

HEALTHY OR HAZARDOUS? THE HIDDEN SIDE OF PUBLIC PARK RECREATION REVEALED BY ITS METABARCODING OF URBAN PARK SOILS

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ABSTRACT

Public parks have been increasingly used for outdoor recreation and leisure activities such as running, aerobic dancing, bird feeding and picnicking. Frequent human interaction with urban birds, particularly pigeons, may increase exposure to potentially pathogenic microorganisms. This study investigated potential health risks associated with environments heavily populated by birds in urban parks. Soil samples in areas of high bird-human interactions were collected from two public parks in Bangkok, Thailand. Fungal communities in the soil samples were analysed using internal transcribed spacer (ITS) metabarcoding combined with bioinformatics approaches to assess microbial diversity and identify potentially pathogenic taxa. Results revealed that Ascomycota was the dominant fungal phylum across all samples, accounting for 89.9% of fungal reads. Beta diversity analysis demonstrated compositional differences in fungal communities between the two parks, although neither beta nor alpha diversity differences were statistically significant, likely due to limited statistical power with three samples per site. Functional guild analysis showed that Pathotroph-Saprotroph-Symbiotroph, Saprotroph, and Pathotroph-Saprotroph were the dominant trophic modes. Several fungal genera with known opportunistic pathogenic potential, including *Aspergillus*, *Fusarium*, *Curvularia*, and *Chaetomium*, were also detected. Environmental observations further indicated that areas with higher bird abundance and more frequent human-bird interactions were associated with site-specific fungal community compositions. As ITS metabarcoding detects DNA rather than viable organisms, these findings indicate potential environmental reservoirs rather than a demonstrated health hazard, highlighting the need for microbial ecological considerations in urban park management.

Keywords: Public Parks, Fungal Pathogens, ITS Metabarcoding, Bird-Associated Pathogens, Public Health Risk

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INTRODUCTION

Urban green spaces, particularly public parks, play a vital role in promoting physical and mental well-being in urban populations. As public health awareness grows, participation in outdoor recreational activities such as jogging, exercising, and relaxation has significantly increased. Urban parks also function as complex ecological interfaces where intense interactions among humans, wildlife, and environmental microorganisms occur. An inappropriate anthropogenic activity observed in urban parks is bird feeding, particularly involving feral pigeons (*Columba livia*). This human-mediated feeding artificially inflates bird populations and concentrates their activity in localized areas. Consequently, the heavy accumulation of bird droppings creates nutrient-rich substrates enriched with nitrogen and phosphorus that facilitate the growth, proliferation, and persistence of various microorganisms, including fungal communities.

Substantial evidence indicates that bird-contaminated environments may serve as major reservoirs for potentially pathogenic fungi. For instance, urban recreational areas in Bangkok, Thailand, harbor diverse environmental yeasts, including *Candida*, *Cryptococcus*, *Rhodotorula*, and *Pichia*, several of which pose opportunistic health risks to humans (Singkum et al., 2025). Avian feces have been documented to sustain a myriad of human-pathogenic fungi derived from soil and airborne propagules (Lee et al., 2017). Specifically, Soltani et al. (2013) identified *Candida albicans* as a frequently isolated yeast, alongside *Penicillium* species as dominant molds in pigeon droppings. More critically, *Cryptococcus neoformans*, a high-consequence opportunistic pathogen, is consistently isolated from these niches.

Beyond localized accumulation, birds actively contribute to fungal dispersal through their foraging behavior, physical movement, and nesting activities (Elliott et al., 2019). Soils in high-density avian zones exhibit high loads of pathogenic molds and yeasts, such as *Aspergillus* and *Candida* species, suggesting that bird-influenced soils act as persistent environmental reservoirs for clinically relevant fungi (Naz et al., 2017).

Although previous studies have established the presence of pathogenic fungi in bird-associated habitats, the specific environmental health risks associated with human exposure in recreational settings remain poorly understood. Most existing research relies on conventional culture-based methods, which inherently underestimate fungal diversity by omitting unculturable or slow-growing taxa. Furthermore, there is a distinct lack of research integrating bird density, high-resolution fungal community composition, and quantitative human recreational behavior.

To address these knowledge gaps, this study investigates fungal communities in bird-influenced urban park soils using internal transcribed spacer (ITS) metabarcoding via next-generation sequencing (NGS). Concurrently, systematic behavioral observations of park visitors were conducted to evaluate potential exposure risks, providing an integrated assessment of microbial ecology and public health safety in urban recreational environments.

LITERATURE REVIEWS

Bird-Associated Fungi in Urban Reservoirs

Fecal contamination from urban bird populations, particularly pigeons, transforms public park soils into specialized ecological niches for micro fungi. Avian excreta possess high concentrations of organic nitrogen, uric acid, and phosphates, which serve as selective enrichment substrates for specific fungal groups (Lee et al., 2017). Genera commonly enriched in these environments include *Candida*, *Cryptococcus*, *Aspergillus*, *Penicillium* and *Rhodotorula* many of which encompass opportunistic human pathogens capable of causing diseases ranging from superficial

mycoses to systemic infections in immunocompromised individuals (Lee et al., 2017; Naz et al., 2017; Singkum et al., 2025).

Pigeon droppings act as an environmental sink, trapping fungal spores from the surrounding air, dust, and soil, while providing the moisture and nutrients necessary for their germination (Lee et al., 2017). Previous mycological surveys established that *C. albicans* thrives in these organic matrices, while *Penicillium* strains often dominate the filamentous fungal profile (Soltani et al., 2013). Of primary clinical concern is the persistence of the *Cryptococcus neoformans/gattii* species complex; these encapsulated yeasts utilize the abundant nitrogenous compounds in bird droppings for growth and capsule synthesis, posing a respiratory biohazard when dry fecal dust becomes airborne.

In addition to acting as a growth medium, avian vectors facilitate the spatial dynamics of these fungi. Birds transport fungal propagules mechanically on their feathers and feet, or biologically via gastrointestinal passage, distributing pathogens across distant urban zones (da Silva et al., 2019; Elliott et al., 2019). This continuous shedding disrupts the natural soil microbiome, shifting the baseline community structure toward an elevated abundance of clinically significant species, such as *Aspergillus fumigatus* and *Candida* spp., in areas characterized by heavy human-wildlife overlap (Naz et al., 2017).

ITS Metabarcoding and Next-Generation Sequencing in Fungal Ecology

Characterizing microbial communities in highly heterogeneous matrices such as soil has historically been limited by the biases of culture-dependent isolation methods. Traditional plating methods favor fast-growing, copiotrophic fungi, while overlooking unculturable, slow-growing, or dormant taxa, which may constitute the majority of environmental microbial diversity (Rappé & Giovannoni, 2003; Lloyd et al., 2018). Next-generation sequencing (NGS) circumvents these limitations by analyzing total environmental DNA (eDNA), offering enhanced sensitivity and taxonomic resolution (Quince et al., 2017).

For fungal community profiling, internal transcribed spacer (ITS) metabarcoding is the universally accepted standard. The ITS region—comprising the ITS1 and ITS2 sub-regions flanking the 5.8S rRNA gene—exhibits high interspecific variation but conserved primer-binding sites, making it an ideal genetic marker for species-level or genus-level identification (Nilsson et al., 2019).

Applying ITS metabarcoding to urban soil ecosystems allows researchers to characterize the true breadth of fungal diversity, uncovering rare, cryptic, and unculturable pathogenic lineages that evade classic surveillance (Batovska et al., 2017). In bird-influenced settings, this molecular approach provides the statistical power needed to correlate anthropogenic activities such as feeding sites with specific shifts in the fungal microbiome.

Human Exposure Dynamics in Recreational Environments

Urban public parks are vital hubs for public recreation, meaning human populations experience prolonged, close-contact exposure to soil- and air-bound microorganisms (Abrego et al., 2020). Bird-associated soils may function as potential risks for environmental exposure (Irga et al., 2016; Halder et al., 2017). When humans engage in activities like jogging, playing, or sitting near feeding zones, they can disturb surface soils, inducing the aerosolization of fungal spores and hyphal fragments (Qian et al., 2014).

Despite the potential public health implications, conventional environmental monitoring rarely integrates microbial metagenomics with patterns of human behavior. Most studies focus primarily on hazard identification—the presence of potential pathogens—rather than exposure assessment, including how, where, and how frequently humans encounter these hazards (Naz et al., 2017; Lee et al., 2017; Lakmuang et al., 2025). By combining high-throughput ITS sequencing with

systematic spatial observations of human activity, this study provides an integrated framework for examining potential exposure pathways and improving understanding of possible health risks arising from human interaction with bird-influenced urban soils.

RESEARCH METHODOLOGY

Sample Collection

Six soil samples were collected from two urban parks in Bangkok on 18 March 2026. Sites were selected based on observable bird presence. Three sampling points per park were selected using a targeted observational sampling approach in areas characterised by frequent human-bird interactions, including feeding zones and recreational areas such as picnicking and running areas, where bird density, particularly of pigeons (*Columba livia*), was high. Sampling points were separated by a minimum distance of 5 m to limit potential spatial dependence among samples. The points were distributed across different sections of each park to capture spatial variation in bird-associated soil communities, and the GPS coordinates of all sampling locations were recorded to document their positions and facilitate reproducibility. Soil samples were collected at 5-10 cm depth using sterile spatulas and stored in 15 mL sterile tubes (Lakmuang et al., 2025). Human and bird activity data were also recorded at each site. Both parks had comparable urban characteristics, including infrastructure and human activity levels, enabling controlled comparison of fungal distribution under different bird community compositions.

A.



B.



Figure 1 Characteristics of two public park sites. (A) Site A, lakeside area with exposed soil, and birds appear along the path. (B) Site B, grassy lakeside area, moderate tree cover, localized human activity, and noticeable bird presence near people.

Both sites (Figure 1) represent heterogeneous urban park environments with similar structural features, including grassy areas, lakesides, tree cover, and infrastructure. However, differences were observed in bird and human activity patterns. Site A (Figure 1A) had a higher abundance of bird species than Site B (Figure 1B). Site A showed a more dispersed bird distribution across varied activity zones, whereas Site B exhibited more spatially aggregated birds associated with localized human activities, such as bird feeding and picnicking. These patterns suggest that the type and intensity of human activity influence bird distribution. Areas with higher food availability and greater human interaction had higher bird density, increasing potential human exposure to environmentally associated microorganisms, including pathogenic fungi.

Microbial DNA Extraction and Metabarcoding

Soil samples of 0.25 g each were subjected to DNA extraction using the DNeasy® PowerSoil® Pro Kit (QIAGEN, Hilden, Germany) following the manufacturer's guidelines. The extracted DNA was kept in a -20 °C freezer for subsequent analysis. Fungal DNA was amplified by targeting the Internal Transcribed Spacer (ITS) region with ITS1 and ITS2 as primers (Lakmuang et al., 2025). Polymerase chain reaction (PCR) amplification was conducted in a thermocycler under standard thermocycling conditions. High-Throughput Sequencing (HTS) was then conducted utilizing the Illumina HiSeq system, producing paired-end reads in a 2 × 250 bp configuration.

Bioinformatics and Information Analysis

Fungal sequencing data were pre-processed using AMPtk (Amplicon Toolkit, v1.6.0) (Palmer et al., 2018), following the standard pipeline including demultiplexing, paired-end merging, quality filtering, denoised using unoise3, and removal of possible index-bleed contamination. Taxonomy was assigned using the UNITE version 9.0 database, and ecological features of fungal amplicon sequence variants (ASVs) were assigned using FUNGuild (Nguyen et al., 2016). Community-level analyses were conducted using the phyloseq package (McMurdie & Holmes, 2013) and the vegan package (Oksanen et al., 2024) in R version 4.5.3 (R Core Team, 2026) with Rstudio version 2026.01.1+403.pro11 (Posit team, 2026). Alpha diversity was assessed using the observed richness index, and differences between sites were evaluated using the Wilcoxon rank-sum test. Beta diversity was assessed using Bray-Curtis dissimilarity, visualised through principal coordinate analysis, and tested for significance using permutational multivariate analysis of variance with the adonis2 function (Anderson, 2001; Oksanen et al., 2024). Taxonomic composition, FUNGuild composition, and heatmap analyses were also performed (Ibrahim et al., 2026).

RESEARCH FINDINGS

Environmental Characteristics and Human–Bird Activity

Environmental observations revealed clear differences in bird abundance, species composition, and human activities between the two study sites (Table 1). A total of 24 birds were recorded at Park Site A, compared to 43 birds at Park Site B. Pigeons (*Columba livia*) were the dominant bird species at both sites, accounting for 14 and 36 individuals in Park Site A and Park Site B, respectively. Ravens were observed at both locations, whereas mynas were only detected at Park Site A.

Human activity patterns also differed between sites. Park Site A was primarily associated with relaxing and fish-feeding activities, with an average of three people observed per sampling location. In contrast, Park Site B was characterized by picnicking and bird feeding activities, with an average of five people recorded per location. The highest bird abundance was observed in areas where food-related activities occurred, particularly bird feeding and picnicking.

Table 1 Summary of bird abundance, bird species composition, human activity, and average number of people per sample location observed in Park Site A and Park Site B.

Parameter	Park Site A	Park Site B
Total birds	24	43
Pigeons	14	36
Ravens	9	7
Mynas	1	-
Average number of people per sample location	3	5
Main activities	Relaxing, fish feeding	Picnicking, bird feeding

Overall, Park Site B exhibited greater bird abundance and a higher level of human-bird interaction than Park Site A. These differences may contribute to variation in the accumulation of bird-derived organic matter within soils and provide ecological context for the differences in fungal community composition and functional structure observed in subsequent analyses.

Functional Guild Composition

Functional guild analysis using FUNGuild revealed that the dominant trophic modes were Pathotroph-Saprotroph-Symbiotroph (39.6%), Saprotroph (24.2%), and Pathotroph-Saprotroph (22.8%) (Table 2 and Figure 2). Minor trophic groups included Symbiotrophs, Saprotroph-Symbiotrophs, and Pathotrophs.

Table 2 Relative and total abundance table generated from FUNGuild parse files, documenting the total abundance and relative abundance of major fungal trophic modes identified within the urban park soil metagenome.

Trophic Mode	Total Abundance	Relative Abundance (%)
Pathotroph–Saprotroph–Symbiotroph	74 196	39.6
Saprotroph	45 295	24.2
Pathotroph–Saprotroph	42 715	22.8
Pathotroph–Saprotroph–Symbiotroph	13 548	7.24
Symbiotroph	6214	3.32
Saprotroph–Symbiotroph	2841	1.52
Pathotroph	2112	1.13
Pathotroph–Symbiotroph	281	0.15

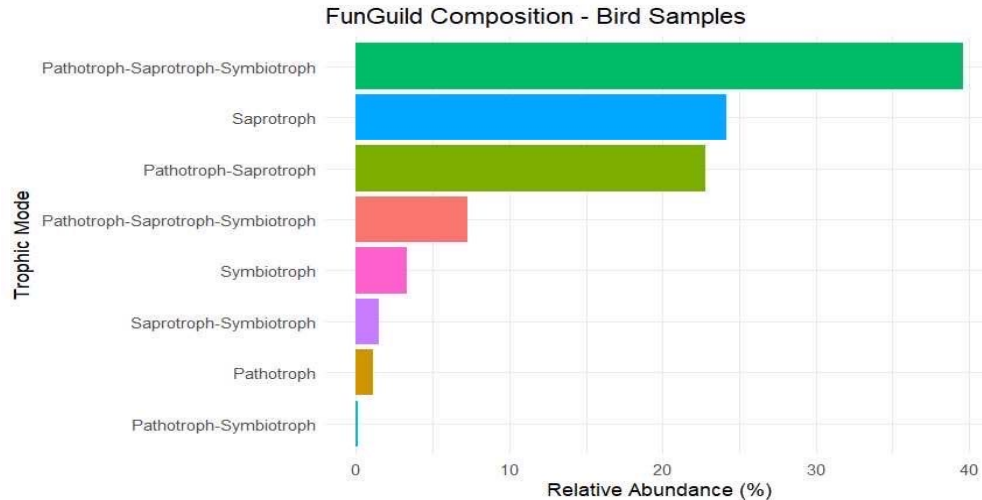


Figure 2 Horizontal bar chart illustrating the FUNGuild composition and relative abundance (%) of fungal trophic modes across bird-associated samples, highlighting the predominance of multi-trophic functional strategies (Pathotroph-Saprotroph-Symbiotroph).

The dominance of saprotrophic and pathotrophic-associated guilds suggests that bird-associated urban soils provide nutrient-rich ecological conditions favorable for fungi with flexible ecological strategies. These findings indicate that accumulated organic matter, including bird fecal material, may promote fungal persistence and functional diversity within the two recreational park environments. Furthermore, the presence of pathotrophic-associated fungi supports the possibility that these environments may serve as reservoirs for fungi with opportunistic pathogenic relevance.

Taxonomic Composition of Fungal Communities

Fungal community profiling revealed that Ascomycota was the dominant phylum across all bird-associated soil samples collected from both urban parks (Figure 3). Relative abundance analysis showed that Ascomycota accounted for 89.9% of fungal reads, followed by Basidiomycota (8.57%), whereas Rozellomycota contributed 1.20%. Other phyla, including Glomeromycota, Anthophyta, Blastocladiomycota, Zoopagomycota, and Mortierellomycota, were detected at substantially lower abundances (<0.2% each). Certain samples also contained unidentified fungal taxa (NA), indicating the presence of unclassified environmental fungi within the urban soil microbiome.

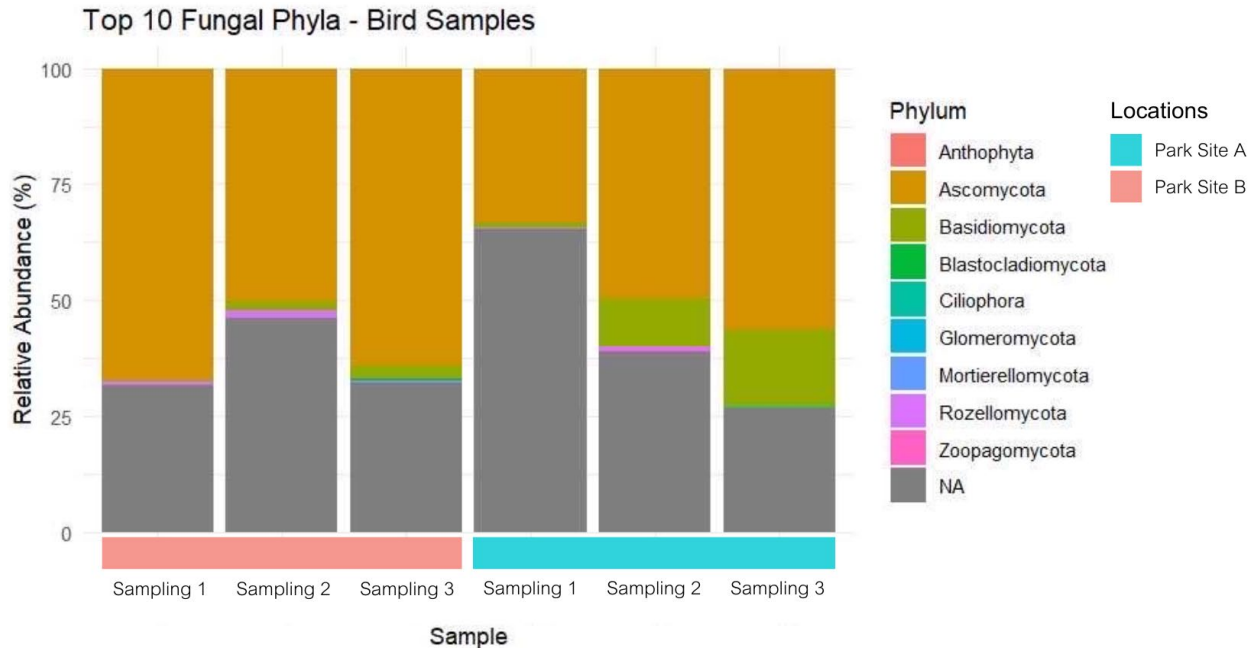


Figure 3 Relative abundance of fungal phyla across soil samples from Park Sites A and B. Gray bars denoted as "NA" represent unclassified fungal sequences at the phylum level.

The dominance of Ascomycota suggests that bird-associated urban soils support fungal groups commonly involved in organic matter decomposition and environmental nutrient cycling (Egidi et al., 2019; Ma et al., 2013). Importantly, Ascomycota also includes several genera known to contain opportunistic pathogenic species, indicating that these recreational environments may function as potential environmental reservoirs of clinically relevant fungi (Egidi et al., 2019; Naz et al., 2017).

Alpha Diversity of Bird-Associated Soil Fungi

Alpha diversity analysis using the observed richness index revealed that Park Site B exhibited higher and more consistent fungal richness across samples than Park Site A. The median observed ASV richness was 502 ASVs for Site B (IQR: 482–508), compared with 333 ASVs for Site A (IQR: 268.5–362) (Figure 4). Site B also showed lower within-site variability, as indicated by its narrower interquartile range, whereas Site A displayed greater variability among samples. Although Site B exhibited higher ASV richness than Site A, the difference was not statistically significant according to the Wilcoxon rank-sum test ($W = 9$, $p = 0.10$). However, with only three samples per site, the test has limited statistical power, and the smallest achievable two-sided p -value for this sample size is 0.05. The non-significant result should therefore be interpreted with caution, as it may reflect insufficient power rather than a true absence of difference. Nevertheless, the observed differences in richness and variability suggest a less uniform fungal community structure at Site A and indicate that beta diversity analyses are warranted to further evaluate structural differences in fungal assemblages between the two parks.

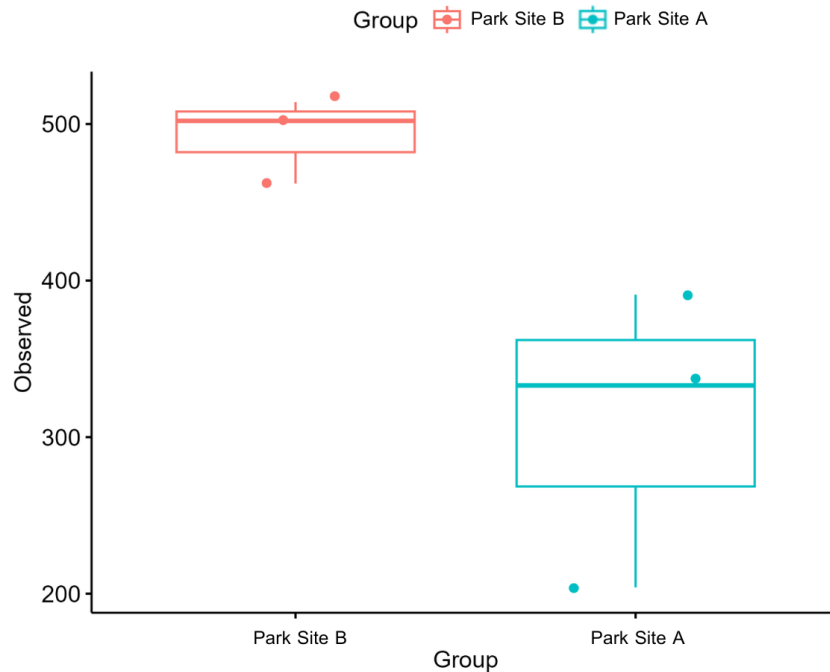


Figure 4 Boxplot analysis of alpha diversity measured via the observed index showing differences in fungal community diversity between Park Site A and Park Site B.

Beta Diversity and Community Structure

Principal Coordinate Analysis (PCoA) based on Bray-Curtis dissimilarity revealed separation between fungal communities from Park Site A and Park Site B (Figure 5). The first two principal coordinate axes explained 30.5% and 21.2% of the total variation, respectively, accounting for 51.7% of the overall community variation. Samples from Park Site B clustered more closely together, whereas Park Site A samples exhibited greater dispersion within the ordination space, suggesting higher within-site compositional variability. PERMANOVA analysis indicated that sampling site explained 30.3% of the variation in fungal community composition ($R^2 = 0.303$, pseudo- $F = 1.739$, 999 permutations), although the difference was not statistically significant ($p = 0.10$). As with the alpha diversity comparison, the small sample size limits statistical power, and this result should be interpreted cautiously.

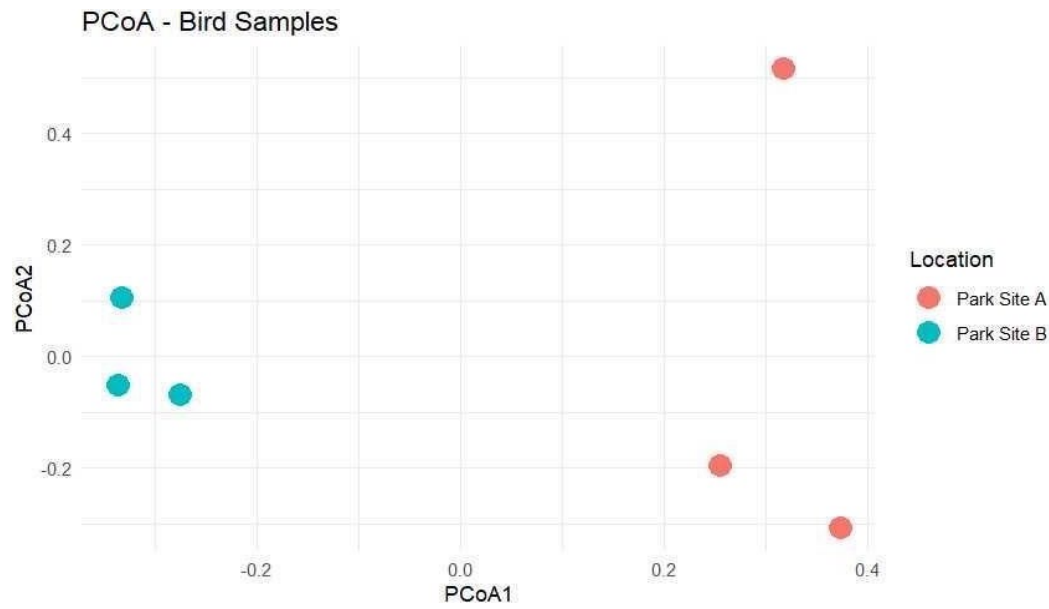


Figure 5 ASV-level Principal Coordinate Analysis (PCoA) based on Bray–Curtis dissimilarity showing beta diversity of fungal communities across soil samples from Part Site A and Park Site B.

Distribution of Dominant Fungal Taxa

Heatmap analysis of dominant fungal ASVs demonstrated clear variation in taxonomic distribution between the two park sites (Figure 6). Several fungal genera with known opportunistic pathogenic potential were identified, including *Aspergillus*, *Fusarium*, *Curvularia*, and *Chaetomium*. *Chaetomium* was the most abundant pathogenic genus at both sites, accounting for 21.22% of the fungal community in Park Site B and 30.45% in Park Site A. *Fusarium* represented 17.22% and 14.33% of the fungal community in Park Site B and Park Site A, respectively. *Aspergillus* was more abundant in Park Site B (11.67%) than in Park Site A (5.61%), whereas *Curvularia* showed the opposite pattern, accounting for only 0.48% of sequences in Park Site B but 8.65% in Park Site A. These findings indicate distinct differences in the composition of potentially pathogenic fungal genera between the two park sites and provide context for assessing potential exposure risks associated with human-bird interactions.

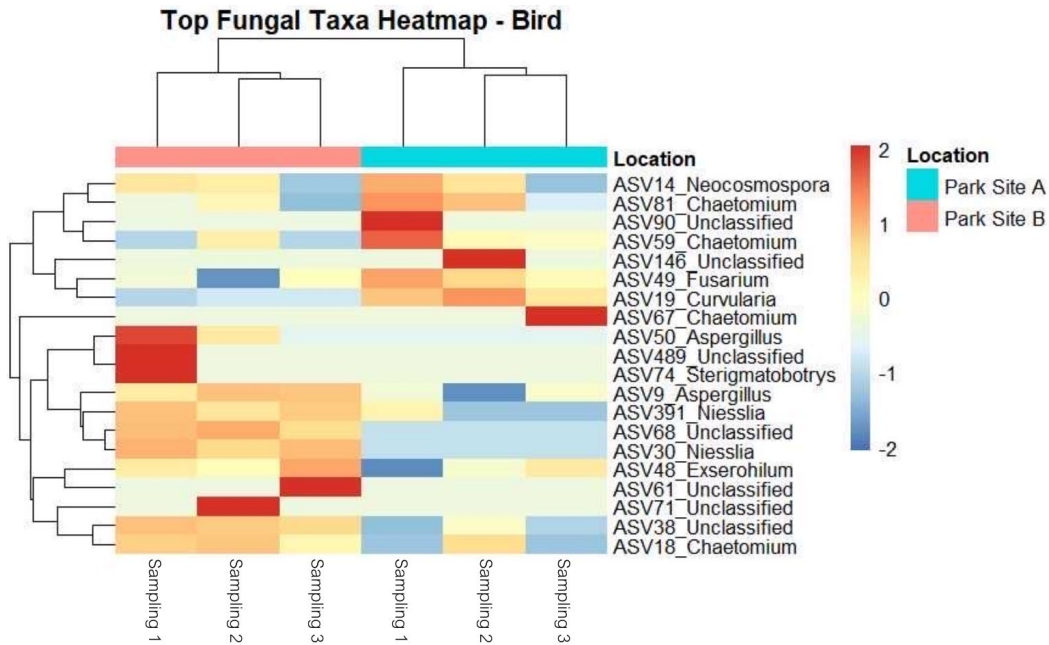


Figure 6 Hierarchically clustered heatmap of top fungal taxa of Park Site A and Park Site B, mapping the relative abundance (z-score scale) of dominant fungal ASVs.

Distinct enrichment patterns of these taxa were observed among samples, further supporting the compositional differences identified in the PCoA analysis. Many of the detected fungi are commonly associated with soil environments, airborne spores, and organic-rich substrates such as bird-contaminated soils (Halder et al., 2017; Naz et al., 2017; Egidi et al., 2019). Some genera identified in this study are also associated with respiratory allergies, opportunistic infections, or mycotoxin production under specific clinical conditions (McCormick et al., 2010; Nobile & Johnson, 2015). However, clinical relevance depends on fungal viability, airborne spore loads, and host susceptibility (McCormick et al., 2010; Almeida et al., 2019), which is outside the scope of this study

CONCLUSION AND DISCUSSION

This study investigated fungal communities in bird-associated urban park soils using ITS metabarcoding and explored their potential implications for environmental exposure in recreational environments. Environmental observations revealed that Park Site B supported a greater abundance of birds and higher levels of human-bird interaction than Park Site A, particularly in areas associated with picnicking and bird-feeding activities. These observations suggest that human activities may influence bird aggregation patterns and contribute to localized environmental conditions that support microbial persistence.

Fungal community analysis demonstrated that Ascomycota was the dominant fungal phylum across all samples. This finding is consistent with previous studies of urban and agricultural soils, which frequently report Ascomycota as the predominant fungal phylum due to its ecological role in organic matter decomposition and adaptation to disturbed environments (Lakmuang et al., 2025; Ibrahim et al., 2026). The dominance of Ascomycota in the present study suggests that bird-associated urban soils provide environmental conditions similar to those reported in other anthropogenically influenced ecosystems.

Although alpha diversity analysis revealed that Park Site B showed higher median observed richness and greater consistency across samples compared to Park Site A, which displayed considerably wider variability among samples. Within-site variability in soil fungal communities is well documented and is commonly attributed to fine-scale spatial heterogeneity driven by uneven disturbance (Abrego et al., 2020). The greater variability at Site A may reflect heterogeneous distributions of human activity and soil disturbance across sampling points, while the more consistent richness at Site B may indicate relatively uniform environmental conditions sustained by concentrated bird activity and associated organic matter enrichment (Haldar et al., 2017; Naz et al., 2017).

Beta diversity analysis revealed clear separation of fungal communities between the two locations. Similar shifts in fungal community structure have been reported in studies examining environmental gradients and anthropogenic influences, where differences in habitat characteristics significantly altered microbial composition (Lee et al., 2017; Ibrahim et al., 2026). In bird-associated environments specifically, differences in bird density, excreta deposition, and localized organic matter accumulation have been shown to create distinct microenvironmental conditions that drive divergence in fungal community composition (Irga et al., 2016; Haldar et al., 2017). This suggests that the observed separation may reflect differences in bird abundance, feeding activities, and localized nutrient inputs between the two parks.

Heatmap analysis further supported these findings by demonstrating differences in the distribution of dominant fungal taxa between the two parks. Park Site B showed relatively higher abundance of *Aspergillus*, while Park Site A was characterised by greater representation of *Chaetomium*, *Fusarium*, and *Curvularia*. The detection of these fungi agrees with previous investigations of bird-associated environments and urban recreational areas, which identified *Aspergillus* and other potentially pathogenic fungi in soils and pigeon-contaminated habitats (Lee et al., 2017; Naz et al., 2017). *Aspergillus* species are particularly important because some members of this genus are recognized as opportunistic pathogens capable of causing respiratory infections in susceptible individuals (McCormick et al., 2010). Similarly, *Chaetomium*, *Fusarium*, and *Curvularia* have been documented as emerging opportunistic pathogens, particularly in immunocompromised individuals (Egidi et al., 2019; McCormick et al., 2010). The detection of potentially pathogenic genera across both sites suggests that both parks may represent potential sources of clinically relevant fungi. However, ITS metabarcoding detects DNA rather than viable organisms (Quince et al., 2017), and the genera detected are commonly reported in urban and anthropogenically influenced soils (Egidi et al., 2019; Abrego et al., 2020). Actual infection risk depends on fungal viability, aerosolization potential, exposure duration, and host immunological status (McCormick et al., 2010; Almeida et al., 2019), none of which were assessed in this study. These findings therefore indicate potential environmental reservoirs rather than a demonstrated health hazard.

Functional guild analysis revealed the dominance of Pathotroph–Saprotroph–Symbiotroph, Saprotroph, and Pathotroph–Saprotroph trophic modes. These results suggest that bird-associated urban soils provide favorable ecological conditions for fungi with diverse nutritional strategies. Similar functional patterns have been reported in soils enriched with organic matter, where saprotrophic fungi dominate because of their ability to decompose complex substrates (Ma et al., 2013). The abundance of saprotrophic fungi indicates active decomposition processes, whereas the presence of pathotroph-associated guilds reflects the occurrence of fungi capable of interacting with living hosts under suitable conditions. Together, these findings suggest that accumulated organic matter and bird activity may contribute to increased fungal persistence and functional diversity within recreational park soils (Haldar et al., 2017; Naz et al., 2017).

One of the strengths of this study is the integration of environmental observations with fungal metabarcoding data. By combining information on bird abundance, human activity, fungal taxonomy, community diversity, and ecological function, this study provides a more comprehensive understanding of microbial ecology within urban recreational environments than approaches that focus solely on hazard identification (Lakmuang et al., 2025; Irga et al., 2016). The findings demonstrate that areas characterized by intensive human–bird interaction may also support distinct fungal communities with potentially important ecological and public health implications.

Nevertheless, this study should be considered a preliminary assessment due to the limited number of sampling sites and samples. Furthermore, ITS metabarcoding identifies fungal DNA but cannot determine whether detected fungi are viable, infectious, or capable of causing disease (Quince et al., 2017). Future studies incorporating larger sampling scales, seasonal monitoring, environmental parameters, and airborne fungal assessments would provide a more comprehensive understanding of fungal exposure dynamics in public parks.

From an urban planning and public health perspective, the observed association between intensive human-bird interaction and distinct fungal community composition suggests that park management strategies should aim to minimize excessive bird aggregation in heavily used recreational areas. Measures such as regulating public bird-feeding activities, improving waste management, and implementing routine cleaning of areas with high bird activity may help reduce the accumulation of bird-derived organic matter that supports fungal persistence. In addition, periodic environmental monitoring of microbial communities in urban parks could serve as an early-warning tool for identifying locations where potentially pathogenic fungi are enriched. Although the present study does not demonstrate direct health risks, the findings support the incorporation of microbial ecological considerations into urban park design and maintenance practices to promote safer and more sustainable recreational environments.

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