

Integrated Disease Management Strategies for Bacterial Citrus Cankers: Insights, Prospects and Future Directions

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Abstract

Citrus canker, caused by *Xanthomonas citri* subsp. *citri* (Xcc), remains one of the most destructive bacterial diseases affecting citrus production worldwide, causing significant yield losses, reduced fruit quality, and increased management costs. Although copper-based bactericides remain the primary control measure, their long-term effectiveness is increasingly constrained by the emergence of copper-tolerant pathogen populations, environmental concerns, and regulatory restrictions. This review critically synthesizes current knowledge on the biology, epidemiology, and pathogenicity of Xcc and evaluates the effectiveness, limitations, and field applicability of conventional, biological, and molecular management strategies within an integrated disease management (IDM) framework. Evidence indicates that no single management approach provides durable disease suppression across diverse production systems. Conventional measures such as quarantine, sanitation, windbreaks, and chemical control remain important but are insufficient when implemented in isolation. Biological control agents, bacteriophages, plant-derived antimicrobials, and induced resistance strategies offer environmentally compatible alternatives, although their performance under field conditions remains variable. Advances in molecular breeding, genome editing, anti-virulence approaches, and precision disease surveillance provide promising opportunities for improving disease management but face technical, regulatory, and economic challenges. Major research gaps include limited long-term field validation of biological and molecular technologies, insufficient understanding of citrus microbiome-mediated disease suppression, and inadequate integration of economic and adoption considerations into management programs. Collectively, current evidence supports the adoption of multidisciplinary IDM strategies that integrate cultural, chemical, biological, and genomic approaches to achieve sustainable and resilient citrus canker management under changing agricultural and environmental conditions.

1. Introduction

Citrus species (family Rutaceae) are among the most economically important fruit crops worldwide, contributing substantially to global food security, nutrition, and agricultural trade [1–3]. Citrus fruits are valued for their high content of vitamins, minerals, dietary fiber, and bioactive compounds, which support both fresh consumption and processing industries [2, 3]. Beyond their nutritional significance, citrus production supports millions of livelihoods through cultivation, processing, transportation, and international trade. Consequently, factors that threaten citrus productivity have far-reaching economic and social implications.

Despite continued expansion of citrus cultivation, production remains constrained by numerous biotic stresses, among which bacterial diseases are particularly challenging because of their rapid dissemination, limited curative treatment options, and capacity to cause substantial economic losses [4, 5]. Among these diseases, citrus canker remains one of the most destructive and widely distributed bacterial diseases affecting commercial citrus production worldwide [4, 6].

Citrus canker is caused by *Xanthomonas citri* subsp. *citri* (Xcc), a Gram-negative phytopathogenic bacterium capable of infecting a wide range of citrus species and cultivars [6, 7]. The disease is characterized by raised necrotic lesions surrounded by chlorotic halos on leaves, stems, and fruits, resulting in reduced photosynthetic capacity, premature fruit drop, diminished fruit quality, and severe economic losses [6, 8]. Under favorable environmental conditions, epidemics can significantly reduce marketable yield and increase production costs through intensified management interventions [4, 9].

The epidemiology of citrus canker is strongly influenced by climatic factors, particularly high temperature, rainfall, humidity, and wind-driven precipitation, which facilitate bacterial dissemination and infection [10, 11]. Disease severity is further exacerbated by injuries caused by the citrus leaf miner (*Phyllocnistia citrella*), which creates entry points that increase host susceptibility and accelerate epidemic development [12–14]. Consequently, citrus canker remains a major phytosanitary concern in both endemic and non-endemic citrus-producing regions, where outbreaks can disrupt local production systems and international trade [5, 15].

Historically, citrus canker management has relied heavily on exclusion, eradication, copper-based bactericides, sanitation practices, and quarantine regulations [16–19]. While these measures have contributed to disease suppression in several production systems, their effectiveness is often constrained by biological, environmental, economic, and regulatory factors. In particular, extensive and repeated use of copper-based compounds has led to increasing concerns regarding environmental accumulation, non-target effects, and the emergence of copper-tolerant Xcc populations [20, 21].

Similarly, eradication programs involving large-scale removal of infected and exposed trees have achieved varying levels of success and often face substantial economic, logistical, and social challenges [32–34]. Although biological control agents, host resistance, and molecular breeding approaches have emerged as promising alternatives, their widespread adoption remains limited by inconsistent field performance, regulatory constraints, and insufficient validation under diverse production environments [20, 22]. These limitations highlight the need for more holistic and sustainable disease management strategies that integrate multiple complementary approaches rather than relying on individual control measures.

Integrated disease management (IDM) has emerged as a comprehensive strategy for managing complex plant diseases by combining cultural, biological, chemical, regulatory, and host resistance-based approaches within a coordinated framework. Unlike conventional single-tactic approaches, IDM seeks to reduce pathogen pressure while minimizing environmental impacts, delaying resistance development, and enhancing long-term system resilience [23].

Recent advances in molecular diagnostics, biological control, microbiome research, precision agriculture, and genome editing have expanded the range of tools available for citrus canker management [7, 22]. However, translating these advances into effective field-level solutions remains challenging. Many promising technologies demonstrate efficacy under controlled conditions but lack sufficient validation across different agroecological regions, production systems, and economic contexts. Furthermore, the integration of emerging technologies with conventional management practices has received comparatively limited attention, creating important knowledge gaps in the development of durable disease management programs.

Several reviews have examined the biology, epidemiology, and management of citrus canker [4, 15, 20]. However, most have focused on specific aspects of the disease, including pathogen biology, symptom development, or individual control measures. Rapid advances in biological control, molecular breeding, genome editing technologies, and precision agriculture now warrant a reassessment of citrus canker management within a broader integrated disease management framework.

This review provides a critical synthesis of current knowledge on *X. citri* subsp. *citri* and evaluates conventional, biological, and molecular approaches for disease management. Particular emphasis is placed on comparing the strengths, limitations, scalability, and practical applicability of available management strategies. In addition, the review identifies major research gaps, discusses emerging challenges such as copper resistance and climate variability, and highlights future opportunities for the development of sustainable, evidence-based, and integrated disease management programs for citrus canker.

2. Biology and Epidemiology of Citrus Canker

2.1 Taxonomy and Host Range of *Xanthomonas citri* subsp. *citri*

Citrus canker is caused primarily by *X. citri*, a Gram-negative, rod-shaped bacterium belonging to the family Lysobacteraceae [15, 24, 25]. Among the recognized forms of citrus canker pathogens, the Asiatic strain (Pathotype A) is the most widespread and economically important due to its broad host range and high virulence [24]. Other pathotypes, including A* and Aw, exhibit narrower host specificity and more restricted geographical distribution [15].

Host susceptibility varies considerably among citrus species and cultivars (Table 1). Grapefruit (*Citrus paradisi*), Mexican lime (*C. aurantiifolia*), and several sweet orange cultivars are generally highly susceptible, whereas certain mandarins and their hybrids exhibit varying levels of tolerance [15, 26]. However, complete and durable resistance remains rare within commercially important citrus germplasm. This limitation has important implications for disease management because it restricts the effectiveness of host resistance as a standalone control strategy and reinforces the need for integrated approaches.

Table 1
Host range of *X. citri*.

Pathotype/Variant	Hosts	Host Range Description	Distribution	References
Canker A (Asiatic)	Most Citrus spp., many cultivars and hybrids	Very broad	Worldwide	[9, 15]
Canker Aw/A	Mexican lime, alemow	Very narrow	South America	[24, 26]
Cancrosis B	Lemon, Mexican lime, sour orange, pummelo	Moderate	South America	[9]
Cancrosis C	Mexican lime, sour orange	Very narrow	Brazil	[24]

2.2 Symptomatology and Disease Development

The characteristic symptoms of citrus canker include raised corky lesions surrounded by water-soaked margins and chlorotic halos on leaves, stems, and fruits [8, 26]. Although symptom expression is useful for field diagnosis, symptom severity is influenced by host genotype, tissue age, environmental conditions, and pathogen population density [4].

Disease development begins when bacterial cells enter host tissues through natural openings such as stomata or through wounds created by mechanical damage, wind abrasion, or insect feeding [12–14]. Following entry, Xcc colonizes the intercellular spaces of susceptible tissues, where it multiplies and induces hyperplastic and hypertrophic cellular responses that give rise to the characteristic canker lesions [27]. Importantly, lesion formation is not merely a symptom of infection but also a critical epidemiological process, as lesions serve as reservoirs of inoculum that facilitate secondary disease spread. Consequently, symptom development directly contributes to pathogen survival, dissemination, and epidemic progression.

2.3 Disease Cycle and Survival Strategies

The disease cycle of citrus canker is driven by the continuous production, dissemination, and reinfection of bacterial inoculum (Fig. 1). Active lesions on infected leaves, twigs, and fruits constitute the primary sources of inoculum, releasing bacterial cells during periods of rainfall, irrigation splash, or high humidity [11, 15]. Disseminated cells are transported by wind-driven rain, contaminated equipment, infected nursery stock, and human activities, enabling both local and long-distance spread [15, 16].

A key factor underlying the persistence of Xcc is its ability to survive under diverse environmental conditions. The pathogen can persist in lesions for extended periods and maintain viable populations in infected plant debris and asymptomatic tissues [15]. Biofilm formation further enhances survival by protecting bacterial cells from environmental stress and antimicrobial exposure [28–30]. These survival mechanisms contribute to recurrent disease outbreaks and complicate eradication efforts, particularly in regions where favorable environmental conditions coincide with continuous citrus production.

From a management perspective, understanding pathogen survival is critical because many control failures arise from overlooking inoculum reservoirs that sustain reinfection cycles. Therefore, successful disease suppression requires interventions that target both pathogen dispersal and long-term survival.

2.4 Epidemiology and Drivers of Disease Spread

The epidemiology of citrus canker is strongly influenced by interactions among the pathogen, host, and environment. Warm temperatures, high relative humidity, and frequent rainfall create conditions conducive to bacterial multiplication, dispersal, and infection [9, 11]. Wind-driven rain is particularly important because it facilitates both bacterial dissemination and wound formation, thereby increasing infection opportunities [10, 15].

The citrus leaf miner (*Phyllocnistia citrella*) plays a significant epidemiological role by creating feeding galleries that expose internal leaf tissues and enhance bacterial entry [12–14]. Multiple studies have demonstrated that leaf miner infestations can substantially increase disease incidence and severity, highlighting the importance of integrating insect management into citrus

canker control programs [13, 14]. This interaction exemplifies the limitations of pathogen-focused management strategies and underscores the need for broader ecosystem-based approaches.

Human-mediated movement of infected propagative material remains one of the most significant pathways for long-distance pathogen dissemination [15]. Consequently, quarantine regulations and certification programs continue to play an essential role in preventing disease introduction into disease-free regions. However, increasing global trade, climate variability, and intensified agricultural production systems may create new opportunities for pathogen establishment and spread [20].

Collectively, these epidemiological factors indicate that citrus canker is not solely a pathogen management problem but a systems-level challenge requiring coordinated interventions that address inoculum sources, environmental drivers, host susceptibility, and anthropogenic pathways of dissemination.

3. Pathogenicity and Host–Pathogen Interactions

3.1 Type III Secretion System and Effector-Mediated Virulence

The Type III secretion system (T3SS) is the principal virulence machinery of Xcc and is indispensable for pathogenicity [25, 27]. This needle-like protein complex enables the direct delivery of effector proteins into host cells, where they manipulate cellular pathways to facilitate bacterial colonization and suppress plant immune responses [27]. Among these effectors, transcription activator-like effectors (TALEs), particularly PthA proteins, play a central role in symptom development and disease progression by reprogramming host gene expression and promoting cell hypertrophy and hyperplasia [24].

The importance of the T3SS (Fig. 2), extends beyond pathogen biology because it represents one of the most promising molecular targets for disease control. Unlike conventional bactericides, which aim to eliminate bacterial populations, strategies targeting T3SS activity may suppress virulence without imposing strong selective pressure for resistance development. However, despite substantial advances in understanding T3SS function, translation of this knowledge into commercially viable disease management tools remains limited. Consequently, the development of anti-virulence compounds targeting effector delivery and function represents an important research priority.

3.2 Biofilm Formation and Disease Persistence

Biofilm formation is a critical adaptive strategy that enhances bacterial survival, persistence, and colonization efficiency [28–30]. During biofilm development, Xcc cells become embedded within a self-produced extracellular matrix composed primarily of xanthan gum, proteins, and extracellular DNA. This matrix facilitates adhesion to host surfaces and provides protection against environmental stresses, antimicrobial compounds, and host defense responses [30].

From an epidemiological perspective, biofilms contribute significantly to pathogen persistence within orchards by increasing bacterial survival on leaf surfaces and within lesions. This persistence can undermine disease management efforts, particularly when control programs focus solely on reducing bacterial populations without disrupting established biofilms. Consequently, emerging approaches aimed at inhibiting biofilm formation or destabilizing mature biofilms may enhance the efficacy of existing chemical and biological control measures. However, relatively few studies have evaluated biofilm-targeting strategies under commercial orchard conditions, highlighting an important gap between laboratory findings and field application.

3.3 Quorum Sensing and Pathogen Communication

Successful infection by Xcc depends not only on individual bacterial cells but also on coordinated population-level behavior. This coordination is achieved through quorum sensing, a cell-density-dependent communication system that regulates the expression of genes associated with virulence, motility, biofilm formation, and environmental adaptation [28, 31]. Through the production and detection of diffusible signaling molecules, bacterial populations synchronize physiological activities that enhance infection success.

The role of quorum sensing in regulating multiple virulence-associated traits makes it an attractive target for disease management. Quorum quenching strategies, which disrupt bacterial communication without directly affecting cell viability, have attracted increasing interest because they may reduce disease pressure while minimizing the risk of resistance development. Nevertheless, the stability, specificity, and field performance of quorum-quenching compounds remain insufficiently understood. Further research is therefore required to determine their practical value within integrated disease management programs.

3.4 Host Defense Responses and Induced Resistance

Plants possess sophisticated defense systems that recognize invading pathogens and activate a range of local and systemic immune responses [22, 32]. Following pathogen recognition, citrus plants induce signaling pathways involving salicylic acid, jasmonic acid, and ethylene, which coordinate the expression of defense-related genes and antimicrobial compounds [22]. However, Xcc has evolved multiple mechanisms to suppress or evade these defenses, contributing to successful infection and disease establishment.

Because host immunity plays a central role in disease outcomes, considerable attention has been directed toward enhancing natural defense responses through induced resistance strategies. Such approaches are particularly attractive because they complement conventional disease management measures and may reduce dependence on chemical bactericides.

3.4.1 Systemic Acquired Resistance

Systemic acquired resistance (SAR) is a long-lasting defense response triggered following localized pathogen infection or treatment with specific resistance-inducing compounds [22, 33]. Activation of SAR is typically associated with salicylic acid signaling and the accumulation of pathogenesis-related proteins that enhance resistance against subsequent pathogen attack.

Several SAR-inducing compounds have shown potential for reducing citrus canker severity under experimental and field conditions [34]. Nevertheless, their effectiveness often varies depending on cultivar, environmental conditions, disease pressure, and application timing. Consequently, SAR inducers should be viewed as complementary components of IDM programs rather than standalone disease control solutions.

3.4.2 Induced Systemic Resistance

Induced systemic resistance (ISR) is commonly triggered by beneficial rhizosphere and endophytic microorganisms, including species of *Bacillus*, *Pseudomonas*, and *Trichoderma* [22, 23]. Unlike SAR, ISR is predominantly mediated through jasmonic acid- and ethylene-dependent signaling pathways and often enhances the plant's capacity to respond rapidly to pathogen invasion.

The integration of ISR-inducing microorganisms into citrus canker management offers a promising avenue for reducing disease severity while promoting plant health. However, the reliability of ISR under field conditions remains inconsistent because microbial establishment, environmental variability, and host genotype can strongly influence outcomes. Long-term multi-location studies are therefore needed to determine the durability and scalability of ISR-based management approaches.

4. Conventional Disease Management Strategies

4.1 Exclusion and Quarantine

Exclusion remains the most cost-effective strategy for preventing citrus canker establishment in disease-free regions [15, 16, 35]. Because long-distance dissemination primarily occurs through the movement of infected propagative materials, nursery stock, and contaminated equipment, quarantine regulations and certification programs play a critical role in limiting pathogen introduction [15, 18]. Countries that have implemented strict phytosanitary measures have generally achieved greater success in preventing disease incursions than those relying primarily on post-introduction management [15].

Despite their effectiveness, quarantine measures face increasing challenges associated with globalization, expanding international trade, and increased movement of plant materials [16, 20]. Moreover, asymptomatic infections and latent

pathogen populations may escape visual inspection, reducing the reliability of conventional surveillance approaches [19]. These limitations highlight the importance of integrating quarantine programs with sensitive diagnostic tools and continuous monitoring systems to improve early detection and rapid response capabilities.

4.2 Eradication and Tree Removal

Eradication programs involving the removal of infected trees have historically been employed to eliminate inoculum sources and prevent disease spread [16–18, 35]. The underlying principle is epidemiologically sound because active lesions serve as reservoirs of bacterial inoculum capable of sustaining local epidemics [10]. Early eradication efforts successfully delayed disease establishment in several regions and remain valuable under low disease incidence scenarios [35].

However, the effectiveness of eradication declines substantially once the pathogen becomes widely established. Large-scale tree removal programs often incur considerable economic costs, generate social resistance, and may fail to eliminate cryptic infections beyond the designated removal zones [16, 18]. Experiences from major citrus-producing regions have demonstrated that eradication alone rarely provides a sustainable long-term solution once endemicity has been reached [15, 16]. Consequently, eradication is most effective when implemented as part of broader containment and suppression strategies rather than as an isolated intervention.

4.3 Sanitation and Orchard Hygiene

Sanitation practices aim to reduce pathogen inoculum by removing infected plant materials and minimizing opportunities for pathogen dissemination [15, 20, 36]. Routine destruction of infected twigs, leaves, and fallen fruits can lower local inoculum pressure and reduce the likelihood of secondary infections [36, 37]. Similarly, disinfection of pruning tools, machinery, and harvesting equipment helps limit mechanical transmission of bacterial cells between orchards and production areas [20, 36].

Although sanitation is widely recommended, its effectiveness is strongly influenced by implementation consistency and disease prevalence. Under conditions of high disease pressure, sanitation alone is insufficient because environmental dissemination through wind-driven rain can rapidly reintroduce inoculum from surrounding sources [10, 15]. Nevertheless, sanitation remains an essential component of IDM because it directly targets inoculum reservoirs and complements both chemical and biological control measures.

4.4 Pruning and Canopy Management

Pruning contributes to disease suppression by removing infected tissues and modifying the orchard microclimate [36]. Improved air circulation and light penetration reduce leaf wetness duration, thereby creating less favorable conditions for bacterial survival and infection [15]. Removal of symptomatic branches can also reduce localized inoculum levels, particularly during the early stages of disease development [36].

However, pruning can unintentionally facilitate disease spread if conducted under wet conditions or without proper tool disinfection [37]. Furthermore, excessive pruning may induce vigorous flush growth that increases the availability of susceptible young tissues. Consequently, the timing and intensity of pruning are critical determinants of its effectiveness. When properly implemented, pruning serves as a valuable cultural practice that enhances the performance of other IDM components.

4.5 Windbreaks and Environmental Modification

Wind-driven rain is one of the most important drivers of citrus canker epidemics because it promotes both bacterial dispersal and host injury [11, 37]. Windbreaks reduce wind velocity and consequently limit the distance and intensity of bacterial dissemination [20, 38]. Numerous studies have reported lower disease incidence and severity in orchards protected by effective windbreak systems compared with unprotected plantings [38].

Beyond reducing pathogen spread, windbreaks may improve overall orchard resilience by moderating environmental extremes and reducing physical damage to plants [38]. However, their effectiveness depends on species selection, orientation, maintenance, and compatibility with orchard design. Although windbreaks alone cannot prevent disease outbreaks, they

represent one of the most practical and environmentally sustainable cultural practices available for long-term disease suppression.

4.6 Chemical Control

Chemical control remains the most widely adopted strategy for managing citrus canker, particularly in regions where disease pressure is high and susceptible cultivars dominate commercial production [20, 21]. Nevertheless, growing concerns regarding resistance development, environmental sustainability, and regulatory restrictions have prompted renewed evaluation of the long-term viability of chemical-dependent management programs [30, 38–40].

4.6.1 Copper-Based Bactericides

Copper compounds remain the cornerstone of citrus canker management due to their broad-spectrum antibacterial activity and relatively low cost [21, 39, 40]. Copper ions inhibit bacterial growth through disruption of membrane integrity, enzyme activity, and cellular metabolism [40, 41]. Numerous field studies have demonstrated that appropriately timed copper applications can significantly reduce disease incidence and severity, particularly when synchronized with periods of susceptible tissue development [15, 42].

Despite their effectiveness, copper-based programs face increasing challenges. Repeated applications have contributed to the emergence of copper-tolerant Xcc populations in several citrus-producing regions, potentially reducing long-term efficacy [40, 43]. In addition, copper accumulation in agricultural soils raises environmental concerns and may adversely affect beneficial microorganisms and ecosystem functions [40]. These limitations suggest that copper should be viewed as one component of IDM rather than the sole basis for disease management.

4.6.2 Antibiotics and Antibacterial Compounds

Antibiotics such as streptomycin and oxytetracycline have been evaluated for citrus canker suppression due to their ability to inhibit bacterial growth and multiplication [44, 45]. In some production systems, these compounds have demonstrated greater efficacy than copper treatments, particularly under severe disease pressure [44, 46].

However, the use of antibiotics in crop protection remains highly controversial. Concerns regarding antimicrobial resistance, environmental persistence, and potential impacts on non-target microbial communities have resulted in strict regulatory restrictions in many countries [44]. Consequently, the long-term sustainability of antibiotic-based management remains questionable. While antibiotics may provide short-term disease suppression under specific circumstances, reliance on these compounds is unlikely to represent a durable solution for citrus canker management.

4.6.3 Plant Defense Inducers

Plant defense activators represent an alternative strategy that enhances host immunity rather than directly targeting the pathogen [47–49]. Compounds capable of activating systemic acquired resistance (SAR) can reduce disease severity by priming defense pathways prior to infection [49, 50].

Although defense inducers are generally associated with lower environmental risks than conventional bactericides, their performance can be inconsistent across cultivars and environmental conditions [48, 51, 52]. Furthermore, they rarely provide complete disease suppression when applied alone. Their greatest value therefore lies in complementing other IDM components and reducing dependence on repeated bactericide applications.

4.6.4 Citrus Leaf Miner Management

Management of the citrus leaf miner (*Phyllocnistia citrella*) is an often-overlooked but critical component of citrus canker suppression [12–14]. Leaf miner feeding creates wounds that facilitate bacterial entry and substantially increase disease severity [13, 14]. Consequently, disease management programs that ignore leaf miner populations frequently achieve suboptimal outcomes despite intensive bactericide use.

Integrated management of leaf miner populations through biological control, selective insecticides, and cultural practices can significantly reduce infection opportunities and improve overall disease suppression [13, 20]. This interaction illustrates the importance of adopting ecosystem-based approaches that address multiple drivers of disease development rather than focusing exclusively on the pathogen itself. Certain processes, benefits, and constraints of antibacterial agents employed in the control of citrus canker are summarized in Table 2.

Table 2
Mechanisms, advantages, and limitations of antibacterial compounds used for citrus canker management.

Antibacterial compound	Mode of action	Target process	Advantages	Limitations	References
Copper hydroxide	Membrane disruption and enzyme inhibition	Cellular metabolism	Widely available and effective	Resistance development; environmental accumulation	[41, 42]
Copper oxychloride	Broad-spectrum antibacterial activity	Multiple cellular targets	Long-standing field efficacy	Environmental concerns	[34, 43]
Streptomycin	Inhibits protein synthesis	Ribosomal function	High antibacterial activity	Regulatory restrictions and resistance	[44, 53]
Oxytetracycline	Inhibits bacterial translation	Protein synthesis	Effective under specific conditions	Resistance concerns	[45, 54]
Plant-derived compounds	Membrane disruption and biofilm inhibition	Multiple targets	Biodegradable and eco-friendly	Variable stability and efficacy	[55–57]
Nanoparticle-based formulations	Oxidative stress induction and membrane damage	Cellular integrity	Improved delivery and efficacy	Limited commercialization	[41, 43]

5. Biological Disease Management

Growing concerns regarding copper resistance, environmental contamination, and regulatory restrictions on chemical bactericides have intensified interest in biological disease management as a sustainable component of IDM programs [20, 23, 39]. Biological control strategies aim to suppress Xcc through diverse mechanisms, including antibiosis, competition for ecological niches, induction of host resistance, biofilm disruption, and bacteriophage-mediated lysis [58, 59] (Fig. 3). Although numerous biological agents have demonstrated promising activity under laboratory and greenhouse conditions, their performance under commercial orchard conditions remains variable. Consequently, the value of biological control should be assessed not only in terms of efficacy but also consistency, scalability, environmental adaptability, and integration with other management practices.

5.1 Bacterial Biocontrol Agents

Bacterial antagonists represent the most extensively investigated biological control agents against citrus canker. Their effectiveness is attributed to multiple complementary mechanisms, including production of antimicrobial metabolites, nutrient competition, niche exclusion, quorum-sensing interference, and stimulation of host defense responses [39, 59]. Unlike chemical bactericides, beneficial bacteria may provide prolonged protection through sustained colonization of plant surfaces and tissues.

5.1.1 *Bacillus* Species

Species of *Bacillus* are among the most promising bacterial biocontrol agents due to their ability to produce a wide range of antimicrobial compounds, including lipopeptides, polyketides, and hydrolytic enzymes that inhibit pathogen growth and colonization [21, 59]. In addition to direct antagonism, *Bacillus* species can stimulate induced systemic resistance (ISR), thereby enhancing host defense capacity against bacterial invasion [21, 39].

Several studies have demonstrated significant reductions in citrus canker severity following application of *Bacillus subtilis*, *B. amyloliquefaciens*, and related species under greenhouse and field conditions [59]. However, efficacy often varies among locations and seasons because environmental factors influence bacterial establishment, persistence, and metabolite production. Consequently, formulation optimization and multi-location validation remain critical prerequisites for large-scale adoption.

5.1.2 *Pseudomonas* Species

Members of the genus *Pseudomonas* have received considerable attention because of their ability to produce siderophores, antibiotics, biosurfactants, and other secondary metabolites that suppress phytopathogenic bacteria [21, 38]. These bacteria also contribute to disease suppression through competition for nutrients and ecological niches on leaf surfaces and within the rhizosphere [21].

Among the studied species, *Pseudomonas fluorescens* has consistently demonstrated potential as a biological control agent owing to its strong rhizosphere competence, ISR-inducing capacity, and favorable biosafety profile [39, 59]. Experimental studies have shown that *P. fluorescens* can reduce disease incidence and enhance host defense responses against bacterial pathogens [38, 39]. In contrast, although *Pseudomonas aeruginosa* exhibits strong antagonistic activity against Xcc, its opportunistic pathogenicity to humans raises significant biosafety and regulatory concerns that limit its practical application in commercial agriculture [38]. Therefore, future research should prioritize environmentally safe and regulatory-compliant *Pseudomonas* strains with demonstrated field efficacy.

5.1.3 Other Bacterial Antagonists

Other bacterial genera, including *Burkholderia*, *Paenibacillus*, and *Streptomyces*, have demonstrated antibacterial activity against Xcc through production of bioactive metabolites and competitive exclusion mechanisms [39, 60]. Particularly, *Streptomyces* species are recognized for their capacity to synthesize diverse antimicrobial compounds with potential applications in plant disease management [59].

Despite encouraging experimental results, relatively few bacterial biocontrol agents have progressed to widespread commercial deployment. The gap between laboratory efficacy and field performance remains one of the major constraints limiting biological control adoption. Future studies should therefore focus on formulation technologies, environmental persistence, and compatibility with existing orchard management practices.

5.2 Fungal Biocontrol Agents

Compared with bacterial antagonists, fungal biocontrol agents have received less attention in citrus canker management despite their considerable potential for disease suppression [23, 61]. Beneficial fungi may inhibit pathogens through antibiosis, competition, production of volatile organic compounds (VOCs), induction of host resistance, and modulation of microbial community structure [62].

5.2.1 *Trichoderma* Species

Species of *Trichoderma* are among the most extensively studied fungal biocontrol agents in plant pathology because of their multifaceted mechanisms of action and broad-spectrum antagonistic activity [61, 62]. These fungi produce antimicrobial metabolites, compete effectively for nutrients and colonization sites, and stimulate plant defense responses through ISR-related pathways [63, 64].

Although direct evidence against citrus canker remains less extensive than for fungal diseases, the demonstrated ability of *Trichoderma* species to enhance plant health and suppress bacterial pathogens suggests significant potential for inclusion in citrus IDM programs [64, 65]. Additional field-based studies are needed to evaluate their long-term effectiveness against Xcc under diverse environmental conditions.

5.2.2 Endophytic and VOC-Producing Fungi

Endophytic fungi represent an emerging area of research in citrus disease management. These microorganisms colonize plant tissues without causing disease and may enhance host resistance through production of antimicrobial metabolites and modulation of plant immune responses [62]. Notably, species of *Muscodora* produce complex mixtures of volatile organic compounds capable of inhibiting a wide range of bacterial pathogens, including Xcc [61, 62].

The potential of VOC-producing fungi is particularly attractive because volatile compounds can suppress pathogens without requiring direct physical contact. However, challenges associated with formulation, delivery systems, and environmental stability currently limit large-scale implementation. Consequently, further research is needed to translate promising laboratory findings into commercially viable products.

5.2.3 Prospects and Limitations of Fungal Biocontrol

Although fungal biocontrol agents offer several ecological advantages, their field performance can be inconsistent due to environmental variability, microbial competition, and host-specific interactions [66, 67] (Table 3). Furthermore, most available studies have focused on controlled experimental conditions rather than commercial orchard systems. This discrepancy highlights the need for long-term field evaluations and a better understanding of microbial ecology to support reliable deployment of fungal antagonists within IDM frameworks.

Table 3
Comparative efficacy, mechanisms, and limitations of biological control agents against citrus canker.

Biological control agent	Representative species/strain	Primary mechanism(s)	Reported effect on Xcc	Major advantages	Limitations	References
Bacillus spp.	B. subtilis, B. amyloliquefaciens	Antibiosis, lipopeptide production, ISR induction	Reduced lesion development and bacterial populations	Stable formulations; multiple modes of action	Variable field performance	[21, 39]
Pseudomonas spp.	P. fluorescens, P. putida	Siderophore production, antibiosis, ISR	Reduced disease severity and pathogen colonization	Strong rhizosphere competence	Environmental dependence	[21, 38]
Trichoderma spp.	T. harzianum, T. viride	Antimicrobial metabolites, defense stimulation	Suppression of pathogen growth and enhanced host vigor	Dual disease control and growth promotion	Limited field validation against canker	[63–65]
Bacteriophages	Xcc-specific phages	Pathogen lysis	Significant reduction in bacterial populations	High specificity and environmental safety	UV sensitivity and poor persistence	[68, 69]
Endophytic bacteria	Various isolates	Competition, ISR, antimicrobial production	Reduced infection and symptom expression	Long-term plant association	Inconsistent colonization	[59, 60]
Microbial consortia	Mixed BCA formulations	Complementary mechanisms	Greater disease suppression than single strains	Improved robustness	Formulation complexity	[66, 67]

5.3 Bacteriophage-Based Disease Management

Bacteriophages offer a highly specific biological approach for controlling bacterial pathogens through direct infection and lysis of target bacterial cells [68]. Unlike broad-spectrum bactericides, phages selectively target pathogenic populations while minimizing impacts on beneficial microorganisms and environmental microbiota [70].

Several studies have reported significant reductions in Xcc populations and disease severity following bacteriophage applications under experimental conditions [71, 72]. Furthermore, phages can multiply at infection sites, providing a self-amplifying mode of action that distinguishes them from conventional bactericides [73].

Despite these advantages, practical implementation remains challenging. Environmental factors such as ultraviolet radiation, temperature fluctuations, rainfall, and low humidity can substantially reduce phage survival and efficacy in orchard environments [69]. In addition, the emergence of phage-resistant bacterial strains and regulatory uncertainties may complicate commercialization efforts. Consequently, bacteriophages should not currently be viewed as standalone replacements for conventional management practices but rather as complementary components of integrated disease management systems. Future research should focus on phage cocktails, protective formulations, and integration with other biological and chemical interventions to improve field reliability.

5.4 Plant-Derived Antimicrobials

Plant-derived compounds have emerged as attractive alternatives to conventional bactericides due to their biodegradability, lower environmental persistence, and diverse modes of action [55, 56]. Extracts, essential oils, and secondary metabolites obtained from medicinal and aromatic plants have demonstrated inhibitory activity against Xcc through disruption of bacterial membranes, inhibition of enzyme activity, interference with quorum sensing, and suppression of biofilm formation [57, 74].

Although numerous plant-derived products exhibit strong antibacterial activity under laboratory conditions, their practical application remains constrained by variability in chemical composition, environmental instability, and challenges associated with large-scale production [57, 75]. Furthermore, relatively few studies have evaluated these compounds under commercial orchard conditions. Therefore, while plant-derived antimicrobials represent promising additions to sustainable disease management programs, further validation is required before widespread adoption can be recommended.

Collectively, current evidence suggests that biological control is unlikely to completely replace conventional disease management practices in the near future. Nevertheless, when integrated with cultural, chemical, and host resistance-based approaches, biological agents can play a critical role in improving the resilience, sustainability, and long-term effectiveness of citrus canker management programs. The relative strengths, limitations, and practical applicability of the principal conventional and biological management approaches are summarized in Table 4.

Table 4 Advantages, limitations, and integrated disease management (IDM) relevance of major citrus canker management strategies.				
IDM component	Primary objective	Major advantages	Key limitations	Role in IDM
Quarantine and exclusion	Prevent pathogen introduction	Highly cost-effective	Difficult enforcement	Essential preventive strategy
Sanitation and pruning	Reduce inoculum reservoirs	Low-cost and environmentally friendly	Labor-intensive	Foundation of IDM
Windbreaks	Reduce pathogen dispersal	Long-term protection	Establishment costs	Supports epidemic suppression
Copper bactericides	Reduce bacterial populations	Proven effectiveness	Copper resistance and environmental concerns	Important but should be optimized
Plant defense inducers	Enhance host immunity	Reduced chemical dependency	Variable efficacy	Complementary strategy
Biological control agents	Suppress pathogen and stimulate defenses	Environmentally sustainable	Inconsistent field performance	Core component of sustainable IDM
Resistant cultivars	Reduce host susceptibility	Long-term protection	Limited availability	Strategic long-term solution
CRISPR-based resistance	Modify susceptibility genes	Precise and potentially durable resistance	Regulatory and adoption barriers	Emerging IDM component
Precision surveillance	Early detection and decision support	Improved intervention timing	Infrastructure requirements	Enhances management efficiency

6. Molecular and Genomic Approaches for Citrus Canker Management

6.1 Resistant and Tolerant Citrus Cultivars

Host resistance remains one of the most desirable disease management strategies because it provides season-long protection without repeated external inputs [58]. However, the development of commercially acceptable citrus cultivars with durable resistance to Xcc has proven challenging due to the narrow genetic base of many cultivated citrus species and the complex inheritance of resistance traits [58, 76].

Variation in susceptibility exists among citrus species and cultivars (Table 5). Grapefruit, Mexican lime, and several sweet orange cultivars are generally highly susceptible, whereas certain mandarins and their hybrids exhibit varying degrees of tolerance [77, 78]. Nevertheless, tolerance does not necessarily prevent pathogen colonization or inoculum production, limiting its effectiveness as a standalone disease management strategy.

Recent advances in genomics and marker-assisted breeding have accelerated the identification of resistance-associated loci and candidate genes involved in citrus defense responses [79]. Despite these advances, breeding efforts remain constrained by long juvenile phases, polyembryony, complex reproductive biology, and the need to maintain desirable horticultural traits [76, 80]. Consequently, while host resistance remains a cornerstone of sustainable disease management, conventional breeding alone is unlikely to provide rapid solutions for emerging disease challenges.

Table 5
Relative susceptibility of selected citrus species and cultivars to citrus canker.

Citrus species/cultivar	Relative response to citrus canker	Characteristics	Potential breeding value	References
Mexican lime (Citrus aurantiifolia)	Highly susceptible	Severe lesion development	Experimental host model	[15, 81]
Grapefruit (C. paradisi)	Highly susceptible	High disease incidence	Limited resistance value	[1, 3]
Sweet orange (C. sinensis)	Susceptible	Economically important but vulnerable	Target for resistance improvement	[5, 82]
Lemon (C. limon)	Susceptible	Frequent symptom expression	Moderate breeding value	[8, 23, 26]
Mandarin (C. reticulata)	Moderately resistant	Reduced symptom severity	Useful resistance source	[19, 24]
Mandarin hybrids	Moderately resistant to resistant	Variable resistance levels	Valuable breeding germplasm	[22, 33]
Genome-edited lines (CsLOB1-modified)	Enhanced resistance	Reduced susceptibility gene activation	High future potential	[20, 33, 77]

6.2 Genetic Engineering Approaches

Genetic engineering offers opportunities to overcome some limitations associated with conventional breeding by enabling targeted introduction or modification of resistance-associated genes [76, 77]. Several studies have demonstrated that transgenic expression of antimicrobial peptides, defense-related proteins, and pathogen-responsive genes can reduce citrus canker severity and enhance resistance against Xcc [58, 77].

The principal advantage of genetic engineering is its ability to introduce specific resistance traits without extensive alteration of elite cultivar characteristics. This is particularly important for citrus, where cultivar identity strongly influences market acceptance and economic value [76, 78].

However, the practical deployment of transgenic citrus remains constrained by regulatory approval processes, public perception concerns, and market restrictions in several countries [77, 83]. Furthermore, resistance based on single genes may be vulnerable to pathogen adaptation over time. Consequently, future efforts should focus on pyramiding multiple resistance mechanisms and integrating engineered resistance within broader IDM programs rather than relying exclusively on genetic modification.

6.3 CRISPR/Cas-Based Genome Editing

The emergence of CRISPR/Cas technology has transformed plant disease resistance research by enabling precise modification of host susceptibility genes and regulatory pathways [84, 85]. Unlike conventional transgenic approaches, genome editing can

generate targeted genetic changes without necessarily introducing foreign DNA, potentially improving regulatory acceptance in some jurisdictions [85].

One of the most promising targets for citrus canker management is the susceptibility gene *CsLOB1*, which is activated by transcription activator-like effectors (TALEs) delivered by the Xcc Type III secretion system [86–88]. Genome editing of *CsLOB1* promoter regions has been shown to reduce pathogen-induced gene activation and enhance resistance to citrus canker [86] (Fig. 4). These findings demonstrate how mechanistic understanding of host–pathogen interactions can be translated into practical disease management innovations.

Despite its promise, several challenges remain (Table 5). Efficient transformation and regeneration of citrus plants remain technically demanding, and edited plants require extensive evaluation for trait stability, agronomic performance, and unintended effects [86, 88, 89]. Moreover, regulatory policies governing genome-edited crops differ considerably among countries, creating uncertainty regarding commercialization pathways [85, 89]. Therefore, although CRISPR/Cas technology represents one of the most promising long-term solutions for citrus canker management, widespread deployment will depend on continued technological refinement and regulatory harmonization.

Table 5
Comparative assessment of CRISPR-based targets for improving citrus canker resistance.

Target gene/pathway	Biological function	Editing strategy	Expected outcome	Advantages	Challenges	References
CsLOB1 promoter	Susceptibility gene activation by TAL effectors	EBE disruption	Reduced pathogen recognition	Strong experimental validation	Regulatory approval	[86]
CsLOB1 coding region	Host susceptibility	Gene knockout	Reduced disease susceptibility	Durable resistance potential	Possible pleiotropic effects	[85, 86]
Defense-related genes	Host immunity regulation	Gene activation	Enhanced defense responses	Broad-spectrum protection	Complex regulation	[85, 87]
Negative regulators of defense	Suppression of immunity	Gene disruption	Increased resistance	Improved immune responsiveness	Potential fitness costs	[84, 87]
Multiplex editing targets	Multiple susceptibility loci	Simultaneous editing	Enhanced resistance durability	Reduced resistance breakdown	Technical complexity	[83, 86]

6.4 Molecular Targets for Anti-Virulence Strategies

Increasing knowledge of Xcc virulence mechanisms has created opportunities to develop disease management strategies that target pathogenicity rather than bacterial survival [83, 84]. Anti-virulence approaches are particularly attractive because they may impose lower selection pressure for resistance development compared with conventional bactericides [84].

Several molecular targets have been identified, including components of the Type III secretion system, quorum-sensing pathways, biofilm-associated regulatory networks, and extracellular polysaccharide biosynthesis pathways [86, 87]. Disruption of these systems can reduce bacterial fitness, impair host colonization, and suppress disease development without necessarily eliminating bacterial populations.

Although numerous candidate targets have been identified under laboratory conditions, relatively few have progressed to field evaluation or commercial development. This translational gap remains one of the major limitations of anti-virulence research. Future studies should therefore prioritize validation of molecular targets under realistic production conditions and assess their compatibility with existing IDM practices.

6.5 Advanced Diagnostics and Precision Disease Surveillance

Effective disease management depends on timely and accurate pathogen detection. Conventional diagnostic approaches based on symptom observation are often insufficient because latent infections and asymptomatic carriers can contribute to disease spread before visible symptoms develop [15, 19].

Recent advances in molecular diagnostics, including polymerase chain reaction (PCR), quantitative PCR (qPCR), loop-mediated isothermal amplification (LAMP), and next-generation sequencing technologies, have significantly improved detection sensitivity and specificity [19, 52, 90]. These technologies facilitate early pathogen detection, surveillance, and epidemiological monitoring, thereby supporting more targeted disease management interventions.

Precision agriculture tools are also emerging as valuable components of disease surveillance systems. Remote sensing technologies, unmanned aerial vehicles (UAVs), artificial intelligence (AI)-assisted image analysis, and geographic information systems (GIS) have demonstrated potential for rapid disease detection and spatial risk assessment in perennial cropping systems [83–85]. While many of these technologies remain at early stages of adoption in citrus production, they offer opportunities to improve disease forecasting, optimize intervention timing, and reduce unnecessary pesticide applications.

Nevertheless, implementation challenges remain, particularly in resource-limited production systems where access to advanced technologies and technical expertise may be constrained. Consequently, future research should focus on developing cost-effective and user-friendly surveillance platforms that can be readily integrated into routine disease management programs.

Molecular and genomic technologies are reshaping the future of citrus canker management by enabling targeted interventions that address host susceptibility, pathogen virulence, and disease detection [83, 87, 91]. Compared with conventional management practices, these approaches offer the potential for greater specificity, reduced environmental impacts, and more durable disease suppression.

However, their practical contribution to citrus canker management remains uneven. Resistant cultivars and molecular diagnostics are already contributing to disease management programs, whereas genome editing, anti-virulence technologies, and precision agriculture tools remain largely developmental [84, 85]. Furthermore, technical complexity, regulatory uncertainty, infrastructure requirements, and economic considerations may limit adoption, particularly among smallholder producers.

Current evidence suggests that molecular and genomic innovations are unlikely to replace conventional and biological disease management strategies in the foreseeable future. Rather, their greatest value lies in strengthening integrated disease management programs through improved host resistance, more precise disease detection, and targeted disruption of pathogen virulence mechanisms. Future progress will therefore depend on successful integration of these technologies with cultural, biological, and chemical interventions within comprehensive and adaptable IDM frameworks.

7. Challenges Research Gaps and Future Research Priorities

7.1 Challenges in Current Citrus Canker Management Programs

7.1.1 Emergence of Copper Resistance and Reduced Chemical Efficacy

Copper-based bactericides remain the cornerstone of citrus canker management worldwide; however, their long-term effectiveness is increasingly threatened by the emergence of copper-tolerant Xcc populations [40, 42, 43]. Repeated and intensive copper applications exert strong selection pressure on pathogen populations, facilitating the persistence and spread of resistant strains [34, 41]. In addition to resistance concerns, copper accumulation in agricultural soils may negatively affect beneficial microbial communities and ecosystem functions, raising questions regarding the environmental sustainability of copper-dependent management programs [38, 92].

These challenges suggest that future disease management strategies should prioritize reducing reliance on single-mode-of-action bactericides and promoting diversification of control measures within IDM frameworks.

7.1.2 Inconsistent Field Performance of Biological Control Agents

Biological control agents have emerged as promising alternatives to conventional bactericides; however, their performance under commercial orchard conditions remains highly variable [39, 60]. Environmental fluctuations, microbial competition, host genotype, formulation stability, and orchard management practices can all influence biological control efficacy [21, 38, 59].

A recurring limitation in the literature is the predominance of greenhouse and laboratory-based studies, which frequently overestimate field performance. Consequently, substantial uncertainty remains regarding the long-term reliability, persistence, and economic feasibility of many biological control products. Bridging the gap between experimental efficacy and commercial application remains one of the most important challenges facing biological disease management.

7.1.3 Limited Availability of Durable Host Resistance

Although host resistance is widely regarded as one of the most sustainable disease management strategies, commercially acceptable citrus cultivars possessing durable resistance to Xcc remain limited [58, 79]. The long generation time of citrus, complex reproductive biology, and the need to maintain desirable horticultural traits have slowed the development and deployment of resistant cultivars [76, 77].

Furthermore, resistance based on single genes may be vulnerable to pathogen adaptation, particularly under conditions of extensive selection pressure [76, 78]. Therefore, future breeding programs should prioritize quantitative and multi-gene resistance mechanisms that are more likely to provide durable protection across diverse environments.

7.1.4 Climate Change and Emerging Epidemiological Risks

Climate variability is increasingly recognized as a major factor influencing plant disease dynamics, including citrus canker epidemics [10, 11, 20]. Increased frequency of extreme weather events, changing rainfall patterns, and rising temperatures may alter pathogen survival, dispersal, and infection processes, potentially expanding the geographic range and severity of disease outbreaks [10, 15].

Despite growing recognition of these risks, relatively few studies have systematically evaluated the long-term impacts of climate change on citrus canker epidemiology. Consequently, predictive disease models capable of incorporating future climatic scenarios remain underdeveloped.

7.1.5 Regulatory and Adoption Constraints

The successful implementation of innovative disease management technologies depends not only on biological efficacy but also on regulatory approval, economic feasibility, and stakeholder acceptance [20, 33]. Technologies such as antibiotics, genetically modified crops, genome-edited cultivars, and bacteriophage-based products face varying regulatory requirements across countries, creating uncertainty regarding commercialization and adoption [22, 27].

In addition, many advanced disease management technologies require substantial financial investment and technical expertise, potentially limiting accessibility for smallholder growers. Consequently, future management solutions must be evaluated not only for biological effectiveness but also for their practical suitability within diverse production systems.

7.2 Major Research Gaps

Although considerable progress has been made in understanding citrus canker biology and management, several critical knowledge gaps continue to limit the development of durable disease control strategies.

7.2.1 Lack of Long-Term Multi-Location Validation Studies

Many disease management technologies are evaluated under controlled conditions or within limited geographic regions [15, 23, 24]. Consequently, knowledge regarding long-term efficacy across diverse environmental conditions remains inadequate.

Future studies should prioritize multi-year and multi-location trials to generate robust evidence supporting large-scale implementation.

7.2.2 Limited Understanding of Citrus Microbiome Contributions

Recent advances in microbial ecology have highlighted the importance of plant-associated microbiomes in disease suppression and plant health [19, 27]. However, the role of citrus-associated microbial communities in regulating Xcc populations and influencing disease outcomes remains poorly understood.

Improved understanding of microbiome-pathogen-host interactions may facilitate the development of microbiome-based disease management strategies capable of enhancing ecosystem resilience and reducing dependence on chemical interventions.

7.2.3 Insufficient Translation of Molecular Discoveries

Significant progress has been made in identifying virulence factors, susceptibility genes, quorum-sensing pathways, and host defense mechanisms [76, 80]. However, relatively few of these discoveries have been translated into practical disease management tools. This translational gap represents one of the most significant barriers to innovation in citrus canker management.

Future research should focus on converting mechanistic knowledge into deployable technologies, including anti-virulence compounds, biofilm-disrupting agents, and resistance-enhancing interventions.

7.2.4 Limited Economic and Adoption Studies

Most citrus canker research focuses primarily on biological efficacy, with comparatively little attention devoted to economic feasibility, cost-benefit analysis, and adoption barriers [20]. As a result, management recommendations often lack the socio-economic context necessary for widespread implementation.

Future studies should integrate economic analyses, stakeholder perspectives, and adoption assessments to improve the practical relevance of disease management recommendations.

7.3 Future Research Priorities

7.3.1 Development of Next-Generation Resistant Cultivars

Advances in genomics, molecular breeding, and genome editing provide unprecedented opportunities for developing citrus cultivars with enhanced resistance to Xcc [58, 77, 78]. Future efforts should focus on pyramiding multiple resistance mechanisms and improving resistance durability while maintaining commercially desirable horticultural characteristics.

7.3.2 Exploiting Pathogen Virulence Mechanisms as Control Targets

The increasing understanding of Xcc virulence systems provides opportunities for developing anti-virulence strategies that suppress disease without directly targeting bacterial survival [25, 27, 28]. Future research should prioritize the identification and validation of inhibitors targeting the Type III secretion system, quorum sensing, biofilm formation, and extracellular polysaccharide production.

Such approaches may offer more sustainable alternatives to conventional bactericides by reducing selective pressures associated with resistance development.

7.3.3 Microbiome-Informed Disease Management

The emerging field of microbiome engineering offers promising opportunities for enhancing disease suppression through manipulation of beneficial microbial communities [22, 23]. Future research should focus on identifying keystone microbial taxa, understanding community assembly processes, and developing synthetic microbial consortia capable of providing stable disease suppression under field conditions.

7.3.4 Precision Agriculture and Digital Disease Surveillance

Advances in remote sensing, artificial intelligence, machine learning, unmanned aerial vehicles, and geographic information systems are transforming plant disease monitoring and management [9, 20, 23]. Integration of these technologies into citrus production systems could improve early disease detection, optimize intervention timing, and enhance decision-making processes.

Future research should prioritize the development of cost-effective surveillance platforms that can be readily adopted across both commercial and smallholder production systems.

7.3.5 Climate-Resilient Disease Management Frameworks

Given the anticipated impacts of climate change on disease dynamics, future management strategies must be designed to remain effective under increasingly variable environmental conditions [10, 11, 20]. This will require integration of epidemiological forecasting, climate modeling, resistant cultivars, and adaptive management approaches capable of responding to evolving disease risks.

8. Conclusion

Citrus canker remains one of the most economically significant bacterial diseases affecting global citrus production, largely due to the widespread distribution of *Xanthomonas citri* subsp. *citri*, its capacity for rapid dissemination, and its ability to persist under diverse environmental conditions. Although considerable progress has been made in understanding pathogen biology, virulence mechanisms, and disease epidemiology, sustainable disease management continues to be challenged by the emergence of copper-tolerant pathogen populations, environmental concerns associated with intensive bactericide use, limited availability of resistant cultivars, and inconsistent performance of biological control agents under field conditions.

Evidence reviewed in this study demonstrates that no single management strategy provides durable and economically viable control of citrus canker across all production systems. Conventional approaches such as quarantine, sanitation, windbreaks, and copper-based bactericides remain important components of disease management programs; however, their effectiveness is constrained when implemented in isolation. Similarly, biological control agents, plant defense inducers, and bacteriophages offer environmentally compatible alternatives but require further optimization and validation to ensure consistent field performance. Molecular and genomic technologies, including marker-assisted breeding, genome editing, and advanced diagnostics, provide promising opportunities to enhance disease resistance and improve management precision, although their widespread adoption remains limited by technical, regulatory, and economic considerations.

Collectively, current evidence supports a transition from pathogen-centric control strategies toward IDM frameworks that simultaneously address pathogen survival, virulence, host susceptibility, and environmental drivers of infection. Future progress will depend on strengthening interdisciplinary research, improving the translation of molecular discoveries into field-applicable technologies, and developing management solutions that are biologically effective, economically feasible, and environmentally sustainable. Particular attention should be directed toward microbiome-informed disease management, anti-virulence approaches targeting key pathogenicity mechanisms, development of durable resistant cultivars, and integration of precision agriculture tools for disease surveillance and decision support.

Ultimately, the long-term sustainability of citrus canker management will depend not only on technological innovation but also on effective stakeholder engagement, regulatory support, and adaptive management strategies capable of responding to evolving disease pressures and changing environmental conditions. A holistic and evidence-based IDM approach therefore represents the most realistic pathway toward resilient citrus production and sustainable disease suppression in the decades ahead.

Declarations

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Figures

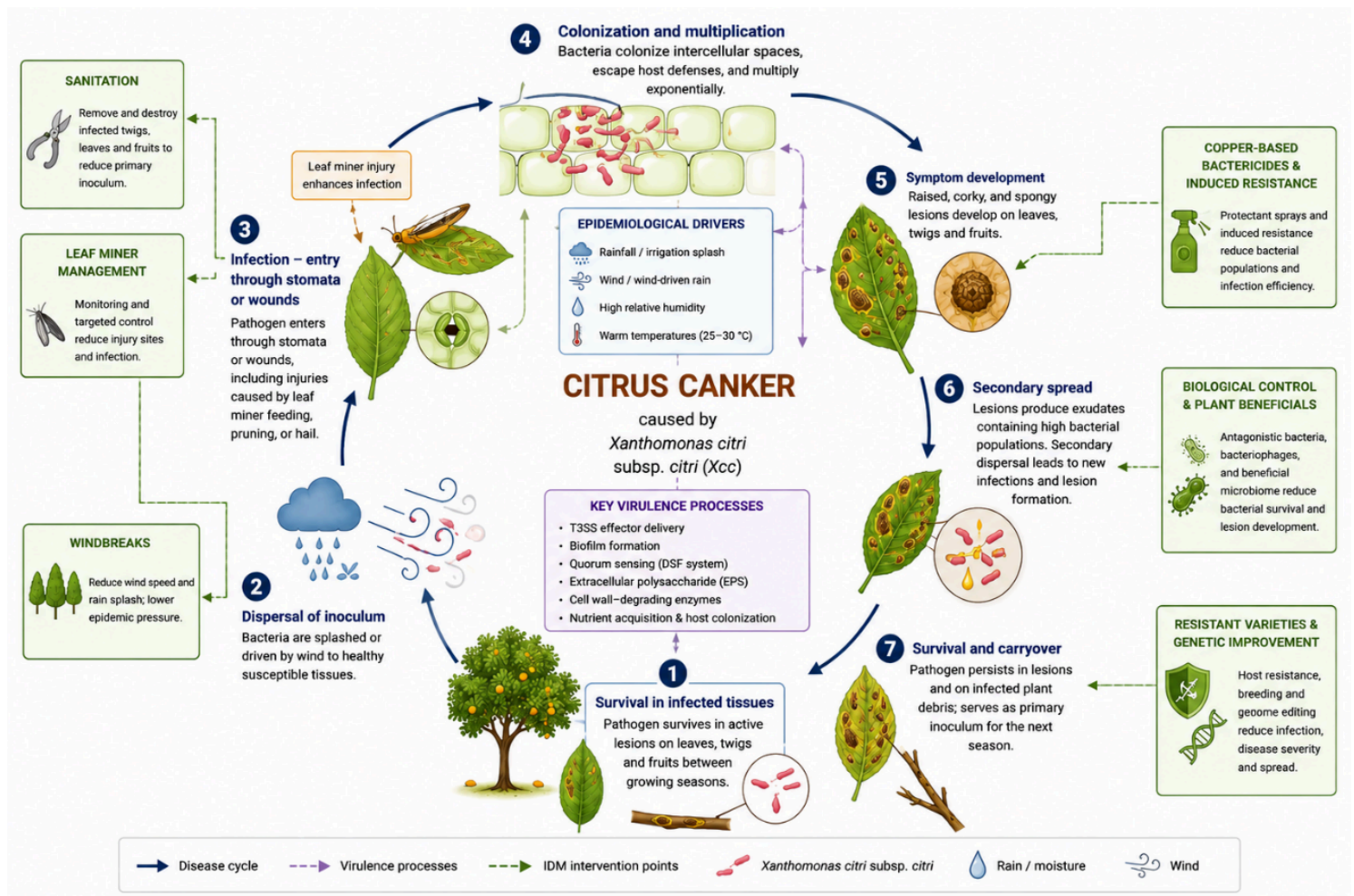


Figure 1

Disease cycle and integrated disease management (IDM) intervention points for citrus canker caused by Xcc. The pathogen survives in infected tissues and is dispersed by rain splash and wind to susceptible hosts, where infection occurs through stomata or wounds, including those caused by citrus leaf miner feeding. Following colonization and multiplication, characteristic canker lesions develop and serve as sources of secondary inoculum, driving disease spread and recurrence. Key IDM intervention points include sanitation, leaf miner management, windbreaks, bactericide applications, biological control, and host resistance strategies.

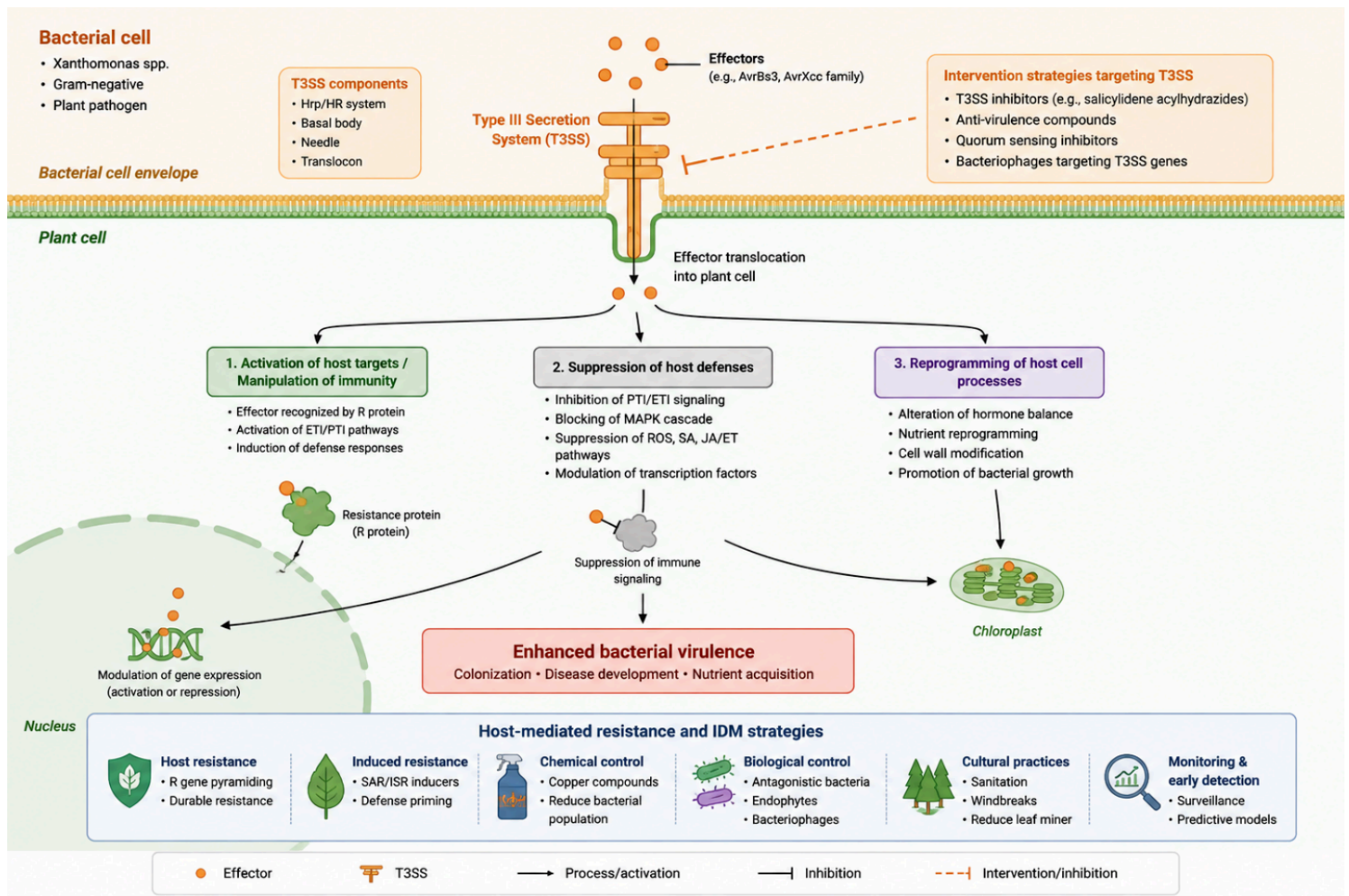


Figure 2

Effector delivery and host manipulation by the Type III secretion system (T3SS) of *X. citri*. T3SS-mediated translocation of effector proteins into host cells modulates gene expression, suppresses immune responses, and reprograms cellular processes to promote bacterial colonization and disease development. The figure also highlights key intervention points for integrated disease management, including host resistance, induced resistance, biological control, chemical suppression, and anti-virulence strategies targeting pathogen virulence mechanisms.

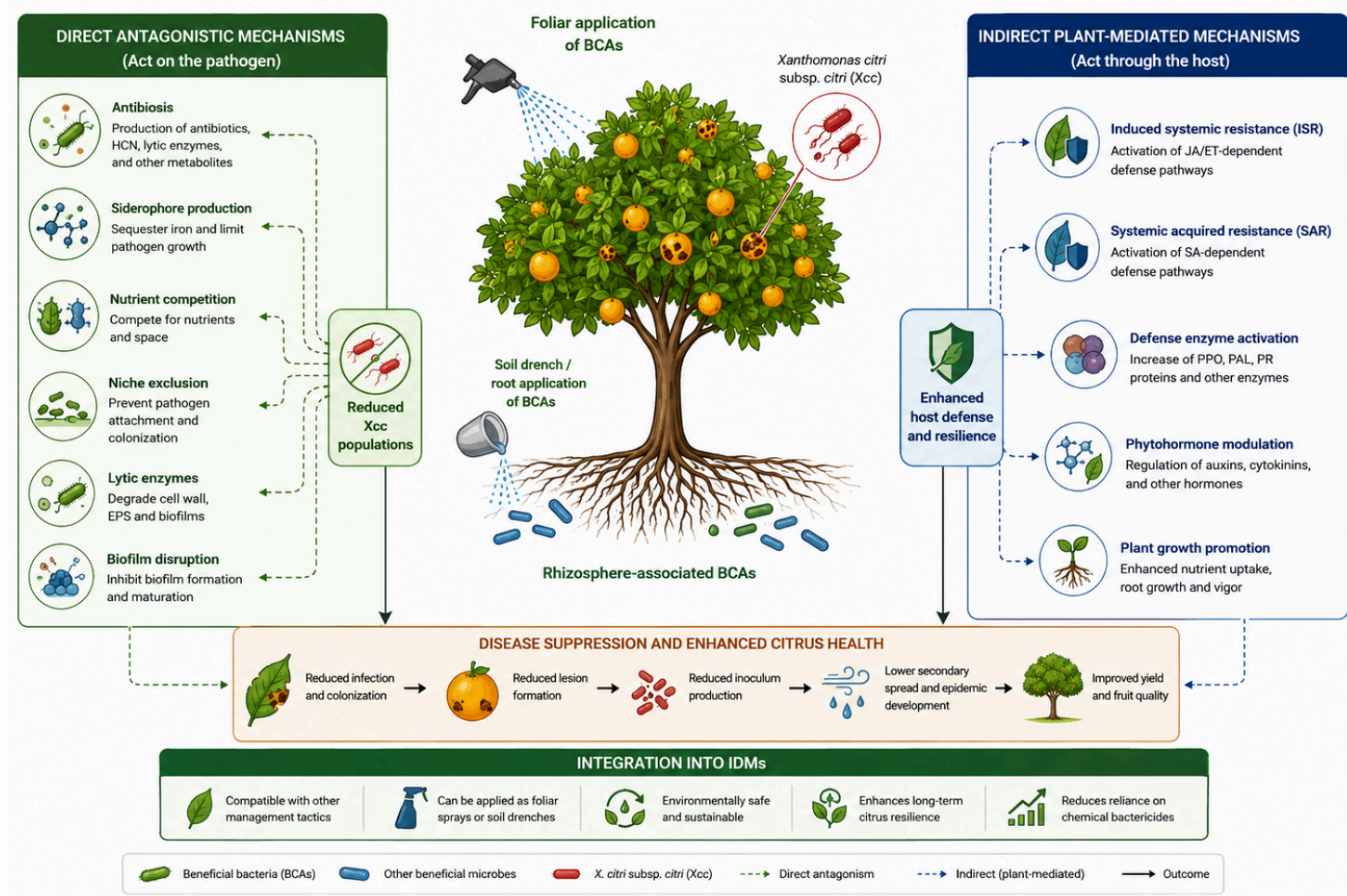


Figure 3

Direct and indirect mechanisms of biological control agents (BCAs) against *Xcc*. Phyllosphere- and rhizosphere-associated BCAs suppress pathogen establishment through direct antagonistic mechanisms, including antibiosis, nutrient competition, niche exclusion, lytic enzyme production, and biofilm disruption, while indirectly enhancing host resistance through induced systemic resistance, defense activation, phytohormone modulation, and plant growth promotion. Collectively, these mechanisms reduce pathogen populations, disease severity, and secondary spread, highlighting the role of BCAs as sustainable components of integrated disease management programs.

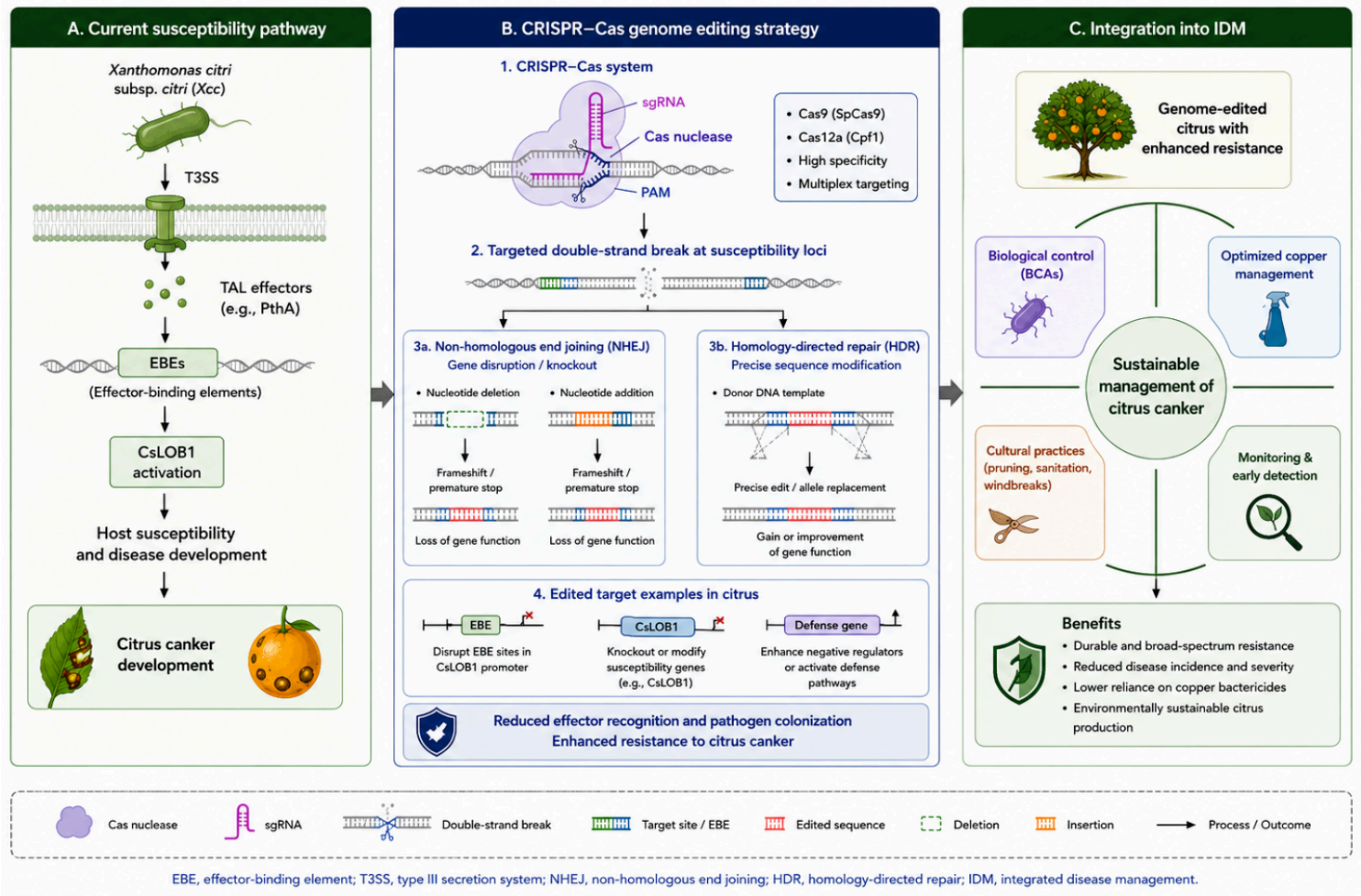


Figure 4

CRISPR–Cas-mediated genome editing strategies for enhancing resistance to Xcc. Genome editing targets susceptibility genes and effector-binding elements associated with pathogen recognition and disease development. Modification of key loci, such as *CsLOB1*, can reduce effector-mediated host susceptibility, limit pathogen colonization, and enhance disease resistance. Integration of genome-edited cultivars with biological, cultural, chemical, and surveillance-based approaches offers a promising strategy for sustainable citrus canker management.

Supplementary Files

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