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Report Title: **Unveiling the Composition of Microbial Communities and Identification of Potential Pathogens in Household Dust**

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Unveiling the Composition of Microbial Communities and Identification of Potential Pathogens in Household Dust

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Abstract

Modern society's increasing reliance on indoor environments has made them significant sources of human exposure to microbes. While previous research has explored factors influencing indoor microbial communities, little attention has been given to microbe dispersion within identical indoor settings. Using PacBio Sequel full-length amplicon sequencing, our study examined microbe distribution in different locations within a single home, identifying potential pathogens and microbial functions. Significant variations in microbial communities were found among indoor sampling sites ($P < 0.05$). Bacterial diversity correlated with human activities and external environment contact at different sites, while fungal diversity remained consistent. Door handles were identified as potential pathogen hotspots, showing enrichment of bacteria and fungi ($P < 0.05$). We also detected a substantial presence of fungal allergens (34.37%–56.50%), relevant to skin conditions and asthma. Cooccurrence network analysis highlighted the crucial role of microbial interactions in supporting a healthy immune system. This study underscores differences in microbial communities within a single indoor environment, revealing potential pathogen distribution and microbial ecological functions. It offers valuable insights for assessing indoor health from a microbiological standpoint.

Keyword:

Indoor microbial health, Bacteria, Fungi, Potential pathogens, Ecological function

Contents

1. Introduction

As urbanization accelerates, people are increasingly confined indoors. Modern individuals now spend an average of 90% of their time indoors for both living and work (Klepeis et al., 2001). Microbes pervade indoor environments, potentially interacting with humans at any moment. Despite reduced microbial exposure compared to the outdoors, indoor spaces foster a distinct microbial environment with profound implications for human health. Diseases like pneumonia, influenza, measles, asthma, and allergies have been linked to indoor microbe exposure and transmission (Fu et al., 2020; Kirjavainen et al., 2019).

Moreover, vulnerable populations such as children and the elderly, who spend more time indoors and have weaker immune systems, are particularly susceptible to harmful pathogens. Nonetheless, some microbes offer benefits by contributing to a robust immune system (Ege et al., 2011; Fu et al., 2021; Soininen et al., 2022). For instance, children raised on farms, exposed to diverse environmental microbes like Alphaproteobacteria and Cyanobacteria, exhibit lower rates of allergic and inflammatory diseases (Ege et al., 2011). Consequently, exploring the diversity and distribution of indoor microbes is crucial to cultivating a health-promoting indoor ecosystem.

Microbial communities exhibit varying structures and diversity across distinct indoor spaces, encompassing households, schools, shopping malls, and hospitals (Adams et al., 2015; Adams et al., 2016; Meadow et al., 2014b). A multitude of factors contribute to the composition of indoor microbial communities, with resident microorganisms, occupant lifestyles, building materials, and the influx of outdoor microbes standing out as predominant influencers (Gilbert and Stephens, 2018). Furthermore, biogeographical patterns have been observed in the distribution of indoor microbes, particularly fungi (Ding et al., 2020). Yet, limited research has delved into the microbial distribution within discrete areas of the same indoor environment. Notably, commonplace human activities like sneezing, walking, and bathing can significantly shape microbe distribution and transmission dynamics (Chen and Hildemann, 2009). Moreover, most studies have relied on dust samples to characterize indoor microbial attributes due to their ease of collection and potential to represent the cumulative indoor microbiota over time (Leppanen et al., 2018).

Surface house dust serves as the primary reservoir of microbes within residential environments, comprising human and animal excretions, skin particles, soil, and plants

(Shan et al., 2019; Macher, 2001). Over time, settled dust provides a comprehensive record of the microbial communities present in an area (Rintala et al., 2012). Notably, it is estimated that an average home accumulates up to 18 kg of dust annually, with resuspended dust accounting for approximately 60% of all indoor air particulate matter (Prussin and Marr, 2015; Fujimura et al., 2014). Consistent research underscores the link between indoor dust microbes and specific health outcomes (Dockx et al., 2023; Kirjavainen et al., 2019). Given their accessibility and widespread use in studies, surface dust samples offer a convenient approach to investigate indoor microbial distribution. As a result, collecting dust samples proves to be an efficient technique for studying indoor microbial dynamics.

In this study, we gathered dust samples from various zones within a household, employing PacBio Sequel full-length amplicon sequencing to delve into microbial diversity and composition. Leveraging full-length gene sequencing offers a more comprehensive and realistic portrayal of microbial community structure, enhancing taxonomic annotation down to the species level (Matsuo et al., 2021). This refinement enables precise identification of potential pathogens and accurate prediction of microbial ecological functions. Moreover, we constructed ecological networks encompassing bacteria and fungi, unveiling interrelations among these microorganisms. Our study's findings present a comprehensive profile of microorganisms inhabiting indoor human environments. This microbial perspective contributes to our grasp of indoor air quality and serves as a steppingstone for establishing a health-promoting indoor environment.

2. Material and methods

2.1. Sample collection

Dust samples were collected from different areas of a single house in Beijing, China (door handle, washroom, bed, floor, dining table, balcony and kitchen). Cleaning was prohibited in the house for 3 days prior to sampling to ensure that the collected dust was representative of the indoor microbial communities. A sterile cotton swab was dipped in buffer containing 0.15 M NaCl and 0.1 % Tween-20 for approximately 10 s, thoroughly moistened, and then vigorously wiped over the surface of the sampling sites. The sampling process took at least 30 s to allow the dust to be evenly distributed on the swab. Full details of the sampling procedure are given in the Supplementary Methods. The swabs were subsequently placed in 10 ml sterile centrifuge tubes, transported to the laboratory within 12 h and stored at−20 °C until DNA extraction.

2.2. Sample DNA extraction

DNA extraction was performed using a FastDNA® Spin Kit (Bio 101Inc., USA) according to the manufacturer's instructions. Modifications were made to better fragment the dust and obtain microbial DNA. Specifically, the frozen swabs were broken into several beads in the tube, and the lysis procedure was performed twice. The purity and concentration of the extracted DNA was measured using the Qubit® Fluorometer (Thermo Fisher Scientific, Waltham, MA, USA). Finally, the dust DNA was stored at−20 °C until analysis.

2.3. Analyses of dust microbial communities

To probe the indoor microbial community, the full-length 16S rRNA gene region for bacteria (27F: AGRGTTTGATYNTGGCTCAG; 1492R: TASGGHTACCTTGTTASGACTT) and the full-length ITS region for fungi (ITS1: F-CTTGGTCATTTAGAGGAAGTAA; ITS4: R-TCCTCCGCTTATTATT ATGC) were used to amplify the dust DNA samples (Guo et al., 2021a). The cycling conditions consisted of 3 min at 95 °C; 25 cycles of 30 s at 95 °C, 30 s at 57 °C and 30 s at 72 °C, and final extension at 72 °C for 3 min. The purified PCR products were obtained as described previously (He et al., 2022; Numberger et al., 2022) using the PacBio Sequel platform at Majorbio Bio-pharm Technology Co., Ltd. (Shanghai, China) for high throughput sequencing.

Bacterial 16S rRNA sequences were not successfully amplified in one sample each from the washroom, bed and kitchen due to insufficient sample size. Serialisation data was processed by SMRT Link (V6.0) to yield clean reads. Clean reads were denoised to generate amplicon sequence variants (ASVs) using the DADA2 algorithm (Callahan et al., 2019). Taxonomy was aligned and assigned utilising the SILVA database (release 138) for bacteria, and the UNITE 8.0 database for fungi (Wang et al., 2022). Alpha diversity of each sample was measured using the ‘vegan’ package in R and represented as the Shannon and Chao1 indices.

Principal Coordinate Analysis (PCoA) based on the weighted UniFrac distance matrix was also performed to observe the differences between different groups of samples. Potential pathogens were identified at the species level by comparing with pathogen database containing 538 pathogenic bacterial species and 317 pathogenic fungal species (Li et al., 2015; Woolhouse et al., 2007). In addition, potential fungal allergens were identified according to the directory of pathogenic microbes infecting human beings issued by the Ministry of Health of the People's Republic of China and published

literature (Ding et al., 2020; Esch et al., 2001). The prediction of microbial function was analysed using the online platform of the Majorbio Cloud Platform (www.majorbio.com).

2.4. Statistical analyses

Differences in alpha diversity and the relative abundance of microbial functional groups among the groups were determined by one-way 0.05 using IBM SPSS version 22 (IBM, Armonk, NY, USA). Linear discriminant analysis (LDA) effect size was applied to identify indicator microbial species within groups ($P < 0.05$, $LDA > 4$). The co-occurrence network was constructed and visualised using the 'igraph' package in R and Gephi respectively (Spearman's $r > 0.7$, $Padj < 0.005$).

3. Results and discussion

3.1. Microbial community diversity among various indoor location

A total of 398,374 and 821,596 high-quality reads were aggregated, forming 3435 bacterial ASVs and 1955 fungal ASVs, respectively. No discernible divergence in fungal community diversity emerged among the distinct indoor locations (Fig. 1a). This outcome can be ascribed to the preponderant influence of factors beyond occupants, with humidity, house age (Kettleson et al., 2015), and georeferenced environmental conditions predominantly steering fungal diversity (Ding et al., 2020).

Conversely, the balcony, kitchen, and dining table exhibited significantly elevated Shannon indices for bacterial communities compared to other sites (Fig. 1a, $P < 0.05$). The balcony and dining table also displayed comparatively heightened Chao1 indices for bacterial communities (Fig. 1a, $P < 0.05$). Diverging from fungal diversity, bacterial diversity variations within homes can be attributed to external environmental factors, indoor habitat structure, or occupants (Dunn et al., 2013). Balconies, serving as the interface between indoors and outdoors, boasted greater bacterial richness than interior spaces (Adams et al., 2014; Guo et al., 2020).

In the kitchen, an array of bacterial communities stems from occupants and influences from food, waste, and heightened illumination (Flores et al., 2013; Kakumanu et al., 2020), culminating in heightened diversity. Similarly, the dining table's elevated bacterial diversity might be linked to an abundance of organic matter and potentially contaminated cleaning cloths within the food court (Dingsdag and Coleman, 2013).

The Weighted UniFrac distance-based Principal Coordinate Analysis (PCoA)

highlighted distinctive microbial community structures among individual indoor sites (Fig. 1b, Adonis test, $P < 0.05$). Notably, the sampled areas encompass diverse human activities, such as cultivating greenery on balconies, excretory practices in washrooms, and dining at tables. This variance in occupant activities and occupancy duration likely underpins the observed disparities in microbial communities (Adams et al., 2015; Barberán et al., 2015; Lax et al., 2014; Meadow et al., 2014a). For instance, research has demonstrated that washroom microbes are chiefly influenced by urine and fecal matter, intricately linked to occupant excretory behaviors (Adams et al., 2015).

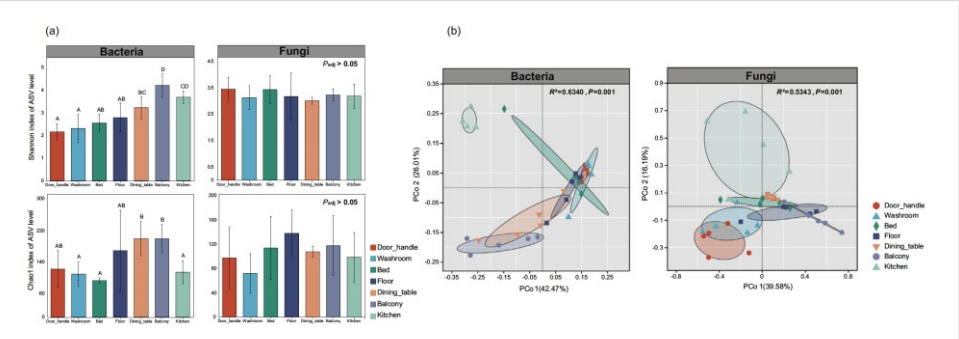

Fig.1 Indoor dust microbial profiles across sample sites. (a) Alpha diversity indices, with different letters representing significant differences among groups, (b) PCoA plot of ASVs based on Weighted UniFrac distance.

3.2. Microbial community composition among various indoor locations

In terms of bacteria, the predominant phyla at the door handle, washroom, and bed were Proteobacteria (81.35%), Firmicutes (10.11%), and Actinobacteriota (5.59%). On the floor, dining table, and balcony, Proteobacteria (65.14%), Firmicutes (10.71%), and Myxococcota (15.21%) were the dominant phyla. In the kitchen, the primary bacteria were Proteobacteria, Firmicutes, and Bacteroidota, with relative abundances of 89.56%, 1.95%, and 5.69%, respectively (Fig. 2a). Proteobacteria and Firmicutes emerged as the prevailing phyla in the indoor environment, consistent with previous studies (Ben Maamar et al., 2020; Dunn et al., 2013). Notably, the presence of Myxococcota, typically associated with soil environments, was widespread in indoor areas influenced by the outdoors.

Source tracking analysis unveiled that indoor bacterial communities largely originated from bacterial populations commonly found on human skin, soil, and plants (Ding et al., 2020). The presence of Bacteroidota in the kitchen aligned with a study examining bacteria distribution on various surfaces in domestic kitchens (Flores et al., 2013). At the genus level, a distinct pattern emerged (Fig. 2b). Apart from the kitchen, Ralstonia

(15.87%–66.12%) exhibited widespread distribution across indoor spaces in this study. Similarly, this genus was abundant indoors but nearly absent outdoors according to Kembel et al. (2012). The washroom exhibited a higher relative abundance of Corynebacterium (7.53%), associated with human skin (Barberán et al., 2015).

Certain Pseudomonas species, considered opportunistic pathogens, were notable on the bed (13.79%), warranting attention. Massilia, predominant in urban dust samples from Beijing, was relatively abundant on the balcony (Hao, 2018), supporting our findings. Furthermore, Acinetobacter, associated with the environment, dominated the kitchen irrespective of geographical location (Adams et al., 2015), aligning with our study where Acinetobacter relative abundance reached 24.77%.

Utilizing a Venn diagram, we identified core bacterial species within the household, mainly belonging to the Ralstonia and Burkholderia-Caballeronia-Paraburkholderia genera. Ralstonia members are common in the human microbiome, while Burkholderia-Caballeronia-Paraburkholderia are linked to soil and plant environments (Guo et al., 2021b; Kaur et al., 2017). This suggests that indoor bacterial community composition arises from dynamic interactions between occupants and the external environment.

Regarding fungi, the indoor microbial communities displayed a prevalence of Ascomycota (39.26%–79.02%) and Basidiomycota (20.72%–63.63%) at the phylum level (Fig. 2c), in accordance with various indoor microbial surveys (Amend et al., 2010; Ding et al., 2020; Fu et al., 2020). Prominent fungal genera in the indoor environment encompassed Coprinellus (12.13%–25.18%), Alternaria (9.18%–31.95%), and Cladosporium (6.74%–19.85%) (Fig. 2d). Alternaria and Cladosporium emerged as pervasive indoor taxa, aligning with culture-based investigations (Amend et al., 2010; Barberán et al., 2015). The wood-degrading fungi Coprinellus likely colonized the wooden floor in this study house (Slimen et al., 2020).

Malassezia species, skin-associated yeasts, can be emitted into the indoor environment through shedding. Nevertheless, studies indicated that indoor fungi mainly originate from outdoor air, with Malassezia predominantly present on the door handle (30.85%), washroom (16.65%), and bed (3.25%), reflecting their proximity to human skin. Utilizing a Venn diagram, core fungal species within the household were identified, primarily belonging to Cladosporium and Coprinellus genera. Research has shown that indoor Cladosporium species are airborne fungi largely derived from outdoor environments (Adams et al., 2013; Prussin and Marr, 2015). Conversely, Coprinellus is associated with wooden building materials (Slimen et al., 2020). This underscores that

unlike bacterial communities, the primary influencers of indoor fungal community composition are taxa from the outdoor environment and architectural design.

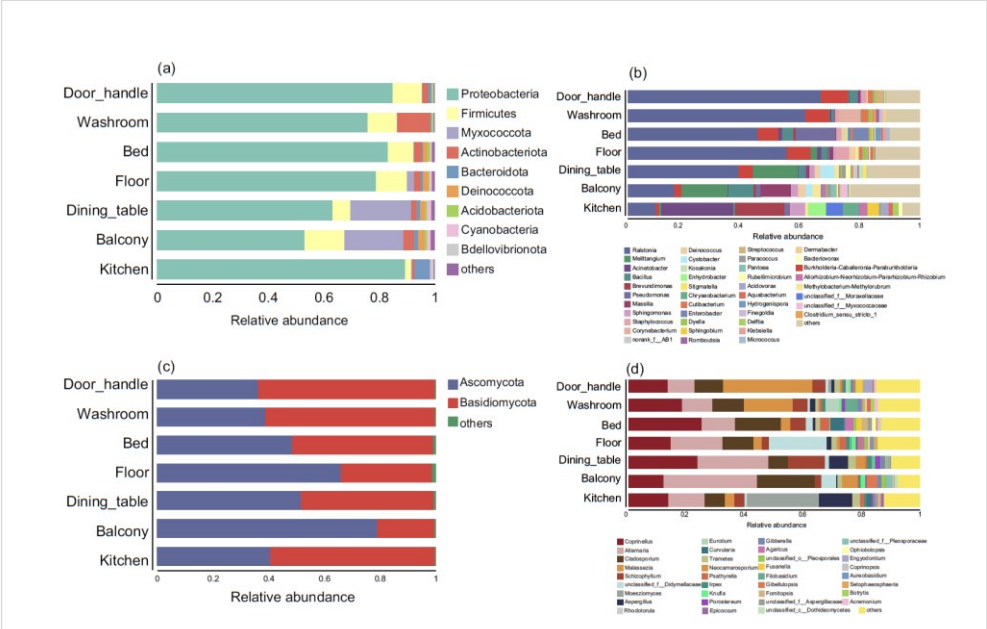

Fig. 2. The microbial composition of indoor dusts. (a) Bacterial composition at phylum level, (b) bacterial composition at genus level, (c) fungal composition at phylum level, (d) fungal composition at genus level.

3.3. Potential bacterial pathogens and fungal allergens

A total of 19 bacterial ASVs with potential pathogenic attributes, representing 14 species, were identified across all dust samples. Among these ASVs, Brevundimonas diminuta, Haemophilus haemolyticus, and Neisseria subflava emerged as the primary potential pathogenic bacteria, with average abundances of 0.71%, 0.03%, and 0.03%, respectively (Fig. 3a). The collective relative abundance of potential pathogenic bacteria ranged from 0.00% to 5.69% in the samples, exhibiting noteworthy enrichment in kitchen and door handle samples (Fig. 3a, $P < 0.05$). Additionally, a greater diversity of potentially pathogenic bacterial species was observed on the door handle, whereas the kitchen primarily hosted B. diminuta (relative abundance, 5.66%). B. diminuta, encountered in water, soil, and plant rhizospheres (Rathi and K N, 2021), stands as an infrequent human pathogen that predominantly affects immunocompromised individuals. Its presence was also noted on the floor, where human activities may introduce soil microbes (Zhu et al., 2021). Given B. diminuta's multi-antibiotic resistance (Han and Andrade, 2005) and challenging clinical diagnosis (Lu et al., 2013), it becomes imperative to monitor kitchen-derived pathogens for immunocompromised individuals residing at home.

The skin constitutes the primary reservoir of human-associated microbes, with hands being particularly exposed to external microbes through contact and various activities (Fierer et al., 2008; Nicas and Best, 2008). Hands serve as a principal conduit for various potential pathogens to infiltrate a residence via the door handle. In this study, N. subflava and Prevotella melaninogenica, significantly linked to bronchiectasis and oral lichen planus, were detected on the door handle.

Moreover, the overall relative abundance of potentially pathogenic fungi in the indoor environment exceeded that of pathogenic bacteria, spanning a range of 0.23%–30.41% (Fig. 3b). A total of 70 potentially fungal pathogenic ASVs belonging to 14 distinct species were identified in the dust samples. The most prominent potential pathogenic fungi were Malassezia restricta, M. globosa, and Schizophyllum commune, with average abundances of 6.52%, 1.18%, and 0.98%, respectively. Notably, potential pathogenic fungi exhibited notably higher relative abundances on the door handle and in the washroom compared to other locations (Fig. 3b, $P < 0.05$).

Malassezia, a superficial commensal bacterium of the skin, can induce inflammatory reactions leading to skin conditions like folliculitis, dandruff, and eczema (Saunders et al., 2012). This genus was particularly prominent in door handle and washroom samples, which commonly involve human skin contact. M. restricta and M. globosa have been shown to predominate on dandruff-prone scalps (Dawson, 2007).

At the genus level, we identified 19 known potential fungal allergens in all samples, primarily Alternaria (averaging 21.04%), Malassezia (8.53%), Aspergillus (4.05%), Cladosporium (3.56%), and Schizophyllum (3.02%), aligning with earlier research (de Ana et al., 2006; Ding et al., 2020). Alternaria and Cladosporium are major mycotoxigenic fungal genera in previous studies (Crawford et al., 2015; Yang et al., 2022), indicating potential risks of indoor fungal contamination. Balconies, with more fluctuating hygrothermal conditions, seem to foster the enrichment of potential allergens like Alternaria and Cladosporium, both of which thrive in humid environments.

While the analysis focused on fungal genus-level relative abundances, identification of potential fungal allergens was based on the directory of pathogenic microbes affecting humans from the Ministry of Health of the People's Republic of China and published literature (Ding et al., 2020; Esch et al., 2001), lending certain reference value. Nevertheless, future studies should integrate toxin assays through culture experiments to provide clearer insights into the potential effects of indoor fungal allergens on human

health.

The door handle emerged as a reservoir of potentially pathogenic bacteria and fungi, underscoring its role as a hotspot for human pathogens. To mitigate the transmission of these potentially harmful microbes, it is advisable for residents to practice routine hand cleaning. Additionally, the cleaning and disinfection of door handles upon entering and exiting the home become essential measures. Ensuring the use of distinct cleaning products is crucial to prevent cross-contamination within the indoor environment (Abney et al., 2021).

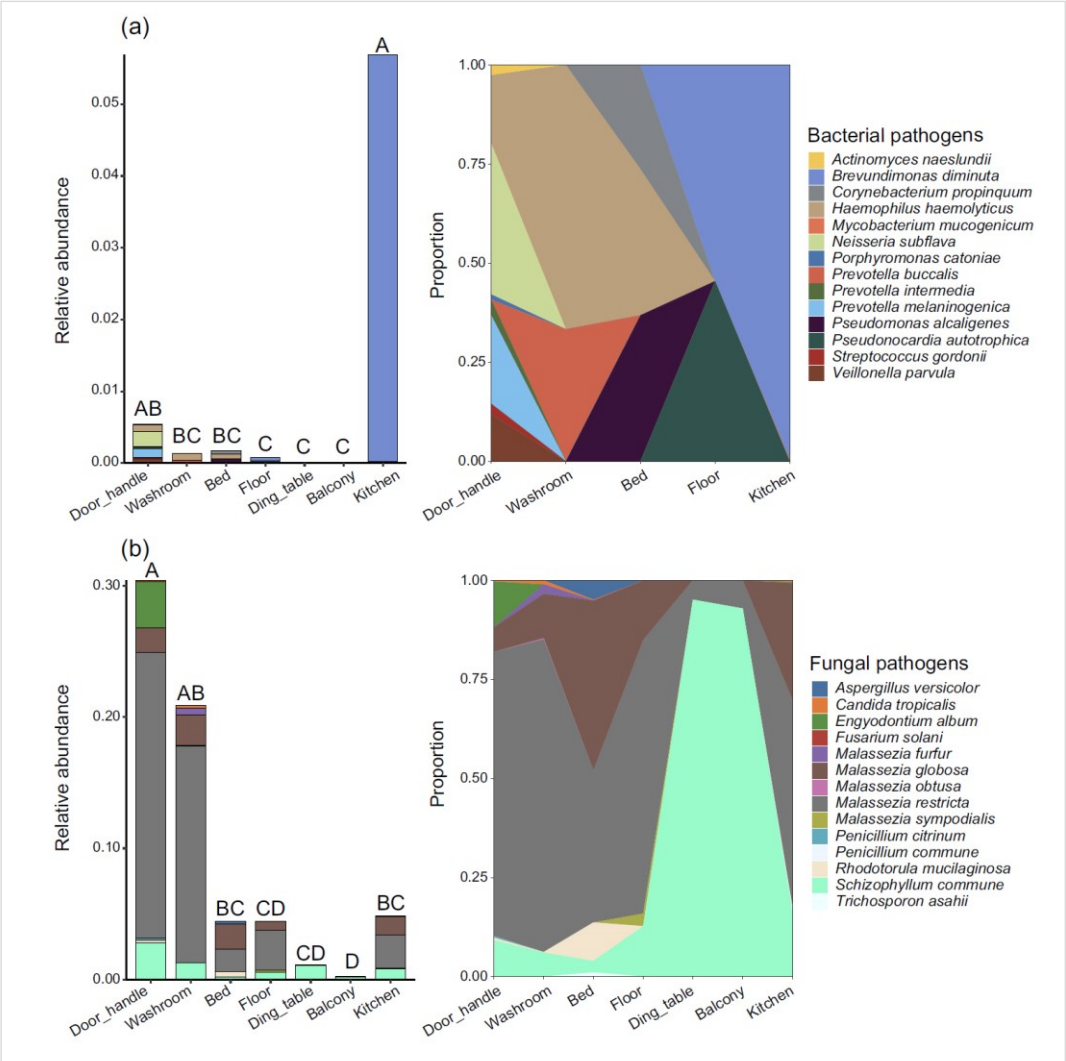

Fig. 3. The relative abundance of potential pathogens in indoor dust and their proportion at different sites. (a) Bacteria, (b) fungi. Different letters representing significant differences among groups.

The door handle was rich in potentially pathogenic bacteria and fungi, suggesting that it is a hotspot for human pathogens, and residents should limit the transmission of

pathogenic microbes by routine hand cleaning. It also appears necessary to clean and disinfect door handles after entering and leaving the home. It is important that cleaning products are used separately to avoid cross contamination of the indoor environment (Abney et al., 2021).

3.4. Functional traits and indicator species of indoor microbes

An indicator species in the washroom, Cutibacterium, holds the distinction of being the most abundant bacterium on sebum-rich human skin sites such as the face and back, emphasizing its significance (Rozas et al., 2021). In the kitchen, bacterial communities were significantly associated with aromatic compound degradation and plant pathogenesis (Fig. 4b, $P < 0.05$), aligning with prior reports where both human occupants and raw food introduced substantial bacterial contributions to this environment (Flores et al., 2013). Notably, the kitchen harbored an indicator species, Acinetobacter, often linked to farm environments and potentially introduced via raw food (Ege et al., 2012). The presence of polymer-degrading microbes, Brevundimonas and Sphingomonas, held significance in food waste decomposition (Peng et al., 2022), designating them as indicator bacteria within the kitchen in this study.

While not displaying significant differences, the bed's bacterial community contained a higher prevalence of human gut-associated microbes, as indicated by Enterobacterales (Fig. 4a). Enterobacterales normally inhabit the human gut (Amaretti et al., 2020) and can be transferred from humans to the environment through shedding or direct contact.

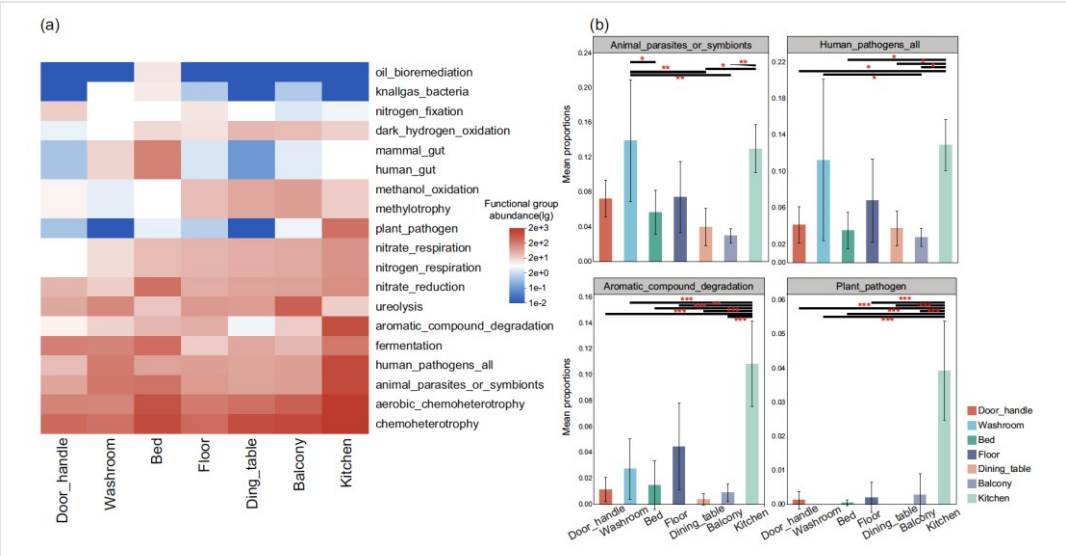

Fig. 4. Bacterial community profiles based on FAPROTAX. (a) Heatmap, (b) functional bacteria with significant differences in relative abundance, asterisks indicate statistically significant (*$P < 0.05$, **$P < 0.01$, ***$P < 0.001$).

Based on FAPROTAX predictions (Fig. 5a), the indoor bacterial communities exhibited potential functions encompassing elemental cycling, organic matter degradation, and human and plant-associated pathogenesis. A noteworthy proportion of animal parasites or symbionts, alongside human pathogens, were notably prevalent in the kitchen and washroom (Fig. 5b, $P < 0.05$), likely attributed to direct human skin contact in these areas.

Using FUNGuild prediction, we determined that indoor fungi predominantly encompassed animal pathogens, plant pathogens, and wood saprotrophic guilds (Fig. 5a). The relative abundance of animal pathogens exhibited a marked elevation in bed, floor, and door handle samples (Fig. 5b, $P < 0.05$). Notably, the indicator species Malassezia on the door handle holds the potential to cause or exacerbate various skin disorders. Similarly, Aureobasidium, enriched on the floor, is linked to cutaneous infections in humans (Chan et al., 2011). Thus, the presence of these fungal species within indoor environments serves as an indicator of potential pathogenic impact and provides insights into the health of indoor microbial communities.

Conversely, the abundance of plant pathogens experienced a significant surge in balcony and kitchen samples (Fig. 5b, $P < 0.05$), primarily influenced by environmental sources. Noteworthy among these is Ustilaginaceae, encompassing a diverse array of plant pathogens (Feldbrügge et al., 2013), and serving as an indicator fungus in the kitchen. Furthermore, the highly prevalent presence of Gibellulopsis on the balcony aligns with its identification as a potential pathogenic fungus.

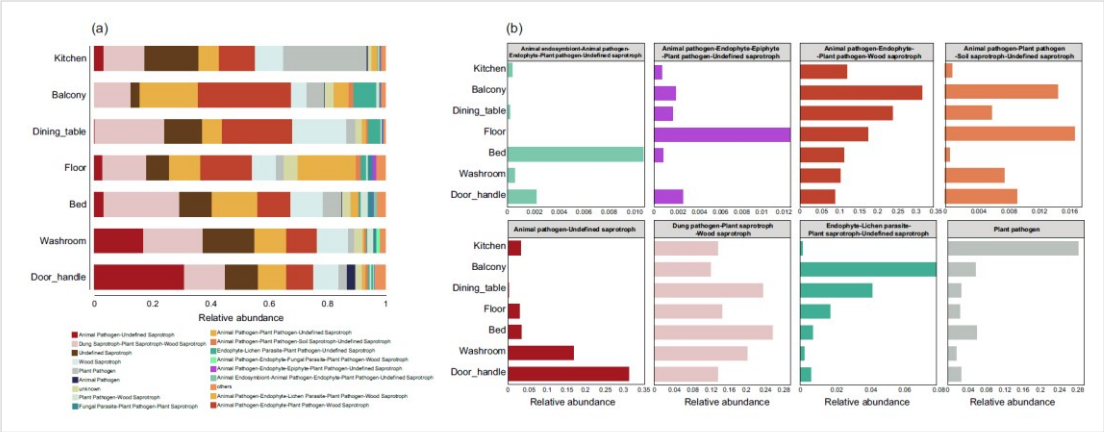

Fig. 5. Fungal community profiles based on FUNGuild. (a) Overall composition, (b) functional fungi with significant differences in relative abundance.

However, the modulation of microbial activity should be taken into account when assessing the presence of dust on surfaces. It's important to recognize that minimal

microbial exposure doesn't necessarily correspond to low levels of living or metabolically active bacteria, as deceased microbes can fragment into minute particles, posing a greater risk to human health (Green et al., 2006; Nevalainen et al., 2015). In essence, various resuspension mechanisms come into play when microbes settle on surfaces, implying that the assumption of their complete removal from the air is not warranted.

In summary, the resuspension of microbes from deposited dust involves multifaceted processes, challenging the straightforward removal assumption. Subsequent research is imperative to establish the nexus between health outcomes and microbial exposure from resuspended dust.

3.5. Co-occurrence network analysis of indoor microbes

Utilizing Spearman correlation analysis, we constructed a co-occurrence network depicting indoor microbial relationships. Post-significance screening, the network comprised 178 nodes and 1044 edges (Fig. 6a). Predominantly, interactions resided within the bacterial domain (71.46%), followed by bacteria–fungi domain connections (24.33%), with the fungal domain accounting for only 4.21%. This distribution can be attributed to the robust biofilm-forming capability of bacteria, fostering heightened interactions within their domain. Various indoor bacteria, including the indicator species Staphylococcus found on the floor in our study, have been shown to excel in biofilm formation (Brągoszewska and Biedroń, 2018).

Analyzing node degrees revealed Alphaproteobacteria and Gammaproteobacteria as the most extensively connected nodes within the co-occurrence network (Fig. 6b). This observation holds significance as members of these groups have been associated with atopy and asthma prevention (Hanski et al., 2012; Parajuli et al., 2018; Roslund et al., 2020; Fu et al., 2021). Notably, studies enhancing indoor microbiology through greenery introduction and green wall installations have highlighted the capacity of enriched Alphaproteobacteria and Gammaproteobacteria to counteract opportunistic human pathogens, fostering a healthy microbiome within built environments (Soininen et al., 2022; AdiWicaksono et al., 2023). This establishes a potential link between indoor microorganisms and a health-supporting environment, implying the role of health-promoting bacteria in indoor microbiology and their potential contribution to regulating microecological well-being indoors.

However, it's important to acknowledge certain limitations in the co-occurrence network analysis, necessitating the development of future research approaches,

potentially incorporating cultivation methods.

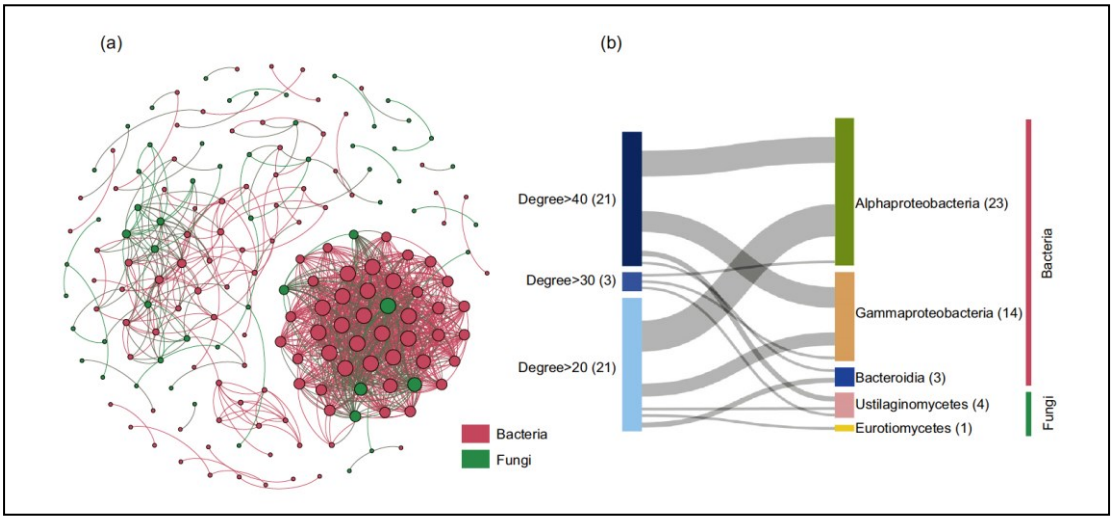

Fig. 6. Correlations of indoor microbes involving bacteria and fungi. (a) Co-occurrence network, (b) distributions of network nodes with degree >20.

4. Conclusion

In conclusion, distinct indoor locations within a household exhibited notable diversity discrepancies in bacterial communities attributed to human activities and external influences. Conversely, the fungal community's diversity appeared primarily influenced by geographic location, resulting in significant microbial community structure variation across sites. The intimate connection between indoor microbes and occupant health was evident, particularly in the substantial relative abundance of potential pathogens. Notably, fungal allergens, known contributors to skin conditions and asthma, were prominent.

Furthermore, predictive functional analysis unveiled the presence of human and animal pathogens within both bacterial and fungal communities. Remarkably, a robust correlation emerged between Alphaproteobacteria and Gammaproteobacteria, recognized for their positive impact on human health and immunity, and various taxa within the microbial co-occurrence network. This suggests the potential for orchestrating beneficial bacterial components to foster a more health-supporting indoor air environment.

In essence, while the detection of potential pathogens within the indoor setting is significant, the pivotal role played by health-promoting bacteria within the co-occurrence network indicates their potential in pathogen regulation and the establishment of a relatively healthful microecological milieu.

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Acknowledgments

Research Background

My journey into the world of microbiology was sparked by an unexpected source -- stray cats. These stray cats, frequent visitors around our household, became a considerable nuisance due to my diagnosis of a level 2 severity cat allergy, a measure that scales from 1 to 3. My symptoms, ranging from swelling to itchy eyes, would often flare up when I'm in certain areas of the house, piquing my curiosity about the underlying cause. For that unsolved curiosity, navigating on searching engines, I first found the root of the allergen: their saliva. Because cats have a habit of cleaning their fur by licking their hair, and intriguingly, this saliva is teeming with diverse microbes that produce specific chemicals, the true culprits behind my allergic reactions. This revelation sparked a profound interest in microbiology, leading me down a path to explore the microscopic world that coexists with us.

One evening, as I sat at my table, a thought struck me: if different areas in our homes serve distinct purposes, like the bathroom for personal hygiene and the kitchen for food preparation, could these areas also harbor unique microbial compositions? This question spurred my research into the microbial distribution in different household settings. My initial findings revealed a significant variation in microbial distribution across different areas within a home. However, while intriguing, these results did not conclusively link the purpose and function of a specific area to its microbial composition. This gap in knowledge has ignited my curiosity, and it's a question I hope will be unravel in my future research.

Relationship between advisors and student

Dong Zhu and Yong-guan Zhu are the extracurricular advisors on Biology classes without any payment. Two advisors taught Jia-Cheng Zhou fundamental Biology knowledge and basic skills of biological experiments.

During this study, Jia-Cheng Zhou completed the collection of on-site samples, DNA extraction independently. Jia-Cheng Zhou, Dong Zhu and Yong-Guan Zhu worked together on the conceptualization, methodology, investigation and formal analysis of the experiment, and report writing and editing.

Other

Yi-Fei Wang was in charge of software support and Funding acquisition and jointed the paper Writing and editing.