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Pathogenesis, Epidemiology, and Control of Colletotrichum Species Infecting Cucurbitaceous Crops: A Comprehensive Review

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Abstract: Colletotrichum species are recognized as some of the most devastating fungal pathogens impacting cucurbitaceous crops globally, causing anthracnose disease that results in significant yield and quality losses. These pathogens exhibit a complex taxonomy, with several species complexes such as Colletotrichum orbiculare, C. lagenarium, and C. truncatum being frequently associated with infections in cucurbits like cucumber, watermelon, melon, and pumpkin. The infection process typically begins with the germination of conidia on the host surface, followed by the formation of appressoria, which facilitate penetration into host tissues. Disease development is highly influenced by environmental conditions, particularly humidity and temperature, which affect spore germination and pathogen proliferation. Recent advancements in molecular diagnostics, including PCR-based assays and genome sequencing, have greatly improved the accuracy of pathogen identification and understanding of host-pathogen interactions. Furthermore, efforts in resistance breeding have led to the development of cucurbit cultivars with enhanced resistance to specific Colletotrichum species. Integrated management strategies incorporating cultural practices, resistant varieties, biological control agents such as Trichoderma spp., and targeted fungicide applications are proving effective in reducing disease incidence. The emphasis on sustainable agriculture has further driven research into eco-friendly control measures, offering promising directions for minimizing the impact of Colletotrichum-induced anthracnose in cucurbit production systems.

Keywords: Colletotrichum, cucurbitaceous crops, anthracnose, fungal pathogens, disease epidemiology, molecular diagnostics, resistance breeding

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INTRODUCTION

Cucurbitaceous crops, including watermelon (*Citrullus lanatus*), cucumber (*Cucumis sativus*), and melon (*Cucumis melo*), hold immense significance in global agriculture due to their high economic value and nutritional benefits. These crops are cultivated extensively across tropical, subtropical, and temperate regions, contributing significantly to the income of smallholder farmers and to food security. However, their production is increasingly threatened by anthracnose, a serious fungal disease primarily caused by *Colletotrichum* species, which has emerged as a major constraint to achieving optimal yields and fruit quality. The disease is characterized by the appearance of sunken, dark lesions on leaves, stems, and fruits, often leading to premature defoliation, fruit rot, and reduced marketability (Patel et al., 2023). Among the most commonly implicated pathogens are *Colletotrichum orbiculare*, *C. lagenarium*, and members of the *Colletotrichum truncatum* species complex, each with varying degrees of host specificity and virulence. The life cycle of *Colletotrichum* involves the production of conidia that adhere to plant surfaces, germinate under favorable conditions, and form specialized infection structures known as appressoria. These structures generate turgor pressure that enables the pathogen to breach the host epidermis and colonize plant tissues. Warm temperatures and high humidity favor the rapid spread and severity of anthracnose, with rain splash and mechanical contact serving as primary modes of spore dissemination. In recent years, advancements in molecular biology have deepened our understanding of the *Colletotrichum*-cucurbit interaction, revealing important insights into virulence factors, pathogenicity genes, and host resistance mechanisms. Techniques such as PCR, qPCR, and next-generation sequencing have enabled precise pathogen identification, tracking of disease outbreaks, and development of molecular markers for resistant cultivar selection. Despite these developments, effective disease control remains a challenge due to the genetic variability of the pathogen and the emergence of fungicide-resistant strains. Conventional management practices, including crop rotation, removal of infected plant debris, and use of certified disease-free seeds, remain foundational but are often insufficient when used in isolation. Therefore, integrated disease management (IDM) strategies are increasingly emphasized, combining resistant cultivars, cultural practices, chemical fungicides, and biological control agents. The breeding of resistant varieties, though time-consuming, offers a long-term solution to anthracnose. Breeding programs are incorporating resistance genes from wild relatives and landraces, aided by marker-assisted selection and genomic tools. Moreover, the application of biological control agents such as *Trichoderma* spp., *Bacillus subtilis*, and mycorrhizal fungi has shown promise in suppressing *Colletotrichum* populations and enhancing plant defense responses. The use of environmentally friendly products like botanical extracts and chitosan-based formulations is gaining popularity as part of sustainable agriculture practices. In addition, the development of forecasting models based on weather parameters is being explored to enable timely application of control measures. Given the rising concern over environmental impact and fungicide residues in food, there is a growing shift toward reducing chemical inputs and adopting greener alternatives. International collaboration in research and extension services is also vital for disseminating knowledge, training farmers, and implementing region-specific management recommendations. In summary, anthracnose caused by *Colletotrichum* species remains a significant threat to cucurbitaceous crops worldwide, and its management requires a holistic approach that integrates modern scientific tools with traditional agricultural practices. Strengthening disease surveillance systems, investing in resistant germplasm development, and promoting sustainable disease control strategies are crucial steps toward ensuring the resilience and profitability of cucurbit production systems in the face of this persistent fungal challenge.

Taxonomy and Species Diversity

The genus *Colletotrichum* comprises a diverse array of species complexes, each exhibiting unique morphological characteristics, genetic profiles, and host specificities, making the taxonomy and identification of these pathogens particularly challenging. Among these, *Colletotrichum orbiculare* stands out as the principal causal agent of anthracnose in cucurbitaceous crops, displaying a strong affinity for hosts such as watermelon, cucumber, and melon. However, other species, including *C. gloeosporioides*, *C. truncatum*, and *C. magnum*, have also been frequently reported in association with cucurbit anthracnose, either as primary pathogens or as part of a complex of co-infecting species (Cannon et al., 2012). The presence of multiple pathogenic species complicates both diagnosis and management, especially under field conditions where morphological identification is insufficient. Recent advancements in molecular phylogenetics have shed light on this complexity, with multilocus sequence analysis (MLSA) and genome-based tools enabling the differentiation of closely related taxa. For example, studies conducted in China have revealed the presence of previously unidentified *Colletotrichum* species causing anthracnose in watermelon, leading to the formal description of novel species such as *C. citrulli* and *C. kaifengense* (Zhang et al., 2022). These findings underscore the dynamic nature of *Colletotrichum* taxonomy and highlight the importance of continuous surveillance and molecular diagnostics to accurately identify the etiological agents of anthracnose. The discovery of new species not only expands our understanding of the pathogen diversity but also has significant implications for breeding programs, quarantine regulations, and the development of targeted disease management strategies.

Pathogenesis and Infection Mechanisms

Colletotrichum species are known for their hemibiotrophic mode of infection, a two-phase strategy that enables them to effectively colonize host tissues and cause disease. Initially, the pathogen establishes a biotrophic relationship with the host, during which it derives nutrients from living cells without causing immediate damage. This is followed by a necrotrophic phase where the pathogen kills host tissue and continues to extract nutrients from the dead cells. The infection process begins with the formation of appressoria—specialized, melanized dome-shaped structures that adhere firmly to the plant surface. These structures generate immense turgor pressure, allowing the fungus to mechanically breach the host cuticle and cell wall (Sharma & Kulshrestha, 2015). Once inside, *Colletotrichum* secretes a range of effector proteins that are crucial for suppressing the plant's immune responses and facilitating the establishment of infection. These effectors modulate host cellular processes to the pathogen’s advantage and prevent recognition by the host’s defense systems (Lu et al., 2022). As the infection transitions into the necrotrophic phase, the pathogen produces an array of cell wall-degrading enzymes (CWDEs), such as cellulases, hemicellulases, and pectinases, which break down the structural components of plant cells (Joshi, 2018). This enzymatic degradation leads to extensive tissue maceration, resulting in the typical anthracnose symptoms—sunken, necrotic lesions on leaves, stems, and fruits. The ability of *Colletotrichum* to effectively switch between biotrophic and necrotrophic phases, coupled with its sophisticated arsenal of pathogenicity factors, underscores its adaptability and success as a pathogen across a broad range of cucurbit hosts.

EPIDEMIOLOGY

Disease Cycle

Colletotrichum spp. survive between cropping seasons as **conidia** (asexual spores) or **sclerotia** (hardened masses of mycelium) in infected plant debris and soil. These survival structures allow the pathogen to persist even under unfavorable environmental conditions, ensuring its availability to infect new crops when conditions become conducive. The disease cycle is perpetuated through various means of dispersal and infection:

Seed Transmission

Seed transmission is a primary route for introducing *Colletotrichum spp.* into previously uninfected regions or fields. When seeds are harvested from infected plants, they may carry conidia either on the seed coat or internally. During storage and handling, these infected seeds can remain viable and act as inoculum when planted in a new area. Upon germination, the pathogen can infect the seedling, producing initial symptoms like leaf spots or cotyledon lesions, which later become sources of secondary inoculum for further disease spread. This method of transmission is particularly concerning in commercial agriculture, where seed lots are distributed over wide geographic areas. Hence, seed health testing and certification programs are crucial in managing *Colletotrichum* diseases (UMN Extension, 2023). Treating seeds with fungicides or using resistant varieties can significantly reduce the risk of seed-borne infections. Moreover, farmers are encouraged to source seeds from reliable suppliers and avoid saving seeds from infected plants to curb this mode of pathogen dissemination.

Rain Splash and Irrigation

Rainfall and irrigation practices contribute substantially to the **dispersal of conidia** of *Colletotrichum spp.* Once conidia are produced on lesions of infected plant parts, they are easily dislodged and carried by water droplets to nearby healthy plants. During rainfall or overhead irrigation, the splash effect can propel the spores across short distances, depositing them on susceptible tissues such as leaves, stems, or fruits. If environmental conditions are favorable—specifically high humidity and moderate to warm temperatures—germination and penetration of the host epidermis occur rapidly. This often results in the appearance of new necrotic lesions, typically within 48–72 hours of spore deposition. Moreover, frequent irrigation or dew formation prolongs leaf wetness duration, creating an ideal microclimate for infection. In densely planted fields or greenhouses, water-mediated spore movement can lead to rapid and widespread disease outbreaks. As a preventive measure, growers are advised to adopt **drip irrigation systems**, maintain **plant spacing** for better airflow, and schedule irrigation during periods of lower humidity to reduce splash dispersal risks (NC State Extension, 2023). Additionally, proper mulching and soil management practices can minimize water splash and indirectly reduce the pathogen’s chances of infecting new hosts.

Insect Vectors

Certain insect pests, such as **cucumber beetles**, have been identified as **mechanical vectors** of *Colletotrichum spp.* These insects contribute to the disease cycle in multiple ways. Firstly, when beetles feed on infected tissues, conidia may adhere to their mouthparts, legs, or body surfaces. As they move from plant to plant, especially during feeding or oviposition, they inadvertently deposit viable spores onto healthy plant tissues, facilitating infection. Secondly, their feeding activity creates entry wounds in the plant’s cuticle, which provide easy access for fungal pathogens to invade. In particular, feeding injuries near nodes or growing points become focal areas for infection. In some cases, beetles may even carry conidia internally and excrete them through frass, adding another route for pathogen dissemination. The interaction between insect vectors and plant pathogens like *Colletotrichum* exemplifies a complex ecological relationship where pest management also becomes a vital component of disease control. Integrated Pest Management (IPM) strategies that include insecticide application, trap cropping, and the use of biological controls can help reduce insect populations and subsequently lower the risk of pathogen spread . Monitoring insect activity during early crop stages is critical to prevent vector-facilitated outbreaks

(UMass Extension, 2023)..

Environmental Factors

Warm temperatures ranging between **25–30°C** and **high relative humidity** create ideal environmental conditions for the development and proliferation of *Colletotrichum* infections. Under these conditions, conidia germinate rapidly, leading to swift colonization of host tissues. **Leaf wetness**, especially when maintained for extended periods, further enhances infection rates. Factors such as **dense plant canopies** restrict airflow and prevent foliage from drying, thereby prolonging surface moisture. Additionally, **overhead irrigation** mimics natural rainfall, facilitating splash dispersal of conidia and maintaining a humid microclimate within the canopy. These conditions collectively accelerate the disease cycle and increase epidemic risk (UMass Extension, 2023).

INTEGRATED DISEASE MANAGEMENT

Integrated Disease Management (IDM) for*Colletotrichum* spp. in cucurbit crops combines cultural, chemical, biological, and molecular strategies to provide a holistic, sustainable, and environmentally responsible approach. Since no single method offers complete protection, integration of multiple tactics is essential for effective and long-term disease suppression.

Cultural Practices

Crop Rotation

Practicing crop rotation is a cornerstone of disease management in cucurbit production. By **avoiding the cultivation of cucurbits for 2–3 consecutive years** in fields previously infested with *Colletotrichum* spp., the natural decline of the pathogen in soil and debris is encouraged. This break in host availability drastically reduces the primary inoculum in the subsequent growing season, thereby lowering disease pressure. Rotation with non-host crops like cereals or legumes interrupts the pathogen's life cycle and minimizes soil inoculum buildup (UMass Extension, 2023).

Sanitation

Sanitation is another vital cultural strategy. *Colletotrichum* spp. can persist in **infected plant debris**, continuing to release conidia and initiate infection cycles. Therefore, **removal and destruction of all crop residues after harvest**—including roots, stems, and fallen fruits—is strongly recommended. Proper composting or deep burial of infected material prevents survival and dissemination of the pathogen. Regular sanitation of tools and equipment also limits mechanical transmission within and between fields (UCANR, 2023).

Resistant Varieties

Utilizing **resistant cultivars** has proven to be an effective cultural approach in reducing anthracnose incidence. Breeding programs have introduced **varieties resistant to specific races of *Colletotrichum***, enhancing disease management while reducing chemical input. These cultivars either possess structural defenses or molecular resistance genes that restrict pathogen entry and colonization. While resistance may not be durable against all pathogen strains, rotating resistant varieties and incorporating other IDM components helps maintain effectiveness (Patel et al., 2023).

Chemical Control

Chemical control plays a significant role in curbing anthracnose outbreaks, especially during peak disease periods. **Fungicides like chlorothalonil and mancozeb** are commonly employed as **protective sprays**, inhibiting fungal spore germination and initial infection. These fungicides are particularly effective when applied **before symptom appearance** or at early disease stages. However, repeated and **sole reliance on chemical treatments can lead to fungicide resistance**, diminishing their efficacy over time. Moreover, extensive chemical use raises **environmental and food safety concerns**, necessitating strict adherence to recommended dosages, pre-harvest intervals, and rotation with fungicides of different modes of action to delay resistance buildup (UF/IFAS, 2023).

Biological Control

Biological control agents (BCAs) offer an environmentally sustainable alternative to chemical fungicides. Organisms such as **Trichoderma spp.** and **Bacillus subtilis** are known for their **antagonistic properties** against *Colletotrichum* spp. These biocontrol agents suppress the pathogen through various mechanisms, including **competition for nutrients and space**, **secretion of antifungal metabolites**, **induction of systemic resistance in host plants**, and **mycoparasitism**. Field trials have demonstrated reduced disease severity and improved plant vigor upon application of these beneficial microbes. Moreover, their compatibility with organic farming systems and minimal environmental impact make them ideal for integrated disease management programs (Than et al., 2008).

Molecular Approaches

Recent breakthroughs in **genomics and molecular biology** have opened up new avenues in anthracnose management. **Genome sequencing of both host plants and *Colletotrichum* spp.** has led to the identification of **resistance (R) genes** in cucurbits and **effector proteins** in pathogens that facilitate infection. This knowledge aids in **marker-assisted selection** for breeding resistant varieties and designing **targeted RNA interference (RNAi)** or **CRISPR-based gene-editing** tools to enhance resistance traits. Molecular diagnostics also enable early detection of specific *Colletotrichum* races in seed lots or field samples, facilitating timely interventions. Although still in research and development stages for most crops, these molecular tools represent a promising frontier in disease prediction, prevention, and precision management (Lu et al., 2022).

CONCLUSION

Effective management of *Colletotrichum*-induced anthracnose in cucurbitaceous crops necessitates a comprehensive and integrated disease management (IDM) strategy that addresses both the environmental conditions conducive to disease development and the biological complexity of the pathogen. Cultural practices such as crop rotation, sanitation, and optimized irrigation play a crucial role in reducing primary inoculum sources and interrupting the disease cycle. Avoiding cucurbit cultivation for two to three years in infested fields, removing and destroying infected plant debris, and switching from overhead to drip irrigation can significantly minimize the spread and establishment of the pathogen. In parallel, the use of resistant cultivars developed through plant breeding programs has emerged as a sustainable strategy to counter specific races of *Colletotrichum*, thereby reducing dependency on chemical controls. However, in regions with high disease pressure, the application of fungicides such as chlorothalonil and mancozeb remains a practical option, especially when used judiciously and in rotation to mitigate resistance buildup. Moreover, the incorporation of biological control agents like *Trichoderma spp.* and *Bacillus subtilis*, known for their antagonistic activity, provides an eco-friendly solution by enhancing soil health and suppressing pathogen growth. Importantly, advances in molecular biology and genomics are revolutionizing our understanding of host-pathogen interactions, enabling the identification of resistance genes and pathogen effectors, which in turn support the development of resistant cultivars and targeted interventions. The dynamic and evolving nature of *Colletotrichum* populations, often characterized by high genetic variability and adaptability, underscores the importance of continuous research and surveillance. As climate change alters the epidemiology of plant diseases, sustained investment in integrated, adaptive, and science-driven management approaches is essential. Only through a multifaceted strategy that synergizes traditional agricultural wisdom with modern biotechnological innovations can long-term, sustainable control of anthracnose in cucurbits be achieved.

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