int. 2020;142:105831.
[7] Beggs PJ, Bambrick HJ, True PV, Xu Z, Davies JM, Slobodin T, et al. Climate change and allergic disease. Clin Exp Allergy. 2022;52(1):14–26.
[8] Ahmad NI, Shahrir NF, Omar Hamdan AS, Kamarudin NA, Mohammad Sham N, Mahmood J, et al. Fungi assessment in indoor and outdoor environment of four selected hospitals in Peninsular Malaysia. J Fungi (Basel). 2025;11(3):182.
[9] Park AM, Kim JH, Lee SY. Microbial contamination on reusable face masks during the COVID-19 pandemic. J Appl Microbiol. 2022;133(4):1456–1467.
[10] Zeynab T, Reza A, Mahsa K. Fungal contamination in indoor air: a global review of sources, health effects, and control measures. Atmos Pollut Res. 2020;11(10):1835–1845.
[11] Lanthier-Veilleux M, Généreux M, Baron G. Prevalence of residential dampness and mold exposure in a university student population. Int J Environ Res Public Health. 2016;13(2):194.
[12] Kumar P, Singh R. Microbial indoor air pollution in Delhi Metropolitan City is attributable to severe respiratory and general health effects among residents. Front Public Health. 2025;13:1626827.
[13] Mendell MJ, Mirer AG, Cheung K, Tong M, Douwes J. Respiratory and allergic health effects of dampness, mold, and dampness-related agents: a review of the epidemiologic evidence. Environ Health Perspect. 2011;119(6):748–756.
[14] Aydogdu H, Asan A, Ture M, Ozer U. Diversity and concentrations of airborne fungi and bacteria in three different bioaerosol sites. Indoor Built Environ. 2010;19(5):485–494.
[15] Reponen T, Vesper S, Levin L, Johansson SG, Tomaz CA, Vanka A, et al. Infants' indoor environmental exposures predict allergy symptoms in early childhood. J Allergy Clin Immunol. 2012;129(2 Suppl):AB2.
[16] Efthymiopoulos S, Aktas YD, Altamirano H. Common sampling techniques for the assessment of indoor fungal growth. In: Proceedings of the 2nd International Conference on Moisture in Buildings (ICMB23); 2023.
[17] Cox J, Indugula R, Vesper S, Zhu Z, Jandarov R, Reponen T. Comparison of indoor air sampling and dust collection methods for fungal exposure assessment using quantitative PCR. Environ Sci Process Impacts. 2017;19(10):1312–1319.
[18] Al Hallak M, Verdier T, Bertron A, Mercade M, Lepercq P, Roques C, et al. Efficiency of the Coriolis µ air sampling device for fungal contamination analysis of indoor air: a case study. Pathogens. 2025;14(4):345.
[19] Nevalainen A, Täubel M, Hyvärinen A. Investigation of fungal contamination in indoor air and on surfaces of neonatal intensive care units in Turkey. Indoor Air. 2020;30(6):1185–1196.
[20] Tabatabaei SM, Karimi A, Habibi M, Hosseini SM, Karimi M. Investigation of fungal contamination in indoor air and on surfaces of traditional public baths in a historical city. J Environ Health Sci Eng. 2020;18(2):1277–1287.
[21] Jabeen R, Shahid M, Nawaz M. Bioaerosol assessment in indoor and outdoor environments: a case study of canteens and classrooms. Front Public Health. 2023;11:1070147.
[22] Kauserud H, Martin-Sanchez PM, Estensmo EL, Skrede I, Kolarik M, Kohout P, et al. Yeasts prefer daycares and molds prefer private homes. Microb Ecol. 2025;88(1):7. doi: 10.1007/s00248-025-02505-4.
[23] Dai R, Liu S, Li Q, Wu H, Wu L, Ji C. A systematic review and meta-analysis of indoor

bioaerosols in hospitals: the influence of heating, ventilation, and air conditioning. PLoS One. 2021;16(12):e0259996. doi: 10.1371/journal.pone.0259996.

[24] Adams RI, Bhangar S, Dannemiller KC, Eisen JA, Fierer N, Gilbert JA, et al. Ten questions concerning microbial quality in the built environment. Build Environ. 2021;207:103922.

[25] Eze CE, Ower J, Eze EA. Analysis of mold and mycotoxins in naturally infested indoor building materials. Mycotoxin Res. 2022;38(4):289–301.

[26] Liu Z, Li Y, Zhang Y. Residential airborne culturable fungi under general living scenario: exposure risk assessment and control strategy. Environ Int. 2021;155:106688.

[27] Cervantes A, Pena M, Riesenberger A, Rodriguez J, Henderson N, Gonçalves P, et al. Critical insights on fungal contamination in schools: a comprehensive review of assessment methods. Front Public Health. 2025;13:1557506. doi: 10.3389/fpubh.2025.1557506.

[28] Hosein R, Khan A, Wilson S. Indoor airborne fungal pollution in newborn units in Turkey. Indoor Air. 2017;27(5):1036–1044.

[29] World Health Organization. WHO guidelines for indoor air quality: dampness and mould [Internet]. Copenhagen: WHO Regional Office for Europe; 2009 [cited 2026 Jun 26]. Available from: https://www.who.int/publications/i/item/9789289041683

[30] Blaustein RA, Stinger K, Rubel A. Potential for microbial cross-contamination of laundry from public laundromats. J Imaging. 2022;8(12):320.

[31] Meadow JF, Altrichter AE, Bateman AC, Stenson J, Brown GZ, Green JL, et al. Humans differ in their personal microbial cloud. PeerJ. 2014;2:e512.

[32] Boor BE, Spilak MP, Corsi RL, Novoselac A. Impact of bedding arrangements, pillows, and blankets on particle resuspension in the sleep microenvironment. Build Environ. 2014;81:60–68.

[33] Jones CL, Neumeister-Kemp HG. The 1000 spores/m³ mould threshold revisited: perspectives and reinforcement from post-2023 literature. J Bacteriol Mycol Open Access. 2025;13(2).