



Red Rot Disease of Sugarcane: Current Status, Pathogen Biology, and Integrated Management Strategies

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Abstract: Red rot of sugarcane, caused by the hemibiotrophic fungal pathogen *Colletotrichum falcatum* Went, remains one of the most devastating diseases threatening global sugarcane production.



Characterized by severe yield losses, deterioration of juice quality, and frequent breakdown of host resistance, the disease has earned recognition as the “cancer of sugarcane.” Recent epidemics driven by highly virulent pathotypes such as CF13, along with emerging disease complexes involving *Thielaviopsis paradoxa*, have intensified economic losses, particularly in tropical and subtropical regions. This review critically synthesizes current knowledge on the epidemiology, pathogen biology, molecular determinants of virulence, and host–pathogen interactions underlying red rot disease. Emphasis is placed on advances in understanding genetic resistance, including quantitative trait loci (QTLs) such as qREDROT and key regulatory components like the 26S protease regulatory subunit. The review further evaluates integrated disease management (IDM) strategies encompassing resistant cultivars, sett sanitation, chemical and biological control, rapid phenotyping tools, molecular diagnostics, and genomics-assisted breeding approaches. Emerging technologies, including high-throughput phenotyping, LAMP-based diagnostics, genomic selection, and CRISPR-mediated genome editing, are highlighted as promising tools for achieving durable resistance. Collectively, this review underscores the necessity of a knowledge-driven, integrated, and technology-enabled approach to sustainably manage red rot and safeguard the long-term productivity and profitability of sugarcane cultivation.

Keywords: Sugarcane; Red rot; *Colletotrichum falcatum*; Pathotype variability; Integrated disease management; Host resistance; qREDROT; Molecular diagnostics; Genomics-assisted breeding

I. Introduction

Sugarcane (*Saccharum species hybrid*) is one of the most commercially vital crops cultivated worldwide, recognized as a critical tropical C4 plant belonging to the Poaceae family. It serves as a primary source for global white sugar and bioethanol production. However, the crop’s productivity is constantly threatened by numerous biotic stresses, among which fungal diseases are gaining severe international importance. (Chaudhary et al., 2022). Red rot, caused by the fungal pathogen *Colletotrichum falcatum* Went, stands out as one of the most important and destructive constraints to global sugarcane cultivation. The disease targets the economically important stalk tissues the sugar reservoir leading to profound losses in both yield and quality. This pervasive and often devastating nature has led to the disease being widely and accurately termed the "cancer" of sugarcane. In major growing regions, particularly India, red rot is considered the primary constraint on sugarcane production. (Arshad et al., 2022).

The historical impact of red rot has been catastrophic. The disease has the potential to inflict complete crop failure, with yield reductions reaching up to 100% in highly susceptible varieties. Across India, the estimated average loss in crop profitability due to fungal diseases alone is approximately 31%

(Shukla et al., 2022). This high potential for total loss creates an extremely challenging economic environment for producers, especially considering that typical input investments in sugarcane farming are often relatively low. Consequently, management strategies must be not only highly effective but also economically accessible and sustainable to mitigate the disproportionately high financial risk posed by this pathogen. (Geffersa et al., 2023).

Effective containment of red rot necessitates a sophisticated, multi-layered approach that integrates advanced molecular and conventional phytopathology knowledge. This review provides an expert-level analysis of the current status of red rot, detailing the intricate biology and molecular determinants of *C. falcatum* virulence, the genetics underlying host resistance, and a comprehensive overview of Integrated Disease Management (IDM) strategies. (Hossain et al., 2020). The goal is to synthesize current research into actionable knowledge for breeders, pathologists, and policy makers seeking to develop durable, sustainable management solutions (Rexroad et al., 2019)

2. Current Status, Epidemiology, and Economic Impact

2.1. Global Distribution and Recent Epidemic Outbreaks

C. falcatum is geographically widespread, affecting sugarcane fields throughout tropical and subtropical regions globally. The ability of the pathogen to rapidly generate new, aggressive pathotypes ensures its continued phytosanitary threat (Hossain et al., 2020).

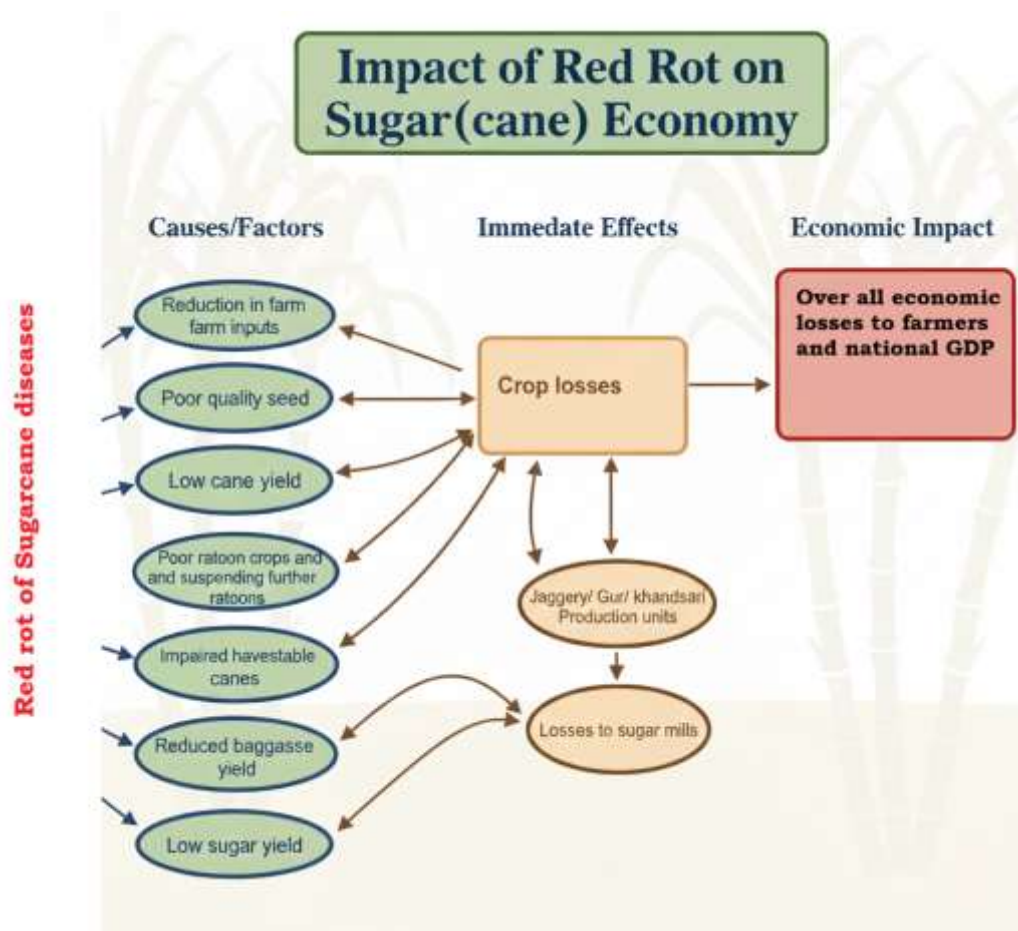
A significant example of this threat is the catastrophic epidemic witnessed in subtropical India. The previously popular cultivar Co 0238 succumbed to severe infection, leading to widespread failure and complete crop losses across thousands of hectares. (Singh et al., 2025). The pathotype CF13 was identified as the primary driver of this recent devastation. These outbreaks resulted in immense economic losses, estimated to range from 0.5 to 1.0 billion USD in different years from 2018 to the present. The pathotype Cf08 also remains a persistent and widespread threat in this zone, capable of harming newly developed cultivars. (Viswanathan et al., 2025)

2.2. Quantification of Yield and Quality Losses

The economic damage caused by red rot extends far beyond simple biomass reduction. Infection by *C. falcatum* severely impacts the industrial quality of the cane juice. Biochemical analysis of infected varieties reveals a harmful imbalance in key macronutrients: there is an observed accumulation of Nitrogen content, but critically, a substantial depletion in the concentration of Phosphorus and Potash. (Jeevanra et al., 2025).

Since Phosphorus and Potash are essential macronutrients required for healthy stalk development and play roles in subsequent industrial sugar extraction processes, their considerable reduction fundamentally degrades the overall industrial value of the harvested cane, even if some yield remains. Therefore, successful red rot management must be benchmarked not only by cane yield recovery but also by the successful restoration of the healthy nutrient profile required for optimal sugar processing (Githumbi et al., 2025).

Figure 1. Flowchart Illustrating the Causes, Immediate Effects, and Economic Impacts of Red Rot Disease on Sugarcane Production and National Economy



2.3. Emerging Disease Complexes: Red Rot and Associated Stalk Disorders

Modern agricultural policy shifts can unintentionally alter disease epidemiology. A notable instance is observed in northwestern São Paulo, Brazil, where the policy transition to "no-burning fully mechanical

harvest" over the past two decades has led to a significant increase in pathogen inocula surviving in crop residues left in the field (Silva et al., 2023).

Surveys in this region confirmed that red rot was widely detected in 88.2% of fields. However, the most economically devastating constraint observed was the stalk internal dry rot. This disorder is defined as a complex associated with the synergistic, simultaneous infection of *C. falcatum* and *Thielaviopsis paradoxa*, the causative agent of pineapple set rot. Total sugarcane yield losses attributable to these stalk disorders in the surveyed fields were estimated at 20.1%. (Baiswar et al., 2021).

The emergence of the highly destructive *C. falcatum* + *T. paradoxa* dry rot complex is directly linked to the accumulation of crop residues following the sustainable policy shift away from burning. (Kaliramana et al., 2019). This phenomenon illustrates that modern, environmentally sound agronomic practices can inadvertently create new ecological niches that favor complex disease interactions and elevated pathogen pressure. Future Integrated Disease Management (IDM) strategies in these regions must therefore be specifically tailored to target both *C. falcatum* and *T. paradoxa* concurrently, placing a strong emphasis on effective residue management and control of associated insect pests that may facilitate entry (Nikpay et al., 2023).

Table 2.1: Synthesis of Global Economic Impact and Key Pathotypes

Region	Key Pathotype(s)/Complex	Observed Impact/Losses	Economic/Quality Significance	Evidence Source
India (Subtropical)	CF13, Cf08	Complete crop loss; Financial losses 0.5–1.0 Billion USD	Rapid breakdown of resistance in major cultivars; Major industrial loss.	⁹
India (General)	Multiple	Estimated average crop loss of 31%	Depletion of P and K content in juice; reduced industrial quality.	³
Brazil (NW São Paulo)	<i>C. falcatum</i> + <i>T. paradoxa</i> (Dry Rot)	Total yield losses estimated at 20.1%	Emergent complex linked to no-burning policy; most important stalk disorder.	¹¹

3. Pathogen Biology: *Colletotrichum falcatum* and Molecular Virulence

3.1. Taxonomy, Morphology, and Unique Hemibiotrophic Lifestyle

The genus *Colletotrichum* encompasses numerous plant pathogens of major agricultural importance globally, particularly in tropical and subtropical systems. *C. falcatum* is classified as a hemi biotroph, a pathogen with a life cycle that transitions from an initial, inconspicuous biotrophic phase to a destructive necrotrophic phase. (Jeevanra et al., 2025). Genomic analysis reveals that *C. falcatum* possesses a draft genome size of approximately 48.16 Mb, encoding 12,270 genes, and shares close phylogenetic relatedness with other anthracnose pathogens, such as *C. graminicola* (maize) and *C. sublineola* (sorghum) (Lemu et al., 2021).

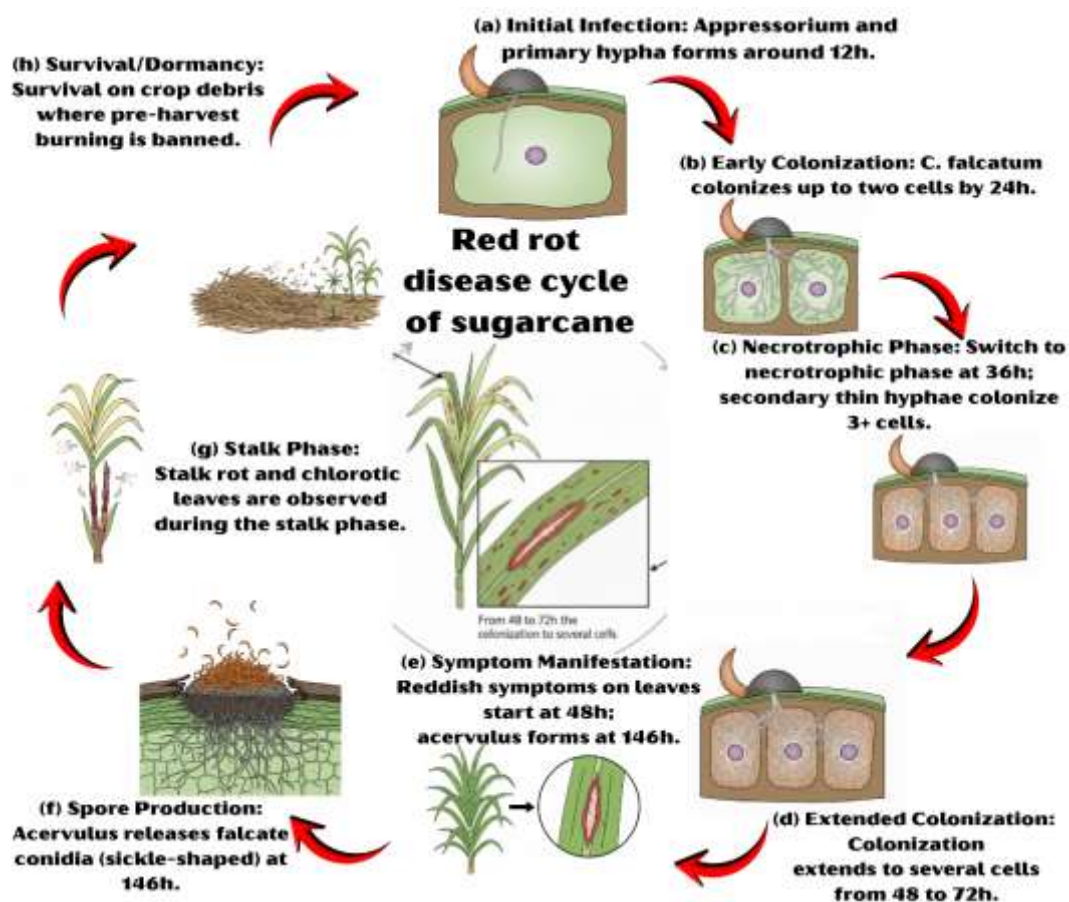
A distinguishing characteristic of *C. falcatum* is its highly specialized lifestyle tailored to infecting the robust stalk tissues of sugarcane. Comparative studies indicate a unique mechanism of penetration into the stalk parenchyma: unlike many other *Colletotrichum* species, *C. falcatum* does not form haustoria within the host cells and shows no apparent mechanical pressure during its initial penetration into the stalk tissue. (Nordzieke et al., 2019). This absence of mechanical pressure strongly suggests a reliance on a highly sophisticated, precise chemical and enzymatic infiltration mechanism. This refined process allows the fungus to navigate the dense cell walls of the stalk parenchyma, differentiating its stalk-infecting behavior from the often more aggressive, wound-dependent or mechanically aided entry seen in typical leaf-infecting anthracnose's. (Toyoda et al., 2016).

3.2. Disease Cycle, Inoculum Sources, and Transmission Pathways

The perennial and clonal nature of sugarcane cultivation facilitates the survival and spread of *C. falcatum*. The primary sources of initial inoculum (primary transmission) are diseased setts (infected planting material) and latent fungal structures persisting in the soil and on unhealthy stalk stubble fragments. These soil-borne structures include appressoria (formed under unfavorable conditions), dense-walled hyphae, chlamydospores, and setae, all of which play crucial roles in disease dispersal and survival. (Kumar et al., 2022).

The pathogen infects standing canes predominantly through natural entry points located in the nodal region, including the leaf scar, growth ring, root primordial, and buds. It enters the node via the inner epidermis of the lower leaf sheath. Secondary transmission, leading to rapid disease spread within a field, is facilitated by irrigation water, rainfall splashing, and field vectors, including insects that create wounds for entry. (Viswanathan et al., 2023).

Figure 3.1 Disease cycle of red rot of Sugarcane



3.3. Pathotype Variability, Evolution, and Adaptation to Host Cultivars

The long term management of red rot is complicated by the significant intra- and interspecific variation exhibited by *C. falcatum*. This variation is driven by genetic mechanisms, including nucleotide substitutions and deletions in key loci, allowing the pathogen to adapt quickly to host defenses. This continuous pathogen evolution explains why new pathotypes arise, leading to the resistance breakdown of commercial varieties, typically rendering them susceptible after only 8 to 10 years of commercial operation. (Fones et al., 2020).

Molecular characterization studies, utilizing tools like Random Amplification of Polymorphic DNA (RAPD) primers, have confirmed high levels of genetic polymorphism among isolates collected from different sugarcane-growing regions. The identification of new isolates, such as R0401 (collected from cv. CoS 8436), which are distinct from established reference pathotypes, definitively confirms the existence and continuous emergence of new aggressive races in the natural environment (Zhan et al., 2015).

3.4. Molecular Determinants of Virulence

The pathogenicity of *C. falcatum* is governed by numerous molecular determinants, including toxins, melanin, and specific enzymes, which regulate associated pathogenicity genes.

A crucial component of fungal virulence involves the deployment of Cell Wall Degrading Enzymes (CWDEs). Studies have demonstrated that the production of pectinolytic and cellulolytic enzymes varies significantly among pathotypes. Specifically, the production of exo-PG (extracellular polygalacturonase) shows a strong positive correlation with the overall virulence of the isolate, highlighting the importance of cell wall degradation as a critical, destructive step in pathogenesis. (Amin et al., 2020).

Genomic studies have identified specific pathogenicity-related genes possessed by *C. falcatum*, including *PKS1*, *HXT1*, and *Pel2*. Functional analysis using RNA interference (RNAi) has strongly implicated the *PKS1* gene in pathogenesis, suggesting a role in the synthesis of polyketide secondary metabolites, which may include toxins or melanin, essential for the infection process. The *Pel2* gene, an ortholog of pectate lyase identified in related *Colletotrichum* species, is observed to be specifically expressed during the necrotrophic phase of infection. (Jiang et al., 2023). The precise temporal correlation between the expression of these virulence genes (like *Pel2*) during the destructive necrotrophic phase and the high correlation between virulence and enzymatic activity (exo-PG production) suggests that management strategies focused on inhibiting these specific virulence effectors, such as CWDE inhibitors, during the transition from the biotrophic to the necrotrophic stage, may offer highly targeted and effective control (Liu et al., 2025).

4. Host-Pathogen Interactions and the Genetics of Resistance

4.1. Biochemical and Cellular Defense Responses in Sugarcane

Resistance in sugarcane is characterized by defined cellular and biochemical responses designed to restrict pathogen colonization. In resistant varieties, initial infection results in confined, dark lesions restricted to a few millimeters, thereby preventing the vertical spread of the fungus within the stalk parenchyma. Conversely, susceptible varieties permit extensive colonization of the nodal region and rapid vertical spread of the lesion, often characterized by limited reddish pigmentation (Scolyer et al., 2024).

A key biochemical marker distinguishing resistance is the defense mechanism leading to the release of anthocyanin pigments upon inoculation. In resistant tissues, methanolic extracts turn reddish due to this

pigment release, whereas extracts from susceptible tissues remain colorless. This reaction serves as a rapid, observable marker for the activation of primary host defenses. (Kaur et al., 2022).

4.2. Genetic Architecture of Resistance: QTL Mapping and Linkage Analysis

Developing resistance to red rot is fundamentally challenging due to the complex genome of sugarcane, characterized by high levels of polyploidy and heterozygosity. These factors make traditional breeding methods cumbersome. Genomic tools, specifically Quantitative Trait Locus (QTL) mapping, have been employed to dissect the genetic architecture of resistance. (Zhang et al., 2024).

A genetic linkage map developed using a selfed population of the popular variety CoS 96268 successfully identified a major QTL linked to red rot resistance, denoted as *qREDROT*. This locus is significant because it explains 26% of the total phenotypic variation observed for the red rot resistance trait. The *qREDROT* region is genetically defined by its flanking Simple Sequence Repeat (SSR) markers, IISR_139a and NKS_32 (Banerjee et al., 2023).

4.3. Identification and Functional Validation of Key Resistance Genes

The genomic region spanning the *qREDROT* locus, approximately 7.6 Mb in size, contains approximately 40 genes implicated in plant defense-related responses. Differential expression analysis and functional validation within this region have identified several critical defense components, including *histone deacetylase 2*, *peroxidase*, *cytochrome P450*, *ABC trans porter*, *putative disease resistance protein RGAI*, *defensin-like protein*, and *MAP kinase 4*. (Hoyos et al., 2022).

However, the most compelling finding involves the plant defense-related gene coding for the 26S protease regulatory subunit. Expression analysis revealed a strong and consistent association between this gene and red rot resistance. Functional validation of this candidate gene demonstrated its practical utility: a specific primer for the 26S protease regulatory subunit was shown to amplify a diagnostic 500 bp product that was found exclusively in red rot-resistant sugarcane varieties. (Fones et al., 2020).

The strong correlation between resistance and a regulatory gene, the 26S Protease Regulatory Subunit, suggests that efficient resistance mechanisms in sugarcane may rely heavily on fine-tuned regulatory processes, specifically those governing targeted protein degradation and recycling essential for rapid signal transduction, rather than sole dependence on simple effector (R) gene recognition. This structural regulatory component offers a robust target for genetic improvement and serves as a highly reliable molecular marker for Marker-Assisted Selection (MAS). (Dinesh Babu et al., 2022).

Table 4.1: Key Molecular Insights into Red Rot Resistance (Based on *qREDROT*)

Mechanism/Gene/Locus	Functional Role/Significance in Resistance	Implication for Breeding	Evidence Source
<i>qREDROT</i> QTL	Explains 26% of phenotypic variation; flanked by IISR_139a and NKS_32.	Primary target for quantitative resistance stacking and MAS.	²
26S Protease Regulatory Subunit	Strongly associated with resistance; key regulatory component in defense signaling.	Reliable, exclusive molecular marker for Marker-Assisted Selection.	²
Putative RGA1, Rp3, MAP kinase 4	Located within the 7.6 Mb <i>qREDROT</i> region.	Candidate genes for pathogen recognition and complex signal network activation.	²
Anthocyanin Pigments	Release correlates with localized lesion formation in resistant cane.	Rapid, visual biochemical marker for early resistance screening.	¹⁴

5. Integrated Disease Management (IDM) Strategies for Red Rot Control

Integrated Disease Management (IDM) represents the most cost-effective and feasible strategic framework for controlling red rot. Studies confirm that IDM practices not only lead to significant reductions in red rot incidence but also concurrently enhance overall growth parameters and improve the quality attributes of both plant and ratoon crops, surpassing the efficacy of non-integrated methods. (NamdeoAiwale et al., 2025).

5.1. Cultural and Agronomic Practices for Inoculum Reduction

The cornerstone of red rot IDM is the deployment of host resistance. The use of recommended resistant and moderately resistant varieties, such as Co 86032, Co 86249, CoSi 95071, and CoC 22, is the most economical, easy, and eco-friendly control measure. However, since pathogen evolution renders resistance varieties susceptible after 8–10 years, resistance breeding remains an unavoidable and continuous priority. (Viswanathan, R., 2021).

5.2. Physical Control Methods

Physical treatments offer eco-friendly and economically advantageous means of eliminating sett-borne pathogens. Recommended protocols include hot water treatment (HWT) at 50°C for 150–180 minutes, or alternatively, aerated stream treatment at 52°C. Although time-consuming, these interventions offer almost complete elimination of setts-borne infection (Noseworthy et al., 2023).

5.3. Chemical Control and Setts Treatment Protocols

While genetic and cultural measures are preferred for long-term sustainability, the application of chemical fungicides remains the only viable option when the disease appears suddenly in an epidemic form (Haq et al., 2020)

Standard chemical management involves dipping the cut ends and entire setts in a fungicide solution before planting. Recommended fungitoxic chemicals include Carbendazim 50 WP (0.5 gm/liter) or related systemic compounds such as Benomyl, Bavistan, or Aretan, often combined with Urea to improve uptake (Sowmya et al., 2025).

A particularly effective modern chemical approach involves the use of combined seed treatments. In high-risk environments, applying a combination of the systemic fungicides azoxystrobin and propiconazole along with the systemic insecticide thiamethoxam to billets has been demonstrated to significantly reduce disease severity, improve germination, and prevent the severe reduction in stand establishment seen in untreated billets. (Ons et al., 2020). The demonstrated success of the fungicide-insecticide combination highlights a critical aspect of red rot epidemiology the systemic insecticide component effectively manages insect vectors, thereby blocking the physical, wound-based entry points that *C. falcatum* readily exploits. This confirms that chemical control must be integrated with pest management to achieve optimal disease suppression, validating the holistic framework of IDM (NamdeoAiwale et al., 2025).

5.4. Biological Control Approaches

Biological control provides a low-input, highly valuable component of IDM, particularly suitable for cost-conscious farmers. Antagonistic Fungi *Trichoderma* species are recognized as highly effective bioagents against *C. falcatum*. In dual culture assays, *Trichoderma harzianum* demonstrated superior efficacy, achieving the highest mycelial growth inhibition against the pathogen (84.4%), although other species like *T. koningii* were also effective (76.2%). The use of *T. harzianum* offers a dual benefit: direct

antagonism against *C. falcatum* and the induction of systemic resistance in plants grown from treated setts. (Shalaby et al., 2022)

Biocontrol Bacteria Screening the sugarcane rhizosphere has identified promising bacterial strains exhibiting both antifungal potential and Plant-Growth-Promoting (PGP) activity. Specific isolates, including *Ochrobactrum intermedium*, *Acinetobacter sp*, and notably, *Escherichia sp* (VRE34), demonstrated high efficacy in suppressing the disease and simultaneously improving plant growth parameters, such as stem diameter and height (Ansabayeva et al., 2025).

Botanical Extracts Plant extracts and essential oils also offer potential control agents. Extracts derived from common botanicals like garlic, onion, and ginger have been reported to inhibit the mycelial development of *C. falcatum* (Poudel et al., 2022).

6. Advanced Tools and Future Perspectives in Red Rot Management

6.1. Modern Screening and Phenotyping Methods

Traditional methods for red rot resistance screening are time-consuming, labor-intensive, and susceptible to environmental variation, often requiring 12 months for final assessment using the standard 0–9 disease severity scale. The slow pace of phenotyping has historically represented a major bottleneck for accelerating sugarcane breeding programs. (Dinesh Babu et al., 2022).

A significant methodological advancement is the development and validation of the innovative two-eye-setts method. This rapid approach involves inoculating two-eye-sets and incubating them under controlled conditions. This method produces excellent symptoms and reduces the required screening time drastically, from over a year to approximately 3 weeks. Furthermore, integrating this method with machine-learning algorithms (such as Classification and Regression Tree analysis) to objectively measure the percentage of symptomatic pixels (image cover) has shown strong correlation ($r=0.88-0.99$) with historical field ratings. (Zhan et al., 2015).

The successful validation of the rapid two-eye-setts method coupled with image analysis provides the necessary High-Throughput Phenotyping (HTP) capability essential for modern genomics-assisted breeding. By overcoming the traditional phenotyping bottleneck, this breakthrough accelerates all subsequent genomic efforts, including the validation of MAS markers and the generation of large-scale phenotypic data required for Genomic Selection (GS) models. (Hoyos et al., 2022).

6.2. Genomics-Assisted Breeding

Genomics tools are essential for overcoming the complexity of the sugarcane genome and accelerating the development of superior, resistant cultivars. Marker-Assisted Selection (MAS) the identification and functional validation of specific markers, such as the sequence exclusive to resistant varieties near the 26S protease regulatory subunit, provide reliable tools for MAS. These markers, alongside identified Single Nucleotide Polymorphism (SNP) sites associated with red rot resistance, offer practical pathways for making the crop improvement process more precise and efficient. (Viswanathan, R., 2021).

Genomic Selection (GS) For traits controlled by multiple complex QTLs, Genomic Selection offers a potent tool for rapid selection and accelerating the breeding cycle. To fully realize the potential of GS in sugarcane, prediction models must integrate the aforementioned HTP capabilities with High-Throughput Genotyping (HTG), machine learning, and speed breeding techniques. (Zhang et al., 2024).

6.3. Molecular Diagnostics for Phytosanitation

Controlling the primary inoculum source infected setts is paramount for IDM success. Molecular diagnostics provide the high specificity and sensitivity required for rigorous phytosanitary certification. (Jiang et al., 2023).

The Loop-mediated isothermal amplification (LAMP) **assay** has been successfully developed for the specific and rapid detection of *C. falcatum* DNA. The LAMP method is highly efficient, amplifying DNA under isothermal conditions. It exhibits a sensitivity up to ten times greater than conventional PCR when testing pure fungal culture DNA. Crucially, the assay provides a visual color change indication in less than one hour and requires minimal post-amplification processing. (Chaudhary et al., 2022). This convenience, speed, and high sensitivity make LAMP an economical and powerful tool suitable for robust, on-farm diagnostics and rigorous certification of planting material. The availability of such high-sensitivity, low-cost molecular diagnostics effectively closes the loop on IDM by ensuring strict control over the primary inoculum source, thereby safeguarding the investment in cultural practices and genetic resistance from inadvertent failure due to infected setts. (Kumar et al., 2022).

6.4. Future Directions: Gene Editing and CRISPR-based Resistance Development

Given the rapid adaptive capacity of *C. falcatum*, which typically breaks host resistance within 8 to 10 years, conventional breeding methods may not be capable of introducing new, durable resistance genes quickly enough. Therefore, future research is centered on utilizing advanced precision biotechnology. (Arshad et al., 2022).

Recent studies have successfully demonstrated efficient and reproducible gene targeting (GT) in sugarcane, allowing for the precise co-editing of multiple alleles via template mediated and homology-directed repair (HDR) mechanisms. (Githumbi et al., 2025). Focusing on transgene-free genome editing holds significant promise for introducing or optimizing resistance genes, such as the 26S protease regulatory subunit, at a speed capable of challenging the pathogen's evolutionary timeline. This advanced capability is essential for establishing truly durable resistance in the face of continuous pathotype emergence. (Shukla et al., 2022).

7. Conclusion

Red rot, caused by the dynamic fungal pathogen *Colletotrichum falcatum*, remains an existential threat to global sugarcane production, exemplified by recurrent billion-dollar epidemics driven by aggressive pathotypes like CF13 and complicated by emerging synergistic disease complexes such as the *C. falcatum* + *T. paradoxa* Dry Rot in certain agricultural systems. (Silva et al., 2023).

Effective, sustainable management demands a comprehensive shift toward knowledge-intensive Integrated Disease Management (IDM). (NamdeoAiwale et al., 2025).

Cultural and Chemical Synergy: Strict sett sanitation, rigorous field hygiene, and the targeted application of fungicide-insecticide combinations to address both the pathogen and the insect vectors that facilitate its entry. (Viswanathan, R., 2021).

Genomic Precision: The accelerated development of resistant varieties achieved through Genomic Selection and Marker-Assisted Selection (MAS), capitalizing on key regulatory components of resistance, particularly the 26S protease regulatory subunit. (Viswanathan, R., 2021).

Technological Innovation: The adoption of High-Throughput Phenotyping (HTP) via rapid methods like the two-eye-setts assay, and the widespread deployment of field-ready molecular diagnostics (LAMP) to ensure zero tolerance for infected planting material, thereby controlling the primary epidemic source. (Shukla et al., 2022).

By leveraging these advanced tools and integrating them with established cultural practices, the agricultural industry can develop durable, proactive resistance mechanisms essential to ensuring the long-term viability and profitability of sugarcane cultivation against this enduring phytosanitary crisis. (Githumbi et al., 2025).

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