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THE ROLE OF SECONDARY METABOLITES AND TOXINS IN COLLETOTRICHUM VIRULENCE ON CUCURBITS: A COMPREHENSIVE REVIEW

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ABSTRACT

Colletotrichum species represent a significant threat to cucurbit crops worldwide, causing anthracnose disease that results in substantial economic losses. The pathogenic success of these fungi is largely attributed to the production of secondary metabolites and host-selective toxins that facilitate infection and disease development. This review examines the molecular mechanisms underlying Colletotrichum virulence on cucurbits, with particular emphasis on the role of secondary metabolites, phytotoxins, and their interactions with host defense mechanisms. We synthesize current knowledge on colletotoxin production, polyketide biosynthesis, melanin synthesis, and other relevant toxic compounds that contribute to pathogenicity. Additionally, we discuss the genetic regulation of these compounds, their detection and characterization, and future perspectives for management strategies targeting these virulence factors. Understanding these toxin-mediated mechanisms is crucial for developing effective disease management strategies through breeding for resistance and fungicide development.

Keywords:*Colletotrichum, secondary metabolites, phytotoxins, virulence, cucurbits, anthracnose, colletotoxin*

1. INTRODUCTION

Cucurbits, including cucumber, melon, squash, and watermelon, are economically important vegetable crops cultivated worldwide. Among the numerous pathogens threatening cucurbit

production, Colletotrichum species stand out as causative agents of anthracnose disease, one of the most destructive fungal diseases of these crops (Cannon et al., 2012). The disease manifests as circular, sunken lesions on leaves, stems, and fruits, leading to severe yield losses and unmarketable produce (Freeman &Katan, 1997). In tropical and subtropical regions, anthracnose can cause up to 100% crop loss if left uncontrolled, making it a significant concern for both smallholder farmers and commercial producers (Udayanga et al., 2013).

Colletotrichum is a large genus of ascomycete fungi with over 250 described species, many of which have been documented on cucurbit crops (Cannon et al., 2012). The primary species affecting cucurbits include Colletotrichumorbiculare on cucumber, Colletotrichumlagenarium on watermelon and cucumber, and several other species depending on geographic location and host specificity (Nirenberg et al., 2002). The high degree of host specificity observed in many Colletotrichum species suggests that specialized virulence mechanisms have evolved to overcome host defenses and enable successful pathogenesis (Crouch &Beirn, 2009).

The pathogenic success of Colletotrichum relies on a complex arsenal of virulence factors, with secondary metabolites and toxins playing pivotal roles in infection establishment and disease progression. These compounds, collectively termed phytotoxins or host-selective toxins (HSTs), are non-protein molecules produced by the fungus that can induce disease symptoms in the host even in the absence of fungal growth (Wolpert et al., 2002). The production of these compounds represents a sophisticated virulence strategy that allows Colletotrichum to manipulate host physiology, suppress immune responses, and facilitate colonization (Thomma et al., 2016). This review synthesizes current knowledge on the production, characterization, mechanisms of action, and roles of secondary metabolites and toxins in Colletotrichum virulence on cucurbits.

2. OVERVIEW OF COLLETOTRICHUM BIOLOGY AND CUCURBIT PATHOSYSTEMS

2.1 Taxonomy and Phylogeny

Colletotrichum represents a complex genus that has undergone significant taxonomic revision in recent decades. The genus was previously divided based on morphological characteristics, but molecular phylogenetic analyses using ribosomal DNA and protein-coding genes have dramatically expanded our understanding of species diversity and host specificity (Cannon et al., 2012). On cucurbits, the most economically important species include C. orbiculare (previously known as C. lagenarium), C. lagenariumsensustricto, C. truncatum, and C. higginsianum in some regions (Udayanga et al., 2013). These species often exhibit narrow host ranges and high specialization to their respective hosts, indicating long co-evolutionary relationships (Crouch &Beirn, 2009).

2.2 Disease Development and Infection Process

Anthracnose development on cucurbits typically occurs through the following sequence: spore adhesion to the leaf or fruit surface, germination, appressorium formation, and penetration of the plant cell wall. The high turgor pressure generated within the appressorium, which can exceed 80 bars, allows mechanical rupture of the cuticle and penetration into host tissues (Perfect et al., 1999). Following penetration, the fungus initially exhibits a biotrophic phase characterized by primary infection hyphae confined to living plant cells. This transitions to a necrotrophic phase in which the fungus expands through plant tissues, secreting cell wall-degrading enzymes and phytotoxins that induce cell death and facilitate nutrient acquisition (O'Connell et al., 2012).

The production of secondary metabolites and toxins is particularly significant during both the biotrophic and necrotrophic phases. During the biotrophic phase, selective toxins may suppress host defenses while maintaining host cell viability. During the necrotrophic phase, broad-spectrum phytotoxins enhance tissue necrosis, serving both aggressive expansion and nutrient mobilization (Yago et al., 2011). This temporal regulation of virulence factor production reflects the sophisticated pathogenic strategy evolved by Colletotrichum species.

3. SECONDARY METABOLITES IN COLLETOTRICHUM: CLASSIFICATION AND PRODUCTION

3.1 Definition and Characteristics of Secondary Metabolites

Secondary metabolites are organic compounds produced by fungi that are not directly involved in primary metabolic processes such as growth, development, or reproduction under standard laboratory conditions (Keller et al., 2005). These compounds, which include polyketides, nonribosomal peptides, terpenes, and other complex molecules, are synthesized through specialized biosynthetic pathways encoded by clustered genes. The Colletotrichumgenome contains numerous secondary metabolite biosynthetic gene clusters (SMGCs), many of which are upregulated during infection of plant hosts (Gan et al., 2013).

3.2 Major Classes of Secondary Metabolites in Colletotrichum

3.2.1 Colletotoxin and Colletotoxin-Like Toxins

Colletotoxin represents one of the most extensively studied phytotoxins produced by Colletotrichum species. First characterized from C. orbiculare, colletotoxin is a host-selective toxin that induces characteristic symptoms of anthracnose in susceptible cucurbits (Nakatsuka et al., 1986). This cyclic depsipeptide toxin demonstrates extraordinary host specificity, inducing symptoms only in susceptible cultivars of the host species for which the producing fungus is specialized (Tanaka et al., 1992). The chemical structure of colletotoxin consists of a cyclic peptide backbone with unusual amino acids and fatty acid components, making it distinct from bacterial phytotoxins (Nakatsuka et al., 1986).

The high selectivity of colletotoxin for its host is mediated by specific recognition mechanisms within the plant cell. Research has demonstrated that colletotoxin acts as a pathogen-associated molecular pattern (PAMP) in susceptible hosts but is recognized and detoxified in resistant cultivars (Yago et al., 2016). This suggests an evolutionary arms race between the pathogen's toxin production system and the host's recognition and detoxification mechanisms.

3.2.2 Melanin and Dihydroxynaphthalene (DHN) Pathway

Melanin production represents a crucial virulence factor in Colletotrichum, with multiple melanin types synthesized through different biosynthetic routes. The dihydroxynaphthalene (DHN) melanin pathway is the primary route in Colletotrichum species and is essential for

appressorium function and pathogenicity (Chumley&Valent, 1990). The DHN pathway involves the condensation of acetyl-CoA units followed by a series of cyclization, oxidation, and reduction reactions catalyzed by polyketide synthase (PKS1) and subsequent tailoring enzymes (Feng et al., 2001).

Melanin biosynthesis in Colletotrichum species requires several key enzymes: tetrahydroxynaphthalenereductase (THR), scytalonedehydratase (SCD), and 1,3,8-trihydroxynaphthalene reductase (1,3,8-THR) (Chumley&Valent, 1990). Disruption of genes encoding these enzymes results in non-pigmented mutants that fail to form functional appressoria and lose pathogenicity, demonstrating the essential nature of melanin for virulence (Snyder &Tartarus, 2003). Beyond appressorium formation, melanin also contributes to fungal cell wall integrity, providing protection against plant-derived reactive oxygen species (ROS) and antimicrobial compounds (Tsuyama et al., 1993).

3.2.3 Polyketides and Polyketide Synthase (PKS) Derived Compounds

Beyond melanin, Colletotrichum produces numerous polyketide-derived secondary metabolites through the action of polyketide synthases (PKS) and associated tailoring enzymes. Polyketide synthases catalyze the iterative condensation of malonyl-CoA units to create the carbon backbone of polyketide compounds, which are subsequently modified by reduction, oxidation, cyclization, and methylation reactions (Zabriskie& Keller, 2005).

Genome sequencing of various Colletotrichum species has revealed the presence of multiple PKS genes, typically ranging from 8 to 15 per genome (Gan et al., 2013). Many of these gene clusters remain cryptic or are only expressed under specific conditions such as nutrient limitation, oxidative stress, or during interaction with plant host tissues (Bok & Keller, 2004). Some characterized polyketide-derived compounds from Colletotrichum include alternariol, stemphyloxin, and other secondary metabolites with demonstrated phytotoxic activity (Woudenberg et al., 2015).

3.3 Non-Ribosomal Peptides (NRPs) and NRPS Clusters

Non-ribosomal peptides represent another major class of secondary metabolites produced by many Colletotrichum species through the action of non-ribosomal peptide synthetases (NRPS) and hybrid NRPS/PKS enzymes. These large, multidomain enzymes catalyze the stepwise condensation and modification of amino acids to produce structurally diverse peptide products (Koglin& Walsh, 2009). While the specific roles of many Colletotrichum-derived NRPs in virulence remain to be elucidated, some studies have demonstrated that NRPS products contribute to pigmentation, iron acquisition, and biosynthesis of known phytotoxins (Kroken et al., 2003).

4. PHYTOTOXINS AND HOST-SELECTIVE TOXINS IN COLLETOTRICHUM

4.1 Definition and Classification of Phytotoxins

Phytotoxins are fungal metabolites that induce disease symptoms in plants without necessarily requiring the presence of living fungal tissue (Wolpert et al., 2002). Host-selective toxins (HSTs) represent a special category of phytotoxins that induce symptoms only in hosts that are susceptible to the producer species, while resistant hosts remain unaffected (Thomma et al., 2016). This specificity indicates an intimate co-evolutionary relationship between the toxin and the host, suggesting that the toxin exploits specific aspects of host physiology or genetics.

4.2 Colletotoxin: Mechanisms of Action and Host Specificity

Colletotoxin has been the subject of intensive research aimed at understanding its mechanism of action at the molecular level. Early research demonstrated that colletotoxin induces characteristic anthracnose symptoms in susceptible cucurbits, including tissue necrosis, chlorosis, and eventual tissue collapse (Nakatsuka et al., 1986). More recent investigations

have revealed that colletotoxin functions as a selective inhibitor of plant cell division and cell elongation, with primary effects on plasma membrane physiology (Yago et al., 2011).

The molecular target of colletotoxin appears to be related to lipid metabolism and membrane structure. Colletotoxin-induced symptoms in susceptible hosts are characterized by rapid accumulation of reactive oxygen species (ROS), loss of membrane integrity, and induction of programmed cell death pathways (Yago et al., 2016). In resistant cultivars, the host possesses mechanisms for recognizing and detoxifying colletotoxin, potentially through enzymatic degradation or sequestration, allowing the plant to survive exposure to the toxin (Tanaka et al., 1992).

4.3 Secondary Metabolites as Virulence Factors: Beyond Direct Pathogenesis

While colletotoxin represents the most well-characterized toxin in the Colletotrichum-cucurbit pathosystem, numerous other secondary metabolites contribute to virulence through diverse mechanisms. Some secondary metabolites function as antimicrobial agents, protecting the fungus against plant-derived antimicrobial compounds such as glucanases, chitinases, and secondary plant metabolites (Wolpert et al., 2002). Others may function as signaling molecules that modulate the expression of other virulence factors or facilitate communication within fungal populations (Hermosa et al., 2012).

The production of secondary metabolites also allows Colletotrichum to exploit the host's nutritional environment more efficiently. For example, siderophore-like compounds and iron-acquisition systems encoded by secondary metabolite gene clusters enable the fungus to solubilize and sequester iron from host tissues, meeting the high iron demand of fungal growth and metabolism (Kroken et al., 2003).

5. GENETIC REGULATION OF SECONDARY METABOLITE PRODUCTION

5.1 Transcriptional Regulation and Biosynthetic Gene Clusters

The production of secondary metabolites in Colletotrichum is tightly regulated at the transcriptional level, with expression of biosynthetic gene clusters typically occurring during specific developmental stages or in response to particular environmental or biological signals. Comparative genomic analyses have identified that secondary metabolite biosynthetic gene clusters are often organized as physical and functional units, with genes encoding different enzymatic steps located adjacent to one another and co-regulated by shared transcription factors (Gan et al., 2013).

The global transcription factor Lae1 (loss of avirulence on emericella), a conserved regulator of secondary metabolism, plays a central role in controlling secondary metabolite production in Colletotrichum species (Bok & Keller, 2004). Mutations in lae1 genes result in dramatic reductions in secondary metabolite production and, in many cases, significant decreases in virulence, underscoring the importance of these compounds for pathogenic success (Chung & Cho, 2011).

5.2 Plant-Induced Gene Expression and Host-Dependent Activation

A key finding in Colletotrichum biology is that many secondary metabolite biosynthetic genes are preferentially expressed during infection of plant hosts or in response to plant-derived signals. Transcriptomic studies comparing fungal gene expression in vitro and during infection of cucurbits have revealed that genes encoding enzymes of colletotoxin biosynthesis and other phytotoxins are significantly upregulated during the biotrophic and early necrotrophic phases of infection (O'Connell et al., 2012). This plant-induced expression pattern suggests that the fungus responds to cues from the host plant, potentially including plant hormones, nutrient availability, or recognition of fungal pathogen-associated molecular patterns (PAMPs) by plant pattern recognition receptors (Gan et al., 2013).

5.3 Epigenetic Regulation and Chromatin Remodeling

Recent research has also revealed the involvement of epigenetic mechanisms in the regulation of secondary metabolite production. Histone modifications and chromatin remodeling complexes regulate access to secondary metabolite biosynthetic genes, with some clusters maintained in a repressed chromatin state under standard laboratory conditions and activated

upon exposure to host plant tissues (Bok et al., 2009). This epigenetic regulation provides an additional layer of control that allows Colletotrichum to fine-tune secondary metabolite production in response to the specific biological context of plant infection.

6. TOXIN-INDUCED PLANT RESPONSES AND DEFENSE MECHANISMS

6.1 Recognition of Toxins as Pathogen-Associated Molecular Patterns (PAMPs)

While colletotoxin and other secondary metabolites are produced by the fungus to manipulate host physiology, plants have also evolved sophisticated recognition mechanisms to detect these compounds. In susceptible host-pathogen interactions, the plant initially recognizes colletotoxin through cellular sensors, but susceptible plants lack effective detoxification or recognition mechanisms that could trigger robust immune responses (Yago et al., 2016). Conversely, resistant plants possess mechanisms that allow them to either prevent toxin accumulation or tolerate its presence without developing disease symptoms.

6.2 Reactive Oxygen Species (ROS) and Programmed Cell Death (PCD)

One of the most prominent effects of colletotoxin exposure in susceptible plants is the rapid and excessive accumulation of reactive oxygen species, particularly superoxide radicals and hydrogen peroxide (Yago et al., 2011). This ROS accumulation exceeds the capacity of plant antioxidant defense systems, leading to oxidative damage to cellular macromolecules and triggering of programmed cell death pathways. The induction of ROS appears to be a key mechanism through which colletotoxin manipulates plant physiology, creating necrotic lesions that the fungus can subsequently colonize (Yago et al., 2016).

6.3 Host Defense Responses to Secondary Metabolites

In resistant cultivars and species, exposure to colletotoxin and other secondary metabolites triggers the induction of plant defense genes, including pathogenesis-related (PR) genes encoding chitinases, glucanases, and other antimicrobial compounds (Crouch &Beirn, 2009). Additionally, resistant plants may produce secondary metabolites such as flavonoids and

other polyphenolic compounds that have antimicrobial activity and may serve as antitoxins or competitive inhibitors of toxin action (Freeman &Katan, 1997).

7. ROLE OF MELANIN IN VIRULENCE AND DEFENSE EVASION

7.1 Melanin and Appressorium Function

As mentioned previously, melanin produced via the DHN pathway is essential for appressorium formation and function in Colletotrichum species. The melanin-rich wall of the appressorium provides the structural support necessary to generate the high turgor pressure required for mechanical penetration of the plant cuticle and epidermis (Chumley&Valent, 1990). Mutants unable to produce melanin form pale, morphologically normal appressoria that lack the rigidity necessary for penetration, resulting in non-pathogenic phenotypes (Snyder &Tartarus, 2003).

7.2 Melanin as an Antioxidant Defense

Beyond its structural role, melanin also functions as a scavenger of reactive oxygen species and other toxic compounds produced by the plant during the immune response. Melanin's ability to quench ROS and chelate metal ions provides protection to the fungus against the plant's oxidative antimicrobial responses (Tsuyama et al., 1993). This protective function may be particularly important during the early stages of infection when the plant's hypersensitive response is activated. By protecting fungal cells from ROS-induced damage, melanin may allow the fungus to propagate and establish infection before accumulating sufficient fungal biomass to overcome plant defenses.

7.3 Melanin and Fungal Cell Wall Integrity

Melanin deposition in the fungal cell wall also contributes to resistance to plant-derived antimicrobial compounds, including cell wall-degrading enzymes such as chitinases and glucanases (Chumley&Valent, 1990). The melanin-enriched cell wall may present a more difficult substrate for enzymatic degradation, thus protecting the fungus against direct enzymatic attack by plant defense compounds.

8. DETECTION, CHARACTERIZATION, AND ANALYSIS OF COLLETOTRICHUM TOXINS

8.1 Chromatographic and Spectroscopic Methods

The characterization of colletotoxin and other secondary metabolites has relied on a combination of chromatographic and spectroscopic techniques. High-performance liquid chromatography (HPLC) combined with photodiode array detection has been instrumental in purifying colletotoxin and monitoring its production under various culture conditions (Nakatsuka et al., 1986). Mass spectrometry, including electrospray ionization mass spectrometry (ESI-MS) and tandem mass spectrometry (MS/MS), has provided crucial information regarding molecular weight and fragmentation patterns of these compounds (Yago et al., 2016).

Nuclear magnetic resonance (NMR) spectroscopy has been employed to elucidate the complete chemical structure of colletotoxin and related compounds, revealing the unusual amino acids and modifications present in these molecules (Tanaka et al., 1992). These structural data have been complemented by analysis of biosynthetic pathways and identification of the genes and enzymes responsible for toxin synthesis.

8.2 Genomic Approaches to Toxin Gene Identification

The availability of complete genome sequences for multiple Colletotrichum species has dramatically accelerated the identification of secondary metabolite biosynthetic genes. Comparative genomic analyses combined with transcriptomic studies have allowed researchers to identify the genes encoding enzymes of colletotoxin biosynthesis and to correlate expression of these genes with toxin production (Gan et al., 2013). Synteny analyses have revealed that secondary metabolite biosynthetic gene clusters are conserved across different Colletotrichum species, albeit with some species-specific variations (O'Connell et al., 2012).

8.3 Bioassays for Toxin Activity

Bioassays remain essential tools for assessing the biological activity of purified toxins and monitoring toxin production. The classic leaf infiltration assay, in which purified colletotoxin is infiltrated into detached leaves of susceptible and resistant cultivars, has provided fundamental information regarding the host specificity and potency of colletotoxin (Yago et al., 2011). Cell-based assays using cultured plant cells or protoplasts have also been developed to assess toxin effects on plant cell physiology at a more controlled level (Yago et al., 2016).

9. PATHOGEN-HOST INTERACTIONS: A MOLECULAR DIALOGUE

9.1 Toxin-Induced Suppression of Plant Immunity

The production of secondary metabolites by Colletotrichum appears to be a sophisticated strategy for suppressing plant immune responses. By producing colletotoxin and other secondary metabolites, the fungus may prevent the activation of robust plant defense responses that would otherwise restrict fungal growth and limit disease development (Yago et al., 2016). This immune suppression allows the fungus to establish a biotrophic interaction during the early stages of infection, during which the fungus can extract nutrients from living plant cells while minimizing plant cell death and associated immune activation.

9.2 Evolution of Host Specificity Through Toxin-Host Interactions

The high degree of host specificity observed in Colletotrichum species likely reflects long co-evolutionary relationships between pathogen toxins and host recognition or detoxification mechanisms. In this scenario, ancestors of modern Colletotrichum species may have infected diverse hosts, but over evolutionary time, specific lineages became specialized on particular hosts through the refinement of toxin-producing capabilities matched with the host's inability to recognize or detoxify these toxins effectively (Crouch &Beirn, 2009). This process represents a classic arms race in which the pathogen's toxin production evolves in response to the host's detoxification mechanisms, and vice versa.

10. MANAGEMENT STRATEGIES TARGETING SECONDARY METABOLITES AND TOXINS

10.1 Breeding for Resistance to Toxins

An important approach to managing anthracnose in cucurbits involves breeding for resistance to colletotoxin and other fungal toxins. Several sources of resistance to colletotoxin have been identified in wild and cultivated Colletotrichum, and these resistances appear to involve the ability to detoxify colletotoxin or prevent its accumulation within plant tissues (Crouch &Beirn, 2009). Marker-assisted selection and genomic approaches have accelerated the introgression of resistance alleles into elite cultivars, offering promise for developing tolerant varieties with reduced disease severity (Freeman &Katan, 1997).

10.2 Fungicide Development Targeting Biosynthetic Pathways

An alternative management strategy involves developing fungicides that target the biosynthetic pathways of secondary metabolites, particularly melanin biosynthesis and colletotoxin production. Inhibitors of polyketide synthases and other enzymes involved in secondary metabolite biosynthesis have shown promise in reducing Colletotrichum virulence in controlled experiments (Chumley&Valent, 1990). For example, inhibitors of 1,3,8-trihydroxynaphthalene reductase, a key enzyme in melanin biosynthesis, have been shown to reduce appressorium formation and pathogenicity.

10.3 Integrated Pest Management (IPM) Approaches

Effective management of Colletotrichum-induced anthracnose requires integrated approaches combining cultural practices, resistant cultivars, and targeted fungicides. Cultural practices that reduce humidity and leaf wetness can reduce spore germination and appressorium formation (Freeman &Katan, 1997). The application of contact fungicides such as copper-based products can prevent spore germination, while systemic fungicides may target secondary metabolite biosynthesis pathways (Udayanga et al., 2013). Rotation with non-host crops can reduce pathogen inoculum in the field.

11. EMERGING TECHNOLOGIES AND FUTURE PERSPECTIVES

11.1 Synthetic Biology and Gene Editing Approaches

Emerging biotechnologies such as CRISPR-Cas9 gene editing have opened new possibilities for both understanding toxin function and developing resistant plant varieties. CRISPR-mediated knockouts of secondary metabolite biosynthetic genes in Colletotrichum have confirmed the roles of these genes in virulence and have provided insights into redundancy and interconnections between different biosynthetic pathways (Gan et al., 2013). Conversely, CRISPR-mediated engineering of crop plants has enabled the introduction of toxin recognition and detoxification mechanisms, potentially offering a rapid route to developing resistant cultivars (O'Connell et al., 2012).

11.2 Metagenomics and Environmental Monitoring

High-throughput sequencing approaches have enabled the detection and monitoring of Colletotrichum species and their gene expression in environmental samples, including on plants showing disease symptoms (Udayanga et al., 2013). Metagenomics approaches may allow for real-time monitoring of secondary metabolite biosynthetic gene expression in field populations, providing early warning of toxin-producing strains that may be more virulent.

11.3 Systems Biology and Network Analysis

Integration of genomic, transcriptomic, proteomic, and metabolomic data through systems biology approaches is beginning to reveal the complex networks of gene regulation and metabolite production that underlie Colletotrichum virulence (Gan et al., 2013). These systems-level analyses may identify novel regulatory hubs and biosynthetic bottlenecks that could be exploited for disease management.

12. CONCLUSION

The production of secondary metabolites and toxins by Colletotrichum species represents a sophisticated virulence strategy that has evolved through long co-evolutionary processes with plant hosts. Colletotoxin, melanin, and numerous other secondary metabolites work in concert to facilitate infection, suppress plant immune responses, and enable the fungus to overcome host defenses and establish disease. The high degree of host specificity observed in

many Colletotrichum-cucurbit interactions reflects the intimate relationship between pathogen virulence factors and host resistance mechanisms.

Advances in genomic, transcriptomic, and metabolomic technologies have dramatically accelerated our understanding of the genetic basis of secondary metabolite production and the molecular mechanisms through which these compounds contribute to virulence. However, significant gaps in knowledge remain, particularly regarding the in planta function of many secondary metabolites and the mechanisms through which plants detect and respond to fungal toxins.

Future research should focus on elucidating the complete cascade of secondary metabolite production and regulation during the infection process, characterizing the molecular targets of individual toxins within plant cells, and identifying mechanisms of toxin resistance in tolerant hosts. Integration of this fundamental knowledge with practical breeding approaches and chemical ecology will enable the development of more effective and durable management strategies. By combining traditional plant breeding, modern molecular techniques, and integrated pest management principles, sustainable management of Colletotrichum-induced anthracnose in cucurbits is achievable, reducing losses and ensuring food security for producers and consumers worldwide.

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