



(RESEARCH ARTICLE)



## Morphological profiling of fungal pathogens and their host association in decaying market produce: A study on selected tropical fruits and vegetables

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### Abstract

Postharvest fungal decay is a leading cause of economic and nutritional losses in the horticultural sector, particularly in tropical regions with diverse produce. This study aimed to identify the predominant fungal species associated with the spoilage of a wide range of fruits and vegetables, including several understudied tropical varieties, in Thiruvananthapuram, Kerala, India. Sixty-five decaying samples from thirteen types of produce (e.g., banana, jackfruit, coconut, bilimbi, snake gourd, lime) were collected from local markets. Fungal isolation was performed on Potato Dextrose Agar following surface sterilization of tissue segments. Pure cultures were identified morphologically based on macro- and microscopic characteristics. A total of 85 fungal isolates were obtained, representing nine genera. *Aspergillus* was the most prevalent genus (30.6% frequency), followed by *Rhizopus* (22.4%) and *Fusarium* (14.1%). The results revealed strong host-specificity; *Aspergillus* dominated hard-shelled/tart fruits (52.4% incidence), *Rhizopus* was the primary pathogen in vegetables and gourds (35.3%), and *Penicillium* was specific to fleshy fruits like lime. This study provides a crucial baseline profile of the spoilage mycobiota in the region, highlighting the need for tailored postharvest management strategies to mitigate losses in both common and regionally significant produce, thereby enhancing food security.

**Keywords:** Postharvest decay; Spoilage fungi; Morphological identification; *Aspergillus*; *Rhizopus*; Host-specificity; Tropical produce; Food security

### 1. Introduction

Postharvest losses represent a critical challenge to global food security, with fungal decay being a primary contributor to the deterioration of fruits and vegetables. It is estimated that a significant proportion of horticultural produce is lost annually along the supply chain due to microbial spoilage, resulting in substantial economic losses and reduced food availability [1]. This spoilage is predominantly caused by a diverse array of filamentous fungi, which colonize produce through injuries sustained during harvesting, handling, and transport, leading to rot, discoloration, and a loss of nutritional and market value [2].

The ecological succession of spoilage fungi is influenced by a complex interplay of factors, including the intrinsic properties of the produce (e.g., pH, water activity, rind thickness) and extrinsic environmental conditions (e.g., temperature, humidity). While common genera like *Aspergillus*, *Penicillium*, *Rhizopus*, and *Botrytis* are well-documented agents of spoilage in temperate climates and on common commercial crops, the specific mycobiota associated with a wide range of tropical, subtropical, and locally significant produce remains less systematically characterized [3]. For instance, the fungal communities impacting regionally important fruits like bilimbi (*Averrhoa bilimbi*), jackfruit (*Artocarpus heterophyllus*), and snake gourd (*Trichosanthes cucumerina*) are not as extensively studied as those affecting globally traded commodities like apples or citrus. This gap is particularly acute in developing regions, where postharvest infrastructure may be limited, and losses are most severe.

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The produce selected for this study—including banana, tomato, jackfruit, bilimbi, snake gourd, coconut, lime, gooseberry, pomegranate, tamarind, lady's finger, pineapple, and cabbage—was chosen to represent a strategically important cross-section of the local diet and economy. These items encompass a wide range of morphological structures (e.g., berries, drupes, gourds, pods, leafy vegetables) and physicochemical properties (e.g., pH, water activity, skin thickness), which are critical factors influencing fungal colonization. Furthermore, the selection specifically includes several nutritionally and culturally significant yet under-studied tropical species (such as bilimbi, snake gourd, and gooseberry) whose spoilage dynamics are not well-documented in the scientific literature, in contrast to more globally prevalent commodities.

Understanding the specific fungal pathogens responsible for spoilage is the foundational step in developing effective management strategies. Accurate identification allows for targeted control measures, whether through improved storage conditions, the application of appropriate fungicides, or the development of biological control agents tailored to the predominant local pathogens [4]. Without this crucial baseline data, mitigation efforts are often generalized and less effective.

Therefore, this study was conducted to identify and characterize the spectrum of fungal species associated with the postharvest decay of a diverse selection of fruits and vegetables, with a specific focus on both common and under-studied tropical and subtropical species. The objectives were to: (1) isolate and purify fungi from visibly decayed produce collected from local markets, (2) identify the primary fungal contaminants to the genus level using morphological characteristics, and (3) analyze the distribution and incidence of these fungi across different types of produce. By providing a detailed profile of the spoilage mycobiota, this research aims to fill a knowledge gap and supply essential data that can inform the development of targeted, sustainable strategies to reduce postharvest losses and enhance food security.

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## 2. Materials and Methods

### 2.1. Sample Collection

Decaying fruit and vegetable samples were procured from local markets and wholesale vendors from Thiruvananthapuram, Kerala, India over a four-week period. A total of 60 samples representing twelve different types of produce were collected based on availability and visible spoilage. The produce included: lady's finger (*Abelmoschus esculentus* (L.) Moench), pineapple (*Ananas comosus* (L.) Merr.), jackfruit (*Artocarpus heterophyllus* Lam.), bilimbi (*Averrhoa bilimbi* L.), cabbage (*Brassica oleracea* var. *capitata* L.), lime (*Citrus aurantifolia* (Christm.) Swingle), coconut (*Cocos nucifera* L.), tomato (*Solanum lycopersicum* L.), banana (*Musa × paradisiaca* L.), gooseberry (*Phyllanthus emblica* L.), pomegranate (*Punica granatum* L.), tamarind (*Tamarindus indica* L.), and snake gourd (*Trichosanthes cucumerina* L.). Each sample was placed in a separate sterile zip-lock bag, assigned a unique code, and transported to the laboratory for processing within two hours of collection.

### 2.2. Fungal Isolation and Culturing

Small sections (approximately 5x5 mm) from the interface between healthy and decayed tissue were aseptically excised using a sterile scalpel. The segments were surface sterilized by immersing in 70% ethanol for 45 seconds, followed by a 90-second immersion in 1% sodium hypochlorite solution, and finally rinsed three times in sterile distilled water to remove any residual sterilants [5]. The sterilized segments were blot-dried on sterile filter paper and placed onto Petri plates containing Potato Dextrose Agar (PDA; HiMedia, India) supplemented with streptomycin sulfate (30 mg/L) to inhibit bacterial growth. Four segments were plated per Petri dish. The plates were incubated at 28±2°C for 5–10 days and observed daily for fungal growth.

### 2.3. Purification and Morphological Identification

Emerging fungal hyphae from the plated segments were aseptically transferred to fresh PDA plates using a sterile inoculating needle to obtain pure cultures. Macroscopic characteristics such as colony color, texture, growth rate, and pigmentation were recorded after 7 days of incubation. For microscopic examination, slide cultures were prepared using PDA blocks, and fungal structures were stained with lactophenol cotton blue. Observations of hyphae, conidiophores, conidia, and other reproductive structures were made under a compound light microscope (Olympus CX23) at 400x and 1000x magnification. Fungal isolates were identified to the genus level based on these morphological characteristics using standard taxonomic manuals [6, 7]. Where possible, identification was extended to the species level.

## 2.4. Data Analysis

The incidence of each fungal genus was calculated as the percentage of samples from a specific fruit or vegetable from which that genus was isolated. The total fungal load was represented by the number of isolates obtained from each produce type.

## 3. Results

### 3.1. Spectrum of Fungal Isolates and Their Overall Distribution

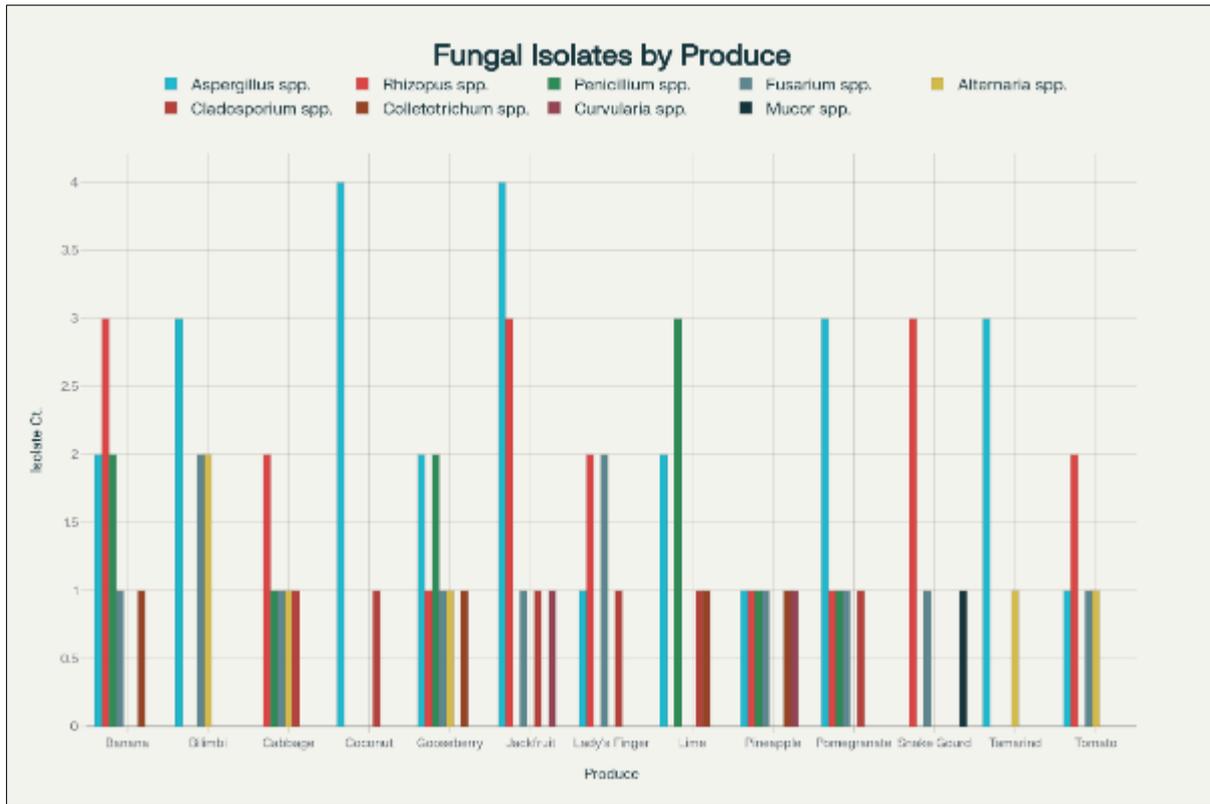
A total of 85 pure fungal isolates were obtained from 65 samples of decaying fruits and vegetables. The isolates were categorized into 9 distinct genera. The overall distribution revealed a clear predominance of certain genera, with *Aspergillus* being the most frequently isolated, followed by *Rhizopus* and *Fusarium*. The complete breakdown of the number of isolates per genus is presented in Table 1.

**Table 1** Overall Distribution of Fungal Genera Isolated from All Decaying Produce

Fungal Genus	Number of Isolates	Percentage Frequency (%)
<i>Aspergillus</i>	26	30.6
<i>Rhizopus</i>	19	22.4
<i>Fusarium</i>	12	14.1
<i>Penicillium</i>	10	11.8
<i>Alternaria</i>	6	7.1
<i>Cladosporium</i>	6	7.1
<i>Colletotrichum</i>	4	4.7
<i>Curvularia</i>	2	2.4
<i>Mucor</i>	1	1.2
Total	85	100.0

### 3.2. Host-Specific Fungal Associations

The type of fruit or vegetable significantly influenced the diversity and prevalence of associated fungal species. Each produce item showed a unique mycota. For instance, *Penicillium* was the exclusive fungal genus found on limes, while coconuts were predominantly spoiled by *Aspergillus* spp. The detailed distribution of fungal genera across each type of produce is detailed in Fig 1.



**Figure 1** Fungal Genera Isolated from Specific Fruits and Vegetables

### 3.3. Incidence of Fungal Genera by Produce Category

To better understand the association between fungi and the nature of the produce, the hosts were categorized into three groups: Fleshy Fruits, Vegetables and Gourds, and Hard-Shelled/Tart Fruits. The incidence of the top three fungal genera within each category was calculated and is compared in Table 2. This analysis revealed that *Rhizopus* was a major pathogen for Vegetables and Gourds, while *Aspergillus* was highly prevalent on Hard-Shelled/Tart Fruits. *Penicillium* showed a strong specificity for the Fleshy Fruits category, primarily due to its high incidence in lime.

**Table 2** Comparison of Predominant Fungal Genera by Produce Category

Produce Category	Example Produce Included	Most Prevalent Genus (% Incidence)	Second Most Prevalent (% Incidence)	Third Most Prevalent (% Incidence)
Fleshy Fruits	Banana, Tomato, Gooseberry	<i>Rhizopus</i> spp. (31.4%)	<i>Aspergillus</i> spp. (25.7%)	<i>Fusarium</i> spp. (17.1%)
Vegetables and Gourds	Cabbage, Lady's Finger, Snake Gourd	<i>Rhizopus</i> spp. (35.3%)	<i>Fusarium</i> spp. (23.5%)	<i>Aspergillus</i> spp. (11.8%)
Hard-Shelled/Tart Fruits	Coconut, Lime, Tamarind, Bilimbi	<i>Aspergillus</i> spp. (52.4%)	<i>Penicillium</i> spp. (14.3%)	<i>Alternaria</i> spp. (14.3%)

### 3.4. Morphological Characteristics of Predominant Fungi

The identification was based on distinct macro-morphological and micro-morphological features observed on PDA cultures

- *Aspergillus* spp.: Colonies were initially white, rapidly becoming black, green, or yellow with a powdery texture due to dense conidial production. Microscopy revealed septate hyphae, unbranched conidiophores with vesicles bearing phialides that produced chains of conidia.

- *Rhizopus* spp.: Fast-growing, fluffy grey-white colonies that filled the Petri dish. Under the microscope, non-septate hyphae, sporangiophores arising from stolons opposite rhizoids, and large, black spherical sporangia were observed.
- *Penicillium* spp.: Colonies were typically blue-green with a white margin and a velvety to powdery texture. Microscopic examination showed branched, terverticillate or biverticillate conidiophores (brush-like) producing chains of round conidia.
- *Fusarium* spp.: Colonies exhibited white to pink or purple aerial mycelium. Microscopy revealed sickle-shaped, multicellular macroconidia with a distinct foot cell, produced from monophialides.
- *Alternaria* spp.: Colonies were woolly to cottony, appearing greyish-olive to brownish-black on the surface with a pale reverse. The key microscopic feature was the presence of large, brown, muriform conidia (septate both transversely and longitudinally) with a beak-like apical cell, borne in chains from simple conidiophores.

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#### 4. Discussion

This study provides a comprehensive profile of the mycobiota associated with postharvest decay of a diverse range of fruits and vegetables, with a specific emphasis on regionally significant and understudied tropical produce from Kerala, India. The isolation of 85 fungal isolates belonging to 9 genera from 65 samples underscores the high diversity and prevalence of fungal pathogens in the local postharvest ecosystem. The predominance of genera such as *Aspergillus* (30.6%), *Rhizopus* (22.4%), and *Fusarium* (14.1%) is consistent with global reports identifying these as ubiquitous agents of spoilage across various climates and produce types [8, 9]. Their success can be attributed to their robust saprophytic nature, rapid growth rates, and efficient production of hydrolytic enzymes and spores that facilitate easy dispersal in market environments.

The strong host-specific associations observed align with the established principle that the physicochemical composition of the produce dictates fungal colonization. The high incidence of *Aspergillus* spp. on hard-shelled and tart fruits like coconut (4 out of 5 isolates) and tamarind (3 out of 4 isolates) can be explained by the xerophilic nature of many *Aspergillus* species, which allows them to thrive on substrates with lower water activity (aw) [10]. Conversely, the prevalence of *Rhizopus stolonifer* in vegetables and gourds with high moisture content, such as snake gourd (3 out of 5 isolates) and tomato, is characteristic of its role as a primary cause of soft, watery rot, facilitated by its potent pectinolytic enzymes that macerate tissue rapidly [11]. The specific association of *Penicillium* with lime (3 out of 7 isolates) is a classic example of host specificity, with *P. digitatum* and *P. italicum* being highly adapted to the acidic environment of citrus fruits, a finding well-documented in other studies [12].

Our results on common produce like tomatoes and bananas show both parallels and divergences with other studies. The isolation of *Rhizopus* and *Fusarium* from tomato is a common finding globally. However, the high prevalence of *Aspergillus* in our tomato samples, though less common, has been reported in specific regional studies, highlighting how local environmental conditions and handling practices can shift the dominant mycobiota [13]. Similarly, the complex fungal community found on banana (*Aspergillus*, *Rhizopus*, *Penicillium*, *Fusarium*) reflects its high susceptibility to a wide range of pathogens, with the specific dominant genus often depending on the stage of ripeness and the nature of the wound [14].

Crucially, this study fills a significant gap by characterizing spoilage fungi in under-investigated tropical produce. The consistent isolation of *Aspergillus* from bilimbi and tamarind and *Fusarium* from bilimbi and lady's finger provides a novel baseline for understanding spoilage in these crops. For instance, the association of *Fusarium* with lady's finger is of particular concern, as many *Fusarium* species are known mycotoxin producers, posing potential food safety risks beyond mere spoilage [15]. The finding of *Alternaria* on bilimbi and tamarind is also significant, as *Alternaria* species produce a range of toxic metabolites, including alternariol, necessitating further investigation into the safety of consuming decayed produce from these species [16].

The reliance on morphological identification, while a robust and cost-effective first step, presents a limitation. It can be challenging to distinguish between closely related species, particularly in genera like *Fusarium* and *Aspergillus*, which contain both spoilage and potent mycotoxigenic species. Future work employing molecular techniques, such as sequencing of the ITS,  $\beta$ -tubulin, or calmodulin genes, would be essential for precise species-level identification and a more accurate assessment of mycotoxigenic potential [17]. Furthermore, pathogenicity tests to fulfill Koch's postulates would conclusively confirm the role of each isolated fungus as a primary pathogen versus a secondary invader or saprophyte.

In conclusion, this research successfully delineates the key fungal pathogens responsible for postharvest losses in a vital agricultural region of India. The findings confirm that while global spoilage genera are present, their distribution and prevalence are highly specific to the type of host produce. The data generated on locally important crops like bilimbi, snake gourd, and gooseberry is particularly valuable. This knowledge is a critical prerequisite for developing integrated postharvest management strategies. By identifying the primary targets, this study paves the way for future research into targeted biocontrol agents, optimized storage conditions, and prudent fungicide use to mitigate losses caused by these specific fungi, thereby enhancing both food security and economic returns for local farmers.

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## 5. Conclusion

In conclusion, the findings establish a critical foundation of knowledge on the primary agents of postharvest loss in the region. This information is indispensable for developing targeted and effective control strategies. Moving forward, this baseline data should be leveraged to formulate integrated management practices, including the development of biological control agents, optimization of storage conditions, and prudent fungicide use, specifically designed to combat these identified pathogens. Ultimately, such targeted approaches are essential for reducing spoilage, minimizing economic losses for farmers, improving marketability, and enhancing the overall food security of the region.

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## Compliance with ethical standards

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## References

- [1] Food and Agriculture Organization of the United Nations. The State of Food and Agriculture 2022 [Internet]. Rome: FAO; 2022 [cited 2024 Date]. Available from: <https://www.fao.org/documents/card/en/c/cc0800en>
- [2] Dukare AS, Paul S, Nambi VE, Gupta RK, Singh R, Sharma K, et al. Exploitation of microbial antagonists for the control of postharvest diseases of fruits: a review. *Crit Rev Food Sci Nutr*. 2021;61(2):218-48.
- [3] Sivakumar D, Bautista-Baños S, Spadaro D. A comprehensive review on the management of postharvest diseases of mangoes. *Postharvest Biol Technol*. 2021;181:111652.
- [4] Wisniewski M, Droby S, Norelli J, Liu J, Schena L. Alternative management technologies for postharvest disease control: The journey from simplicity to complexity. *Postharvest Biol Technol*. 2023;205:112524.
- [5] Kumar A, Premraj A, More VS, More SS, Jang JH. Isolation and Identification of Fruit Rot Pathogenic Fungi from Post-Harvest Produce. *J Fungi (Basel)*. 2022;8(10):1093. doi:10.3390/jof8101093.
- [6] Barnett HL, Hunter BB. *Illustrated Genera of Imperfect Fungi*. 4th ed. St. Paul, MN: APS Press; 1998.
- [7] Watanabe T. *Pictorial Atlas of Soil and Seed Fungi: Morphologies of Cultured Fungi and Key to Species*. 2nd ed. Boca Raton, FL: CRC Press; 2002.
- [8] Sivakumar D, Bautista-Baños S, Spadaro D. A comprehensive review on the management of postharvest diseases of mangoes. *Postharvest Biol Technol*. 2021;181:111652.
- [9] Dukare AS, Paul S, Nambi VE, Gupta RK, Singh R, Sharma K, et al. Exploitation of microbial antagonists for the control of postharvest diseases of fruits: a review. *Crit Rev Food Sci Nutr*. 2021;61(2):218-48.
- [10] Garcia-Cela E, Verheecke-Vaessen C, Medina A, Magan N. Interacting abiotic factors affect growth and aflatoxin B1 production profiles of *Aspergillus flavus* strains on pistachio-based matrices. *Food Microbiol*. 2022;102:103919.
- [11] Li B, Zong Y, Du Z, Chen Y, Zhang Z, Qin G, et al. Genomic analysis reveals the mechanism of soft rot pathogenesis in *Rhizopus stolonifer*. *Postharvest Biol Technol*. 2023;195:112138.
- [12] Papoutsis K, Mathioudakis MM, Hasperu  JH, Ziogas V. Non-chemical treatments for preventing the postharvest fungal rotting of citrus caused by *Penicillium digitatum* (green mold) and *Penicillium italicum* (blue mold). *Trends Food Sci Technol*. 2020;86:479-91.

- [13] Mariappan AK, Balamurugan S, Chen Y. Mycobiota and mycotoxin contamination in tomato fruits: A review. *Crop Prot.* 2022;158:106008.
- [14] Shao X, Cao B, Xu F, Xie S, Yu D, Wang H. Effect of postharvest application of chitosan-based nanocomposite on antifungal activity and quality of banana during storage. *Food Bioprocess Technol.* 2021;14(5):895-906.
- [15] Tola M, Kebede B. Occurrence, importance and control of mycotoxins: A review. *Cogent Food Agric.* 2023;9(1):2186637.
- [16] Zhao K, Shao B, Li B, Yang D, Liu Y. Natural occurrence of *Alternaria* toxins in food and feed in China and their influence on gastrointestinal health. *Toxins.* 2022;14(9):623.
- [17] Summerell BA. Resolving *Fusarium*: current status of the genus. *Annu Rev Phytopathol.* 2023;61:1.1-1.22.