



Available Online at EScience Press

Plant Protection

ISSN: 2617-1287 (Online), 2617-1279 (Print)
http://esciencepress.net/journals/PP

Research Article

Environmentally Safe *In Vitro* Biocontrol Strategies for the Sustainable Management of *Curvularia lunata* Leaf Spot of Rice: Current Advances and Future Perspectives

^aNaematullah Shah, ^aGhulam Hussain Jatoi, ^aManzoor Ali Abro, ^bSadia Khalil, ^cSamina Awan, ^dLaith Khalil Tawfeeq Al-Ani, ^eUmed Ali

^a Department of Plant Pathology, Faculty of crop Protection, Sindh Agriculture University, Tando Jam, Pakistan.

^b Department of Microbiology, Federal Urdu University of Arts, Science and Technology, Karachi, Pakistan.

^c District Shaheed Benazir Abad, School Education and Literacy Department, Government of Sindh, Pakistan.

^d School of Biology Science, Universiti Sains Malaysia, 11800 Minden, Pulau Pinang, Malaysia.

^e Department of Agriculture, Mir Chakar Khan Rind University, Sibi, Balochistan, Pakistan.

ARTICLE INFO

Article history

Received: 9th March, 2026

Revised: 26th June, 2026

Accepted: 27th June, 2026

Keywords

Curvularia lunata

Rice leaf spot

Biological control

Sustainable disease

management

Eco-friendly plant

protection

ABSTRACT

Rice (*Oryza sativa* L.), a cornerstone of global food security and trade, is increasingly threatened by the emerging fungal pathogen *Curvularia lunata*, which causes brown leaf spot, grain discoloration, kernel rot, and substantial yield and grain quality losses. This review synthesizes current knowledge on the biology, epidemiology, pathogenicity, diagnosis, and integrated management of *C. lunata*, with particular emphasis on its increasing importance under changing climatic conditions. The pathogen survives in infected seed, crop residues, and alternate grass hosts, while warm temperatures, prolonged leaf wetness, and high relative humidity favor rapid disease development and repeated secondary infection cycles. Advances in molecular diagnostics, including internal transcribed spacer (ITS) sequencing, multilocus sequence typing, and loop-mediated isothermal amplification (LAMP), have substantially improved the rapid and accurate identification of *C. lunata*. The review further highlights the extensive pathogenic and genetic variability of the pathogen, which complicates disease surveillance and resistance breeding. Sustainable management requires an integrated disease management approach combining certified disease-free seed, field sanitation, residue and weed management, balanced nutrient and silicon application, optimized planting practices, biological control using *Trichoderma* spp., *Bacillus* spp., *Pseudomonas fluorescens*, and antagonistic yeasts, botanical extracts, and the judicious use of fungicides through seed treatment and timely foliar applications. Climate change is expected to further expand the geographical distribution and epidemic potential of *C. lunata*, emphasizing the need for climate-resilient disease management strategies. Future research should prioritize pathogen population genomics, host resistance, rapid diagnostics, biological control optimization, and precision disease forecasting to safeguard rice productivity, grain quality, and global food security.

Corresponding Author: Ghulam Hussain Jatoi

Email: Jatoiighulamhussain@hotmail.com

Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops globally and serves as the primary staple food for more than half of the world's population (USDA, 2024). Belonging to the family Poaceae, rice is predominantly cultivated in tropical and subtropical regions due to its high water requirement and preference for warm climatic conditions (Figure 1). Beyond its role as a major source of dietary energy, rice production contributes significantly to global food security, rural livelihoods, and economic stability, particularly in Asia, which accounts for approximately 90% of global rice production and consumption (Ali, 2020; FAO, 2024). In addition to human consumption, rice generates valuable by-products, including rice bran, husk, and straw, which have applications in bioenergy production, livestock feed, and sustainable agricultural systems (Pandey et al., 2019).

Importance of rice in Pakistan

Pakistan has a predominantly agrarian economy, where crop production is influenced by monsoon rainfall patterns, temperature variability, and seasonal climatic conditions. Rice is an important Kharif crop, mainly cultivated in the provinces of Punjab and Sindh, and contributes substantially to national food security, employment generation, and foreign exchange earnings.

According to the Ministry of National Food Security and Research, Pakistan produced approximately 7.32 million tons of rice during the 2022-2023 cropping season, with around 2.98 million hectares allocated to rice cultivation (MNFSR, 2023; GOP, 2023). During the fiscal year 2024-2025, rice cultivation expanded to approximately 3.90 million hectares, reflecting its increasing economic importance compared with several competing crops (MoF, 2025). Rice contributes about 4.19% to agricultural value addition and approximately 0.6% to Pakistan's gross domestic product (GDP) (MoF, 2025).

Export significance and varietal importance

Pakistan is recognized as one of the leading rice-exporting countries worldwide, ranking among the top four global rice exporters. During 2023-2024, the country achieved a record export volume of approximately 6.3 million metric tons, supported by increased international demand, favorable market prices, and strong consumer preference for both Basmati and non-Basmati rice varieties (Bhuyan et al., 2024; EPBDT, 2025; FAO, 2025). Pakistan's globally renowned Basmati rice, a geographically indicated (GI) variety, is highly valued in international markets due to its characteristic aroma, extra-long slender grains, superior cooking quality, and premium market price, particularly in European and Middle Eastern countries (Ali, 2020).

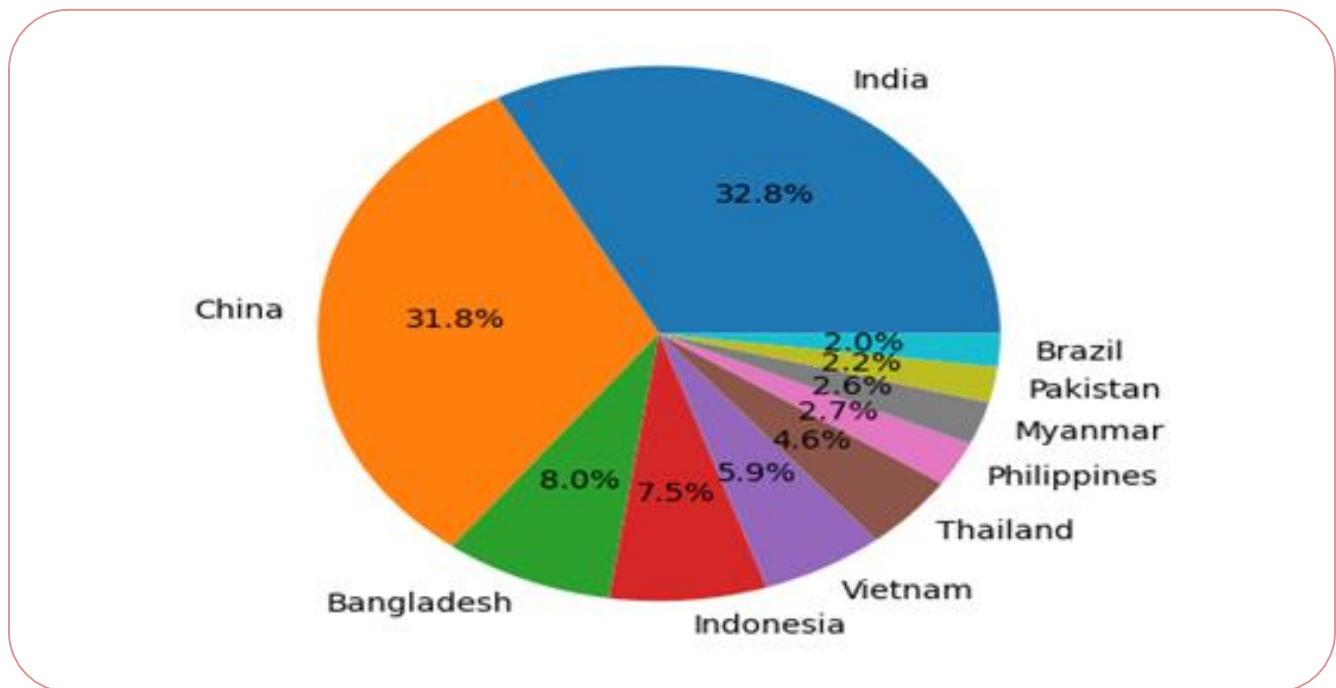


Figure 1. Global rice production has steadily increased and is projected to reach a record 541.28 million metric tons (milled equivalent) in the 2024-2025 marketing year (USDA, 2024). High-yielding hybrid cultivars are increasingly complementing traditional production systems, particularly in Asia, where most global rice production is concentrated.

Despite its economic importance, rice production is continuously threatened by several abiotic and biotic constraints. Among biotic stresses, insect pests and diseases represent major limitations to sustainable rice production by reducing both yield quantity and grain quality. Rice diseases are caused by diverse pathogens, including fungi, bacteria, viruses, and nematodes, which collectively impose substantial production losses worldwide (Wu et al., 2024). Fungal pathogens are particularly destructive because they may survive in seeds, crop residues, and soil, resulting in reduced germination, poor crop establishment, and severe yield penalties under favorable environmental conditions. Seed-borne fungal infections alone have been reported to cause yield losses ranging from 50-80%, depending on pathogen virulence, environmental conditions, and crop susceptibility (Ackaah et al., 2023).

In addition to fungal diseases, insect vectors such as leafhoppers (Cicadellidae) and planthoppers (Delphacidae) contribute significantly to rice production losses by transmitting destructive viral pathogens, including rice tungro virus, rice grassy stunt virus, rice transitory yellowing virus, and rice yellow mottle virus (Chen et al., 2023). Among fungal diseases, rice blast caused by *Pyricularia oryzae* is considered one of the most devastating diseases globally, affecting leaves, nodes, necks, and panicles throughout crop development (Heinrichs et al., 2017; Miah et al., 2017). Bacterial leaf blight caused by *Xanthomonas oryzae* pv. *oryzae* is another major disease, particularly in Asian rice-growing regions (Naqvi, 2019). Although viral diseases generally cause localized losses, epidemic outbreaks of rice grassy stunt virus and rice tungro spherical virus (RTSV) can result in severe yield reductions across Asia (Tennant et al., 2018; Listihani et al., 2024).

Plant-parasitic nematodes also pose a considerable threat to rice production. The rice stem nematode (*Ditylenchus angustus*) causes Ufra disease, which may result in yield losses of 20-90% in affected Asian regions. Similarly, the root-knot nematode (*Meloidogyne graminicola*), particularly prevalent under flooded and irrigated rice systems, can cause yield reductions of up to 80% in upland rice and approximately 73% under irrigated conditions. Other important nematode species include the white-tip nematode (*Aphelenchoides besseyi*) and rice cyst nematodes (*Heterodera* spp.). Collectively, diseases and pests significantly constrain rice productivity, reducing global yield potential by more than 50% under severe

disease pressure (Haque et al., 2021).

Seeds represent a fundamental component of crop production, and the use of healthy, pathogen-free seed is essential for achieving high productivity. Seed-borne pathogens are particularly problematic because they can persist during storage, reduce seed viability, impair germination, and facilitate disease transmission from seed to seedling and subsequently to mature plants. Under severe conditions, seed-borne pathogens may cause yield losses approaching 90% (Gebeyaw, 2020). Among seed-associated fungal diseases, brown leaf spot (BLS) remains one of the most important diseases of rice worldwide, particularly in rain-fed and irrigated ecosystems. Disease-associated yield losses generally range from 12-43%; however, severe epidemics may result in losses approaching 90% under highly conducive environmental conditions (Shaheen et al., 2017; Nawaz et al., 2020).

Brown leaf spot disease is associated with several dematiaceous fungal pathogens, including *Bipolaris oryzae*, *B. sorokiniana*, *Curvularia lunata*, *C. hawaiiensis*, *B. zeicola*, and *Exserohilum rostratum* (teleomorph: *Setosphaeria rostrata*). These fungi infect members of the Poaceae family and cause characteristic necrotic lesions on rice foliage, thereby reducing photosynthetic efficiency and crop productivity (Nawaz et al., 2020). Among these pathogens, *C. lunata* has gained increasing attention due to its expanding geographical distribution, adaptability to changing climatic conditions, and association with grain discoloration complexes (Ferdinandez et al., 2021a).

The association of *C. lunata* with brown leaf spot and grain discoloration of rice has been documented in several rice-growing regions, including Pakistan, India, Malaysia, and Northern Queensland (Kamaluddeen et al., 2012; Kusai et al., 2015; Khemmuk et al., 2016; Majeed et al., 2016). Although historically regarded as a secondary or opportunistic pathogen, *C. lunata* is increasingly recognized as an economically important pathogen due to its contribution to grain discoloration, reduced grain quality, and yield instability under favorable environmental conditions (Ferdinandez et al., 2021b; Ahmed et al., 2022; Araujo Magano et al., 2025). In Pakistan, the pathogen has emerged as a significant concern in rice-wheat cropping systems, particularly in Punjab, where it has been isolated from both foliage and root tissues. Infection results in brown lesions on grains, lightweight and poorly filled panicles, and reduces milling quality, thereby causing considerable economic losses (Majeed et al., 2016; Riegler et al., 2025).

Economic importance of *C. lunata*

Most fungal diseases affecting rice are seed-borne, resulting in substantial economic losses during both seed storage and crop production. Seed-borne pathogens adversely affect multiple stages of crop development, including seed storage, germination, seedling establishment, vegetative growth, and reproductive development. Infected seeds often exhibit reduced germination, serve as primary inoculum for seed-to-seedling transmission, and facilitate the spread of disease throughout the growing season. Among these pathogens, brown leaf spot is one of the most widespread and economically important diseases of rice worldwide. It occurs in both rain-fed and irrigated production systems, where yield losses commonly range from 12% to 43%; however, under severe epidemic conditions, reductions of up to 90% have been reported (Shaheen et al., 2017).

C. lunata, once regarded primarily as a weak or opportunistic pathogen, has emerged as an economically significant pathogen of rice. It is now recognized as a major causal agent of grain discoloration (GD), leaf spot, and premature leaf senescence, thereby reducing both grain yield and quality (Ferdinandez et al., 2021a; Ahmed et al., 2022; Araujo Magano et al., 2025). The economic consequences of *C. lunata* extend beyond quantitative yield reductions, as infection also compromises grain appearance, milling quality, seed viability, and market acceptability, ultimately diminishing the profitability and competitiveness of rice production.

Yield and milling losses

Severe epidemics of *C. lunata* can reduce grain yield by 10-40%, primarily through decreased photosynthetic efficiency, premature leaf senescence, and a reduction in the number of well-filled grains per panicle (Pramesh et al., 2024). In addition to field losses, the pathogen substantially affects post-harvest processing. Infected grains become brittle and structurally weakened, resulting in a greater proportion of broken kernels during milling. This reduction in head rice recovery lowers milling efficiency, commercial grade, and overall market value (Ashfaq et al., 2017; Belete and Boyraz, 2019; Khan et al., 2025a). Such quality deterioration has significant economic implications for major rice-exporting countries. In Pakistan, where annual rice export earnings exceed US\$2.5 billion, losses associated with grain discoloration and poor milling quality represent a substantial threat to national export revenue and the sustainability of the rice industry (TDAP, 2024; MoF, 2025). Consequently,

effective management of *C. lunata* is essential not only for safeguarding crop productivity but also for maintaining grain quality, export competitiveness, and food security.

Disease spread under climate change

Climate change is profoundly altering the epidemiology of plant diseases by influencing pathogen survival, reproduction, dispersal, and host susceptibility. Rising temperatures, elevated atmospheric CO₂ concentrations, and increasingly erratic precipitation patterns are expected to intensify the incidence and severity of numerous plant diseases, thereby posing a significant threat to global food security. Among rice pathogens, *C. lunata* has increasingly transitioned from a relatively minor pathogen to an emerging disease of economic importance, largely driven by climate-induced environmental changes that favor its establishment and epidemic development (Sarma et al., 2023; Hoang et al., 2025; Riegler et al., 2025).

Increased thermotolerance

Global warming, primarily resulting from anthropogenic greenhouse gas emissions, has substantially modified agroecosystems by affecting both abiotic and biotic components (Carrell et al., 2020). Unlike many temperate fungal pathogens, *C. lunata* exhibits remarkable thermotolerance, with optimal growth, sporulation, and infection occurring between 28 and 35°C. Increasing global temperatures are therefore expanding the pathogen's ecological niche, enabling its establishment in previously cooler rice-growing regions. Elevated temperatures also accelerate fungal metabolism, shorten infection cycles, and increase inoculum production, thereby enhancing epidemic potential (Ferdinandez et al., 2021b; Adomako et al., 2025).

Increased host vulnerability

Climate change not only enhances pathogen fitness but also weakens host defense mechanisms. Rice plants subjected to prolonged drought, heat stress, salinity, or irregular rainfall experience physiological stress that compromises innate immune responses, including systemic acquired resistance (SAR). Brown spot disease caused by *C. lunata* is particularly favored under conditions characterized by extended dry periods followed by sudden increases in humidity or rainfall. Drought-induced tissue damage facilitates pathogen penetration, while subsequent humid conditions promote rapid sporulation and secondary infection. Consequently, disease outbreaks are expected to become more frequent and severe in regions experiencing

greater climatic variability, whereas the disease generally remains less destructive in cooler climates or under well-irrigated production systems (Haque et al., 2021; Riegler et al., 2025).

Disease symptoms

Disease development caused by *C. lunata* can be broadly categorized into two distinct phases: (i) the foliar phase (leaf spot) and (ii) the reproductive phase (grain discoloration and spikelet rot). Symptom severity depends on cultivar susceptibility, environmental conditions, and the stage of crop development.

Foliar symptoms (leaf spot phase)

Leaf spot symptoms usually develop during the vegetative stage, particularly under prolonged periods of high relative humidity (> 85%) and temperatures ranging from 25 to 30°C, which are highly conducive to pathogen infection and colonization.

Initial infection

The earliest symptoms appear as minute, pinhead-sized, dark brown to black lesions scattered across the leaf blade. Initially, the lesions are circular to irregular in shape and are distinctly smaller than those produced by *B. oryzae*, whose lesions are typically larger, elongated, and oval. These subtle differences in lesion morphology provide useful diagnostic characteristics during the early stages of disease development (Majeed et al., 2016; Cheng et al., 2025; Varshini et al., 2025).

Lesion expansion

As infection progresses, lesions gradually enlarge to approximately 2-10 mm in diameter and develop into chlorotic spots surrounded by conspicuous brown necrotic margins. A representative outbreak was reported on the rice cultivar Mahsuri in Kampung Tagas, Sabah, Malaysian Borneo (6°9'41.8"N, 116°13'45.1"E), where disease incidence reached approximately 100% and severity approached 60% during the vegetative stage. As lesions expanded, adjacent spots coalesced to form extensive chlorotic areas. For pathogen isolation, symptomatic leaf tissues (5 × 5 mm) excised from lesion margins were surface sterilized following the protocol described by Khoo et al. (2022a).

The characteristic yellow chlorotic halo surrounding the necrotic lesion is primarily associated with fungal phytotoxins, including brefeldin A and related secondary metabolites, which disrupt chloroplast function and accelerate chlorophyll degradation before extensive tissue necrosis occurs. This chlorotic halo represents the advancing zone of host tissue colonization and is

considered a characteristic symptom of *C. lunata* infection (Pramesh et al., 2024; Cheng et al., 2025; Riegler et al., 2025) (Figure 2).

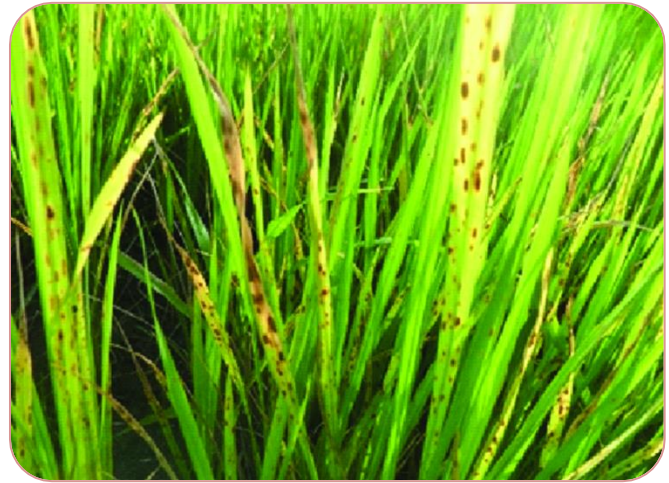


Figure 2. Characteristic symptoms of *C. lunata* leaf spot on rice leaves (adapted from Honger et al., 2022).

Lesion coalescence

Under prolonged periods of favorable environmental conditions, individual lesions enlarge and merge to form extensive necrotic patches that may cover more than 50% of the leaf surface. Severe lesion coalescence results in premature leaf senescence, substantial reduction in photosynthetic capacity, and impaired assimilate translocation to developing grains. Consequently, infected plants exhibit poor grain filling, reduced grain weight, and significant yield losses, particularly when infection occurs before or during the reproductive stage (Tann and Soyong 2017; Wang et al., 2022).

Reproductive symptoms (grain discoloration phase)

The reproductive stage represents the most economically destructive phase of *C. lunata* infection in rice because it directly compromises grain quality and yield. The pathogen primarily infects developing panicles during the milk and dough stages of grain development, resulting in severe panicle and grain abnormalities.

Glume discoloration

Grain discoloration is a complex disease syndrome caused by a consortium of fungal pathogens, including *Alternaria* spp., *Curvularia* spp., *Fusarium* spp., *B. oryzae* (syn. *Helminthosporium oryzae*), *Magnaporthe oryzae* (syn. *Pyricularia oryzae*), *Sarocladium oryzae*, *Sclerotium* spp., *Aspergillus* spp., *Penicillium* spp., *Phoma* spp., and *Cercospora* spp. (Islam and Ahmed, 2017; Persaud et al.,

2019). Among these pathogens, *C. lunata* and *B. oryzae* are the most prevalent and economically important species associated with grain discoloration. Taxonomically, *Curvularia* belongs to the family Pleosporaceae within the class Dothideomycetes (Ariyawansa et al., 2015). The pathogen colonizes the glumes, producing dark brown, purple, or black lesions that progressively enlarge during grain development. Under severe infection, extensive sporulation produces a characteristic velvety black appearance on the grain surface due to abundant conidial production (Ashfaq et al., 2017; Guo et al., 2025; Riegler et al., 2025).

Kernel rot and grain chalkiness

When infection occurs during the early grain-filling stage, the pathogen penetrates the developing endosperm, resulting in kernel rot, incomplete grain filling, and chalky or shriveled kernels. Severely infected grains may become partially or completely hollow owing to the destruction of internal tissues. Such grains exhibit poor milling quality,

reduced market value, and increased susceptibility to breakage during processing (Majeed et al., 2016; Khan et al., 2025b; Riegler et al., 2025).

Sheath rot-like symptoms

In certain cases, *C. lunata* infects the flag leaf sheath enclosing the developing panicle, causing tissue necrosis and sheath rot-like symptoms. Infection restricts panicle emergence, resulting in partially or completely enclosed (choked) panicles that fail to produce viable grains, thereby causing complete yield loss in the affected tillers (Majeed et al., 2016; Khan et al., 2025a; Varshini et al., 2025) (Table 1).

Disease cycle

The disease cycle of *C. lunata* (teleomorph: *Cochliobolus lunatus*) consists of four interconnected stages: survival, primary infection, secondary infection and dissemination, and environmental modulation. These stages collectively facilitate disease persistence and epidemic development under favorable environmental conditions (Majeed et al., 2016; Pramesh et al., 2024; Varshini et al., 2025) (Figure 3).

Table 1. Visual representation and summary of diagnostic cues of *C. lunata* during leaf spot development, grain discoloration, and microscopic examination.

Symptom Stage	Visual Description	Source/Reference
Early Foliar	Pinhead spots with distinct yellow halos on the leaf blade.	Majeed et al. (2016)
Grain Phase	Velvety black or dark brown spots on the glumes; shriveled kernels.	Ashfaq et al. (2017)
Microscopic	Curved, 3-septate conidia with a swollen middle cell.	Pramesh et al. (2024)

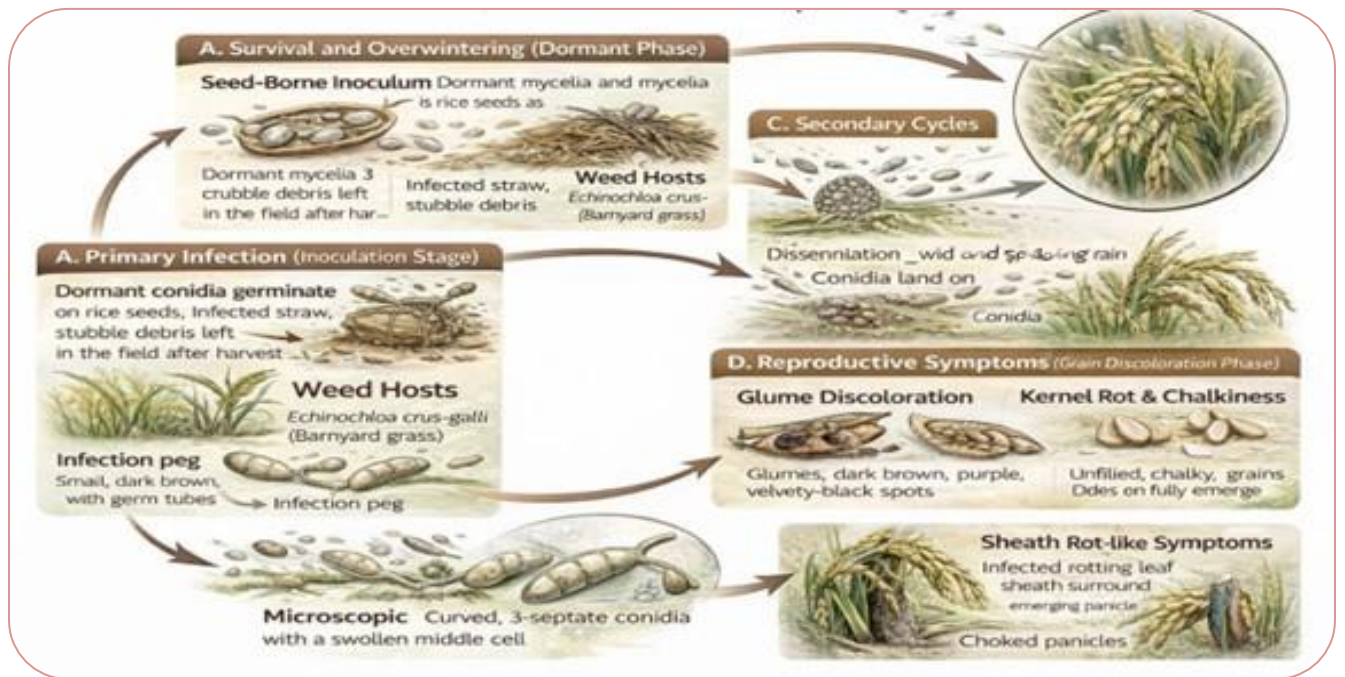


Figure 3. Disease cycle of *C. lunata*, illustrating its transition from dormant survival in seeds and weed hosts to primary and secondary infection cycles, resulting in leaf spot, grain rot, and glume discoloration during the reproductive stage.

A. survival and overwintering (dormant phase)

C. lunata survives between successive rice-growing seasons through multiple reservoirs, enabling rapid disease initiation in subsequent crops.

Seed-borne survival

The pathogen persists externally or internally in infected rice seeds as dormant mycelia and conidia, making seed the primary source of initial inoculum. Infected seeds frequently exhibit discolored hulls or glumes and may become soft, moldy, or partially decomposed (Naik et al., 2025). Following germination, infected seedlings typically emerge weak, chlorotic, and stunted, with reduced vigor and poor establishment (Khoo et al., 2022b). Under severe infection, browning and rotting of the basal stem and root tissues may occur, leading to damping-off and seedling mortality (Limtong et al., 2020; Ackaah et al., 2023).

Crop residues and alternate hosts

After harvest, the fungus survives saprophytically on infected straw, stubble, and other crop residues, serving as an important inoculum reservoir (Ferdinandez et al., 2021b). In addition, several grass weeds function as alternate hosts. Among these, barnyard grass (*Echinochloa crus-galli*) is recognized as an important reservoir that maintains the pathogen between cropping seasons and acts as a “green bridge” for disease transmission in rice-growing regions of Pakistan (Majeed et al., 2016; Adomako et al., 2025; Khan et al., 2025b).

B. Primary infection (inoculation phase)

Primary infection is initiated when dormant conidia germinate under favorable environmental conditions, particularly when relative humidity exceeds approximately 85%. Germinating conidia produce germ tubes that penetrate host tissues either directly through the cuticle via specialized infection pegs or indirectly through stomata and other natural openings. Mechanical injuries and insect feeding sites may also facilitate pathogen entry (Tann and Soyong, 2017; Sepe et al., 2020). Following penetration, the pathogen colonizes the intercellular spaces, secreting cell wall-degrading

enzymes and phytotoxins that induce host tissue necrosis. The earliest visible symptoms appear as minute, dark brown pinhead-sized lesions on infected leaves.

C. Secondary infection, reproduction, and dissemination

Approximately 7-10 days after the initial infection, abundant conidia are produced on necrotic lesions, initiating repeated secondary infection cycles throughout the growing season. These conidia are disseminated primarily by wind and rain splash. Under the warm and humid agroecological conditions prevalent in the rice-growing regions of Punjab and Sindh, multiple infection cycles may occur within a single season, substantially increasing disease severity and facilitating epidemic development (Sarma et al., 2023).

During the heading stage, airborne conidia readily colonize developing panicles, resulting in grain discoloration and kernel infection. Closure of the rice canopy creates a humid microclimate characterized by prolonged leaf wetness, limited air circulation, and elevated relative humidity, conditions that markedly enhance spore germination and infection efficiency (Garcia-Aroca et al., 2018; Adomako et al., 2025). Upon landing on susceptible plant tissues, germinating conidia differentiate specialized appressoria that generate sufficient mechanical pressure to breach the cuticle and penetrate the glumes, thereby initiating grain infection (Pramesh et al., 2024) (Table 2; Figure 3).

D. Environmental catalysts

Disease development is strongly influenced by environmental conditions that regulate pathogen survival, sporulation, dispersal, and host infection. Warm temperatures ranging from 25-32°C, coupled with relative humidity above 85%, prolonged leaf wetness, frequent rainfall, and dense crop canopies, create optimal conditions for conidial germination, host penetration, sporulation, and rapid epidemic progression. Conversely, dry weather and reduced humidity substantially suppress disease development by limiting spore germination and infection efficiency.

Table 2. Disease cycle and environmental drivers illustrating how high humidity and temperature accelerate pathogen transition from latent seed survival to secondary dissemination via wind and rain.

Phase	Activity	Primary Drivers	Reference
Survival	Mycelia in seeds and stubble	Infected residues/Weeds	Ackaah et al. (2023)
Primary Inoculum	Seed germination or wind-borne spores	Rainfall/Initial humidity	Majeed et al. (2016)
Secondary Spread	Rapid conidia production on leaves	Wind and splashing rain	Sarma et al. (2023).
Latent Period	7 to 14 days from infection to spore	High temperature/Humidity	Pramesh et al. (2024)

Pathogenic and genetic variability of *C. lunata*

The ability of *C. lunata* to infect diverse rice cultivars across a wide range of agroecological regions is primarily attributed to its extensive pathogenic and genetic variability. Both conventional pathological assessments and advanced molecular approaches have demonstrated substantial intraspecific diversity within *C. lunata* populations, resulting in marked differences in virulence, host adaptation, and evolutionary potential (Guo et al., 2025; Khan et al., 2025a).

Pathogenic variability (virulence diversity)

Isolate diversity

Studies conducted in major rice-growing regions of Pakistan and India have revealed considerable variation in the pathogenicity of *C. lunata* isolates collected from different geographical locations. Isolates originating from distinct agroecological zones, such as Punjab and Sindh, exhibit significant differences in disease severity, lesion development, and infection efficiency. Highly virulent isolates induce rapidly expanding necrotic lesions, whereas less aggressive isolates produce only small, localized lesions with limited disease progression (Majeed et al., 2016; Pramesh et al., 2024).

Host specificity

Although *C. lunata* possesses a broad host range, certain pathotypes have evolved enhanced virulence toward commercially important rice cultivars, including Super Basmati and Basmati-385. Such host specialization increases disease severity and economic losses in premium export-quality rice, posing a significant challenge to sustainable rice production and resistance breeding programs (Ashfaq et al., 2017; Varshini et al., 2025).

Toxin production and virulence factors

Differences in pathogenicity are closely associated with the production of cell wall-degrading enzymes, including cellulases, pectinases, and xylanases, together with host-selective toxins (HSTs). Highly virulent isolates generally produce greater quantities of these pathogenicity determinants, enabling more efficient degradation of host tissues, enhanced colonization, and accelerated symptom development (Ferdinandez et al., 2021a; Lu et al., 2025).

Genetic variability (molecular diversity)

DNA polymorphism

Molecular marker analyses have revealed extensive genetic polymorphism within *C. lunata* populations. Techniques such as Random Amplified Polymorphic DNA (RAPD), Simple Sequence Repeat (SSR), and other DNA fingerprinting methods have demonstrated substantial

genetic diversity among isolates. In some studies, genetic similarity among rice-derived isolates was reported to be as low as 60%, indicating considerable genomic variation and a high evolutionary potential within natural populations (Khan et al., 2025a).

Phylogenetic analysis

Multilocus phylogenetic analyses based on the Internal Transcribed Spacer (ITS) region and Translation Elongation Factor 1-alpha (TEF-1 α) gene have become the standard approach for accurate identification of *C. lunata* and its discrimination from closely related species, including *C. ricei* and *C. penniseti*. Accurate molecular identification is essential for epidemiological investigations, population genetics, disease surveillance, and the development of effective disease management strategies (Pramesh et al., 2024; Lu et al., 2025).

Integrated management of *C. lunata*

Detection and identification of the pathogen

The detection and identification of *C. lunata* have evolved from reliance on conventional field observations and morphological characterization to comprehensive, multi-tiered diagnostic approaches integrating classical mycology, high-resolution microscopy, molecular diagnostics, and phylogenetic analyses. Contemporary diagnostic techniques provide greater sensitivity, specificity, and taxonomic resolution, enabling early detection, accurate species identification, and effective differentiation of *C. lunata* from morphologically similar *Curvularia* species. These advances facilitate timely disease diagnosis, improve epidemiological surveillance, and support the implementation of targeted and sustainable disease management strategies (Disanayaka et al., 2025).

Detection, identification, and diagnostic characterization of *C. lunata*

Field symptomatology and preliminary diagnosis

The initial diagnosis of *C. lunata* infection is primarily based on characteristic field symptoms. Unlike many rice pathogens that predominantly affect either vegetative or reproductive tissues, *C. lunata* infects both the vegetative (leaves and leaf sheaths) and reproductive (panicles and grains) stages of the crop. Early symptoms appear as small chlorotic lesions surrounded by a conspicuous yellow halo. As disease progresses, the lesions enlarge, coalesce, and develop into dark brown to black necrotic areas, ultimately producing a characteristic blighted appearance (Kamaluddeen et al., 2012). These distinctive field symptoms provide an important basis for preliminary disease diagnosis before laboratory confirmation.

Morphological characterization (microscopic identification)

Microscopic examination remains an essential component of the identification of *C. lunata*. Under a compound microscope, the pathogen exhibits several distinctive morphological characteristics that differentiate it from closely related genera such as *Bipolaris* and *Exserohilum*. The most reliable diagnostic feature is the morphology of the conidia (Figure 4C). Conidia are typically curved (lunate), smooth-walled, brown, and predominantly 3-septate (4-celled). A characteristic feature is the disproportionately enlarged and darker third cell from the basal end, which imparts the distinctive crescent- or moon-shaped appearance to the conidium (Pramesh et al., 2024). Conidiophores are dark brown, septate, simple or branched, and exhibit sympodial (geniculate or zig-zag) growth due to successive conidial production from newly formed apical growing points (Santos et al., 2018; Gore and Shishupala, 2025) (Figure 4A, B, C).

Cultural characteristics on potato dextrose agar (PDA)

Isolation of *C. lunata* on PDA provides additional diagnostic characteristics (Figure 4A). The fungus produces rapidly growing colonies with a velvety to cottony texture and coloration ranging from greyish-black to dark black. Mature colonies frequently develop abundant aerial mycelia, while the reverse side of the culture exhibits intense black pigmentation, reflecting substantial melanin production (Pramesh et al., 2024; Disanayaka et al., 2025). These colony characteristics facilitate routine laboratory identification and isolation of the pathogen.

Advanced molecular identification

Although morphological identification remains valuable, phenotypic characteristics may vary depending on culture media and environmental conditions. Consequently, molecular diagnostic techniques have become the gold standard for accurate and definitive identification of *C. lunata*.

Internal transcribed spacer (ITS) sequencing

Amplification and sequencing of the internal transcribed spacer (ITS) region of ribosomal DNA using the universal primers ITS1 and ITS4 is the most widely employed molecular approach for fungal identification. Comparison of ITS sequences with publicly available databases such as GenBank (NCBI) enables accurate species-level identification. Previous studies have demonstrated that ITS sequencing reliably distinguishes *C. lunata* from closely related species, including *C. geniculata* and *C. oryzae* (Santos et al., 2018; Pramesh et al., 2024; Namdeo Aiwale et al., 2025).

Multilocus sequence typing (MLST)

For greater taxonomic resolution, multilocus sequence typing (MLST) has become increasingly important. This approach utilizes multiple conserved genetic loci, including translation elongation factor 1- α (*TEF-1 α*), glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*), β -tubulin (*TUB2*), and additional housekeeping genes. MLST enables the discrimination of cryptic species within the *Curvularia* complex that cannot be reliably differentiated using morphological traits or ITS sequences alone, thereby improving phylogenetic resolution and diagnostic accuracy (Manzar et al., 2022; Disanayaka et al., 2025).

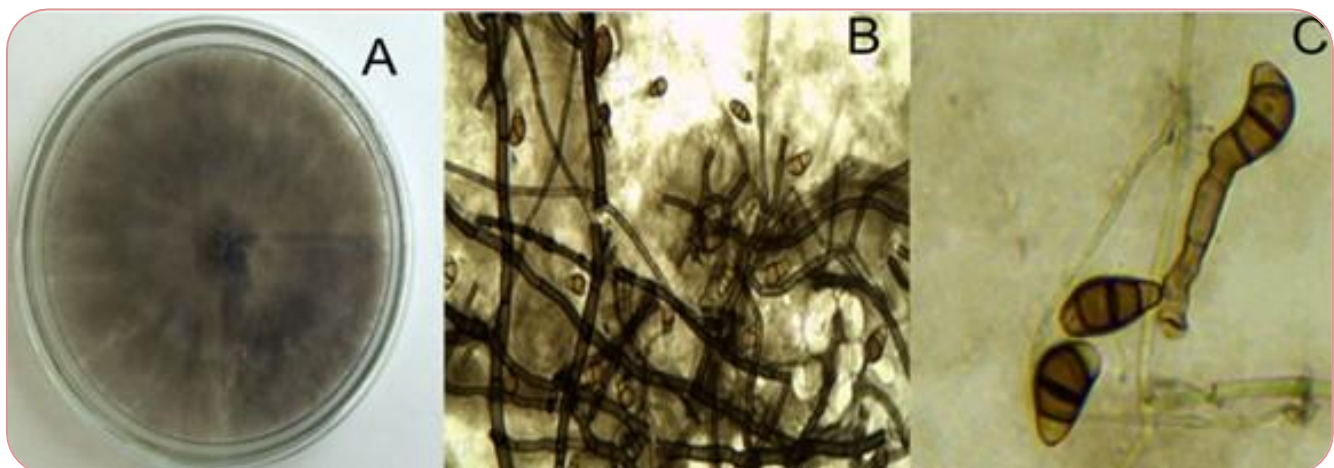


Figure 4. Morphological and cultural characteristics of *C. lunata*. (A) Velvety black fungal colonies growing on PDA medium. (B) Dark brown, septate conidiophores exhibiting a characteristic zigzag pattern. (C) Microscopic view of typically 3-septate, crescent-shaped (lunate) conidia with an enlarged central cell (Honger et al., 2022; Gore and Shishupala, 2025).

Loop-mediated isothermal amplification (LAMP)

Loop-mediated isothermal amplification (LAMP) has emerged as a rapid, sensitive, and highly specific molecular diagnostic tool for detecting fungal pathogens. Unlike conventional PCR, LAMP amplifies DNA under isothermal conditions, eliminating the need for expensive thermal cyclers while reducing assay time and simplifying field implementation (Notomi et al., 2015). The technique has been successfully applied for the early diagnosis, quarantine, disease surveillance, and epidemic forecasting of numerous fungal diseases. For *C. lunata*, LAMP assays enable direct detection of pathogen DNA from infected plant tissues or seed samples within approximately 60 min under constant-temperature conditions, making the method particularly suitable for on-site diagnosis and rapid disease management (Németh et al., 2025).

Seed health testing (standard blotter method)

Because *C. lunata* is an important seed-borne pathogen, seed health testing represents a critical component of disease surveillance and integrated disease management.

Standard blotter method

The standard blotter method remains one of the most reliable techniques for detecting seed-borne fungi. According to the protocol described by Limonard (1968), three sterile, water-soaked filter papers are placed in sterile 9-cm Petri dishes. Twenty seeds are aseptically

arranged equidistantly on the moistened filter papers using sterile forceps. The Petri dishes are sealed and incubated at $25 \pm 2^\circ\text{C}$ under alternating 12-h light and 12-h dark photoperiods for seven days. Following incubation, infected seeds produce characteristic black, fluffy mycelial growth emerging from the seed coat, indicating the presence of *C. lunata*. Seed health testing is of considerable epidemiological importance because infection levels in commercial rice seed lots have been reported to range from 5% to 25%, providing a primary source of inoculum for field epidemics (Rashid, 2001) (Table 3).

Isolation and identification of *C. lunata*

C. lunata, the causal agent of rice leaf spot, was isolated and identified from naturally infected rice cultivars during experimental investigations conducted at the Department of Plant Pathology, Faculty of Crop Protection, Sindh Agriculture University, Tandojam. Seed-borne fungal pathogens were detected using the standard blotter paper technique under the supervision of Dr. Ghulam Hussain Jatoi. Surface-sterilized infected rice seeds were placed on moist sterile filter paper in Petri dishes and incubated at room temperature. Following seven days of incubation, fungal colonies emerged from infected seed tissues, producing characteristic dark mycelial growth and abundant conidia that were subsequently examined for morphological identification (Figure 5).

Table 3. Comparison of detection methods: field-based symptomatology and blotter tests versus laboratory-based microscopy and high-accuracy ITS sequencing.

Method	Ease of Use	Accuracy	Primary Indicator
Symptomatology	High (Field)	Low	Brown spots with yellow halos
Microscopy	Medium	Medium	3-septate, curved conidia
ITS Sequencing	Low (Lab)	Very High	DNA Sequence homology
Blotter Test	Medium	High	Fuzzy black growth on seeds



Figure 5. Samples were collected from infected rice cultivars and incubated on moist blotter paper in Petri dishes. *C. lunata* was identified through detailed microscopic examination, and its identity was confirmed using established morphological keys based on fungal characteristics at the Department of Plant Pathology, Faculty of Crop Protection, Sindh Agriculture University, Tando Jam.

Microscopic confirmation of *C. lunata*

The identity of the fungal isolate was confirmed through detailed microscopic examination using standard taxonomic keys. Diagnostic morphological features observed included:

Conidiophores

Dark brown, septate, simple to branched conidiophores exhibiting characteristic sympodial growth with geniculate (zig-zag or knee-like) apices resulting from successive conidial production.

Conidia

Smooth-walled, brown, lunate (crescent-shaped) conidia consisting predominantly of four cells separated by three transverse septa.

Cell morphology and pigmentation

The third cell from the basal end was consistently larger, darker, and asymmetrically swollen compared

with the terminal cells, producing the characteristic curvature that distinguishes *C. lunata* from other species within the genus. These morphological characteristics correspond closely with the accepted taxonomic descriptions of *C. lunata* and provide reliable confirmation of species identity when integrated with cultural and molecular diagnostic approaches.

Cultural practices

Cultural management represents the first line of defense against *C. lunata* and focuses on disrupting the pathogen’s survival, reproduction, and dispersal during its disease cycle. By reducing the primary inoculum and creating environmental conditions that are less favorable for pathogen establishment, cultural practices can substantially delay epidemic development and reduce disease severity (Asif et al., 2025; Namdeo-Aiwale et al., 2025) (Table 4).

Table 4. Impact of sustainable cultural management practices, field sanitation, nutrient balance (potassium and silicon), and crop spacing on reducing initial inoculum.

Strategy	Target phase	Expected impact	Reference
Deep Plowing	Survival/Inoculum	Reduces soil-borne spores	Heinrichs, <i>et al</i> (2017)
Potassium (K) Application	Penetration Stage	Enhances physical resistance	Zhou <i>et al.</i> (2025)
Wider Spacing	Secondary Spread	Reduces canopy humidity	Cucu <i>et al.</i> (2025)
Seed Sorting	Primary Inoculum	Prevents seedling infection	Xuan <i>et al.</i> (2018)

Field sanitation and residue management

Sanitation is a fundamental preventive strategy that minimizes pathogen reservoirs within the production system. It encompasses the removal and destruction of infected plant tissues, volunteer rice plants, weeds, and crop residues, as well as the disinfection of farm tools, machinery, and equipment to prevent pathogen dissemination. Elimination of weeds and volunteer hosts is particularly important because they serve as alternative reservoirs for *C. lunata* and increase canopy humidity, thereby creating a favorable microclimate for fungal infection and sporulation. In addition, tillage practices that incorporate infected crop residues into the soil expose fungal propagules to adverse environmental conditions, including solar radiation and microbial decomposition, thereby reducing pathogen survival (Barnwal et al., 2013). Since *C. lunata* is a facultative saprophyte capable of surviving on infected crop debris between growing seasons, effective post-harvest residue management is essential for lowering the initial inoculum and preventing disease recurrence.

Consequently, removal and destruction of infected plant materials and crop residues significantly reduce overwintering inoculum and subsequent reinfection in the following cropping season (Bhardwaj, 2025; Araujo Magano et al., 2025).

Removal of infected stubble

Effective management of infected rice stubble is critical for suppressing the primary inoculum. Burning, where permitted, or deep incorporation of infected residues through ploughing can substantially reduce pathogen survival. Heinrichs and Muniappan (2017) reported that these practices can decrease the primary inoculum by up to 60% before the subsequent cropping season. Deep ploughing (20-25 cm) buries fungal conidia beneath the soil surface, thereby limiting their dispersal by wind and reducing the likelihood of infection in newly established rice crops (Pankhurst et al., 2002).

Weed management

C. lunata possesses a broad host range that includes several weed species, such as *Echinochloa crus-galli* and *Cyperus rotundus*, which function as alternate

hosts during the off-season. Maintaining weed-free fields, bunds, and irrigation channels eliminates this “green bridge”, thereby interrupting pathogen survival and reducing inoculum carryover between successive rice crops (Adomako et al., 2025; Araujo Magano et al., 2025).

Balanced nutrient management

Appropriate nutrient management plays an important role in enhancing host resistance. Excessive nitrogen fertilization promotes the development of succulent tissues that are more susceptible to fungal penetration and colonization. In contrast, adequate potassium nutrition enhances cell wall integrity, improves tissue strength, and increases the plant's resistance to fungal invasion. Zhou et al. (2025) demonstrated that potassium supplementation reinforces rice leaf cell walls, thereby providing an effective physical barrier against fungal germ tube penetration (Sopialena et al., 2025).

Silicon amendment

Rice is a silicon-accumulating crop, and silicon fertilization has been widely recognized as an effective strategy for enhancing resistance against fungal diseases. Silicon deposition beneath the cuticle strengthens epidermal tissues and stimulates host defense responses, including increased lignification and accumulation of phenolic compounds. These structural and biochemical changes restrict fungal penetration, confine pathogen spread, and limit lesion expansion following *C. lunata* infection (Detmann et al., 2024; Sopialena et al., 2025).

Sowing and spacing optimization

The microclimate within the rice canopy, particularly relative humidity, air circulation, and leaf wetness duration, plays a decisive role in *C. lunata* spore germination, infection, and disease development. Therefore, optimizing planting geometry and sowing time constitutes an important component of integrated disease management.

Optimal planting density

Excessively dense planting creates a humid, poorly ventilated canopy that favors spore germination, pathogen establishment, and rapid disease spread. Increasing plant spacing enhances air circulation, improves light penetration, and reduces the duration of leaf wetness, thereby creating conditions that are less conducive to fungal infection. Cultural practices such as appropriate plant spacing, thinning, and canopy management effectively

improve ventilation within the crop stand (Vishwakarma et al., 2025). Cucu et al. (2025) demonstrated that increasing hill spacing from 15 to 20 cm significantly reduced canopy humidity and leaf wetness duration, resulting in lower *C. lunata* infection and disease severity.

Adjustment of sowing dates

Modifying sowing dates can reduce disease risk by allowing susceptible crop growth stages to escape periods of environmental conditions favorable for pathogen development. The effectiveness of this strategy depends on regional climate, cultivar characteristics, projected climate variability, and prevailing agronomic and market conditions (Wolfe et al., 2008). Under Pakistani agroecological conditions, early sowing enables rice plants to avoid peak humidity during July and August, particularly during flowering and grain filling, thereby reducing the incidence of grain discoloration caused by *C. lunata* (Vishwakarma et al., 2025; Zhou et al., 2025).

Use of certified disease-free seed

Because *C. lunata* is a well-recognized seed-borne pathogen, the use of certified disease-free seed represents one of the most important cultural practices for preventing primary infection. Reducing the pathogen load in seed lots minimizes the introduction of inoculum into the field and consequently lowers disease incidence during the early stages of crop establishment.

Seed sorting

Seed sorting is an effective approach for reducing the transmission of seed-borne pathogens. Laboratory studies have demonstrated that density-based separation using salt solutions is more efficient than manual sorting for eliminating infected seeds from rice and cowpea seed lots. Simple physical techniques, such as salt-water flotation (brine treatment), selectively remove lightweight, shriveled, and pathogen-infected seeds while retaining healthy, well-filled seeds. Studies by Xuan and Gergon (2018) and Jatoi et al. (2016c) demonstrated that density-based seed sorting significantly reduces seed-borne fungal contamination. Furthermore, the exclusive use of heavy, healthy seeds has been reported to decrease early seedling rot caused by *C. lunata* by nearly 40% (NamdeoAiwale et al., 2025; Vishwakarma et al., 2025).

Biological control strategies

A. Antagonistic fungal agents (*Trichoderma* and *Chaetomium*)

Antagonistic fungi represent one of the most promising biological control options against *C. lunata* because they efficiently colonize the same ecological niches as the

pathogen. Species such as *Trichoderma harzianum* and *T. viride* function as aggressive mycoparasites by directly attacking pathogen hyphae. *Trichoderma* hyphae coil around the mycelium of *C. lunata* and secrete hydrolytic enzymes, including chitinases and β -1,3-glucanases, which degrade the fungal cell wall and suppress pathogen growth. This hyperparasitic mechanism has been reported to reduce the colonization of rice grains by up to 70% (Ali et al., 2023; Dutta et al., 2023).

In addition to *Trichoderma*, species of *Chaetomium* produce potent antifungal metabolites with strong activity against *C. lunata*. Tann and Soyong (2017) demonstrated that chaetoglobosin C extracted from *C. cupreum* exhibits significant biofungicidal activity by suppressing fungal growth and sporulation. Similarly, Ramírez-Olier et al. (2019) reported that the native *Trichoderma* isolates GRB-HA1 and GRB-HA2 completely inhibited the mycelial growth of *Colletotrichum gloeosporioides* and *C. lunata*, with isolate GRB-HA2 showing superior antagonistic activity against *C. gloeosporioides*, *C. lunata*, and *Fusarium oxysporum*. These findings highlight the considerable potential of fungal antagonists as environmentally sustainable alternatives to chemical fungicides (Ashwini et al., 2025; Namdeo Aiwale et al., 2025).

B. Bacterial endophytes and plant growth-promoting rhizobacteria

Beneficial bacteria, particularly plant growth-promoting rhizobacteria (PGPR) and bacterial endophytes, provide long-lasting protection against *C. lunata* by directly inhibiting pathogen development and activating host defense mechanisms.

Species such as *Bacillus subtilis* and *B. amyloliquefaciens* produce a diverse array of antifungal lipopeptides, including surfactin, iturin, and fengycin, which disrupt the integrity of *C. lunata* conidial membranes and inhibit spore germination and mycelial growth (Jatoi et al., 2015; Jatoi et al., 2016a; Muhammad et al., 2026; Ehsan et al., 2023). In addition, *Bacillus* spp. establish endophytic populations within rice tissues, forming an internal protective barrier that provides sustained suppression of pathogen colonization (Maharjan et al., 2025; Jatoi et al., 2016b).

Likewise, *Pseudomonas fluorescens* synthesizes the broad-spectrum antibiotic 2,4-diacetylphloroglucinol (DAPG), which effectively suppresses the growth of *C. lunata*. Seed priming with *P. fluorescens* also induces systemic resistance (ISR), resulting in enhanced activities of

defense-related enzymes, including peroxidase and polyphenol oxidase, thereby strengthening the plant's resistance to subsequent fungal infection (Andriani et al., 2025; Ashwini et al., 2025).

C. Antagonistic yeasts: an emerging frontier

Antagonistic yeasts have recently emerged as promising biological control agents for managing grain discoloration and post-harvest diseases caused by *C. lunata*. Unlike many conventional antagonists, several yeast species suppress fungal pathogens through the production of volatile organic compounds (VOCs), which function as natural biofumigants without requiring direct physical contact with the pathogen.

Khunnamwong et al., (2020) demonstrated that the epiphytic yeast *Wickerhamomyces anomalus* produces VOCs capable of significantly inhibiting the mycelial growth of *C. lunata*. This vapor-phase mode of action is particularly advantageous during grain storage, where direct application of biological agents is often impractical. Consequently, antagonistic yeasts offer an environmentally friendly strategy for reducing grain discoloration and minimizing post-harvest losses throughout the storage phase of the rice production cycle (Figure 6; Table 5).

Botanical extracts and natural compounds

Botanical extracts represent an environmentally sustainable alternative for the management of *C. lunata*. Their antifungal activity is primarily attributed to plant-derived secondary metabolites, including alkaloids, phenolic compounds, flavonoids, terpenoids, and essential oils, which inhibit fungal growth through multiple mechanisms such as disruption of cell membrane integrity, inhibition of enzymatic activity, suppression of spore germination, and induction of host defense responses. Numerous medicinal and aromatic plant species have demonstrated significant antifungal activity against *C. lunata* under both *in vitro* and *in vivo* conditions (Khatun et al., 2025; Namdeo Aiwale et al., 2025; Vishwakarma et al., 2025) (Figure 7).

Neem (*Azadirachta indica*) is one of the most extensively studied botanical fungicides. Neem leaf extracts and seed oil contain biologically active compounds, including azadirachtin, nimbin, and salannin, which disrupt fungal cell membrane permeability and inhibit mycelial growth. Studies have reported that a 10% neem extract reduced the mycelial growth of *C. lunata* by more than 75% (Rao et al., 2021; Jatoi et al., 2019).

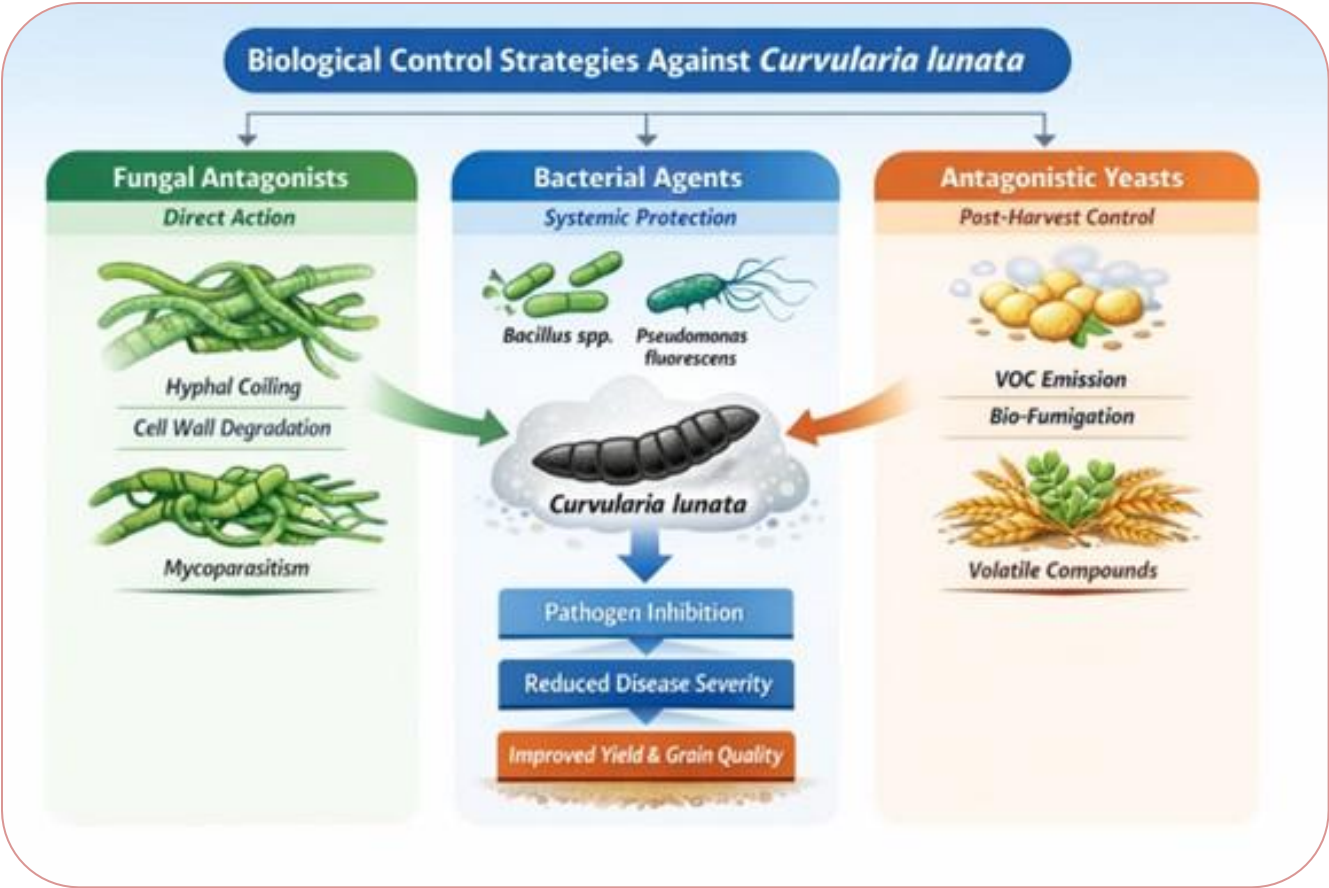


Figure 6. Mechanisms of biological control of *C. lunata* by *Trichoderma*, *Bacillus*, and *Wickerhamomyces* through mycoparasitism, antibiosis, induced systemic resistance, and volatile organic compound (VOC)-mediated inhibition.

Table 5. Mechanisms by which bacteria, yeasts, and beneficial fungi (e.g., *Trichoderma*) suppress pathogen growth through mycoparasitism and antibiosis.

Biocontrol agent	Primary mechanism	Target stage	Reference
<i>Trichoderma harzianum</i>	Mycoparasitism and chitinase	Mycelial growth/Stubble	Dutta et al. (2022)
<i>Bacillus subtilis</i>	Antibiosis (Lipopeptides)	Spore germination	Muhammad et al. (2026)
<i>Chaetomium cupreum</i>	Bio-active metabolites	Foliar lesions	Tann & Soyong (2017)
<i>Wickerhamomyces</i>	VOCs (Bio-fumigation)	Grain discoloration	Khunnamwong et al. (2020)

Garlic (*Allium sativum*) possesses potent antifungal activity due to its high allicin content. Garlic aqueous extracts have been shown to inhibit hyphal development by causing structural disruption and lysis of fungal hyphae, thereby suppressing disease progression (Bello and Sisterna, 2010).

Turmeric (*Curcuma longa*) contains curcumin, a polyphenolic compound that interferes with fungal metabolic pathways and enzyme activity. In addition to its direct antifungal effects, curcumin has shown considerable potential as a seed treatment for reducing seed-borne transmission of *C. lunata* (Ojha et al., 2025).

Clove (*Syzygium aromaticum*) essential oil is rich in eugenol, a phenolic compound with strong fungicidal and fumigant properties. Eugenol effectively inhibits spore germination and mycelial growth, with reports indicating nearly complete suppression of conidial germination even at relatively low concentrations (Abubakar et al., 2026).

Ginger (*Zingiber officinale*) contains bioactive compounds such as gingerol and shogaol, which exhibit broad-spectrum antifungal activity. *In vitro* studies have demonstrated significant inhibition of radial mycelial growth of *C. lunata* following treatment with ginger extracts (Bello and Sisterna, 2010).

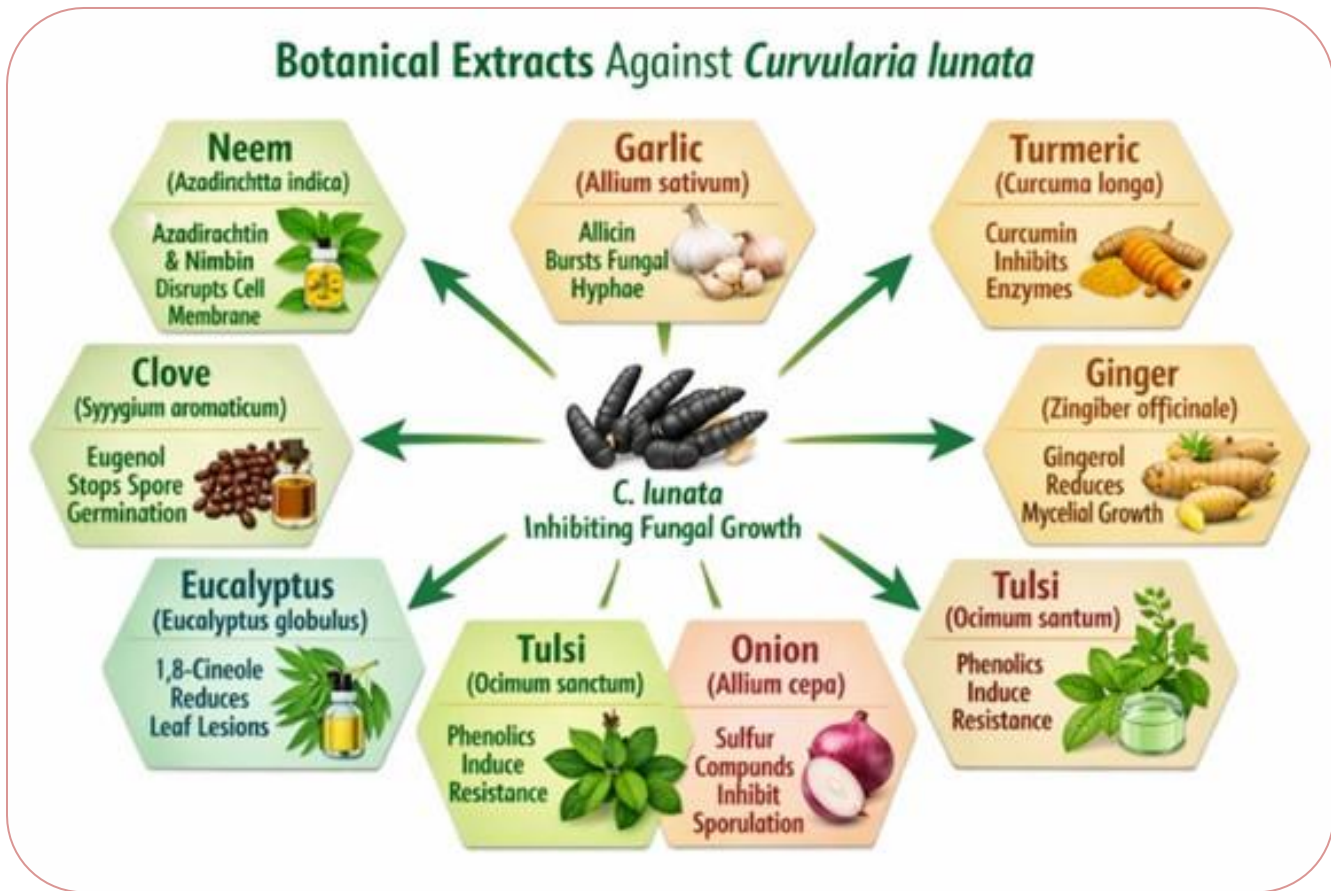


Figure 7. Mechanisms of action of plant-derived compounds from *A. indica*, *A. sativum*, and *C. longa* against *C. lunata*.

Eucalyptus (*Eucalyptus globulus*) essential oil contains high concentrations of 1,8-cineole, which exhibits strong antifungal activity. Foliar application of eucalyptus oil has been reported to reduce lesion development on rice flag leaves and suppress disease severity under field conditions (Yu et al., 2025).

Holy basil (*Ocimum sanctum*) contains phenolic compounds and essential oils that not only inhibit fungal development but also induce systemic resistance in rice plants by activating host defense pathways, thereby enhancing resistance against *C. lunata* infection (Rao et al., 2021).

Onion (*Allium cepa*) contains sulfur-containing compounds similar to those found in garlic. These metabolites inhibit fungal enzymatic systems and significantly reduce sporulation and pathogen reproduction (Abubakar et al., 2026).

Aloe vera (*Aloe barbadensis*) gel contains several bioactive compounds, including aloectin and anthraquinones, which suppress fungal growth and inhibit the production of phytotoxic metabolites by *C. lunata*, thereby reducing host tissue damage (Khatun et al., 2025; Ojha et al., 2025) (Table 6).

Table 6. Impact of plant-derived metabolites, such as allicin from garlic and azadirachtin from neem, on fungal cell membrane integrity and sporulation.

Plant Source	Active component	principal Effect	Reference
Neem	Azadirachtin	Membrane disruption	Rao et al. (2021)
Garlic	Allicin	Hyphal lysis (bursting)	Bello and Sisterna (2010)
Clove	Eugenol	Total spore inhibition	Abubakar et al. (2026)
Eucalyptus	1,8-cineole	Protective foliar coating	Yu et al. (2025)
Turmeric	Curcumin	Metabolic inhibition	Ojha et al. (2025)

Use of chemical fungicides

Chemical fungicides remain an important component of integrated disease management (IDM) strategies for *C. lunata*, particularly under conditions conducive to severe disease outbreaks. Contemporary fungicides are selected based on their systemic activity and specific modes of action, including inhibition of ergosterol biosynthesis, disruption of mitochondrial respiration, and interference with fungal cell division. Their judicious use, integrated with cultural and biological control

measures, provides effective suppression of disease while minimizing the risk of fungicide resistance (Khan et al., 2025b; Namdeo Aiwale et al., 2025) (Figure 8; Table 7).

A. Seed treatment: the first line of chemical defense

Because *C. lunata* is predominantly a seed-borne pathogen, seed treatment before sowing represents one of the most economical and effective approaches for interrupting the disease cycle and preventing early seedling infection.



Figure 8. Integrated application of seed treatments and systemic fungicides (triazoles and strobilurins) for effective management of *C. lunata* through inhibition of ergosterol biosynthesis and disruption of fungal respiration.

Table 7. Strategic application of foliar fungicides (triazoles and strobilurins) and seed treatments for protecting crop yields.

Fungicide category	Common name	Mode of action	Best use stage	Reference
Benzimidazole	carbendazim	mitosis inhibition	seed treatment	Palaki, (2015)
Triazole	propiconazole	sterol biosynthesis	booting stage	Obeng et al. (2021)
Strobilurin	azoxystrobin	energy/Respiration	heading stage	Palaki, (2015)
Dithiocarbamate	mancozeb	multi-site contact	preventive/early	Yu, et al. (2022)

Carboxin + Thiram

The combination of the systemic fungicide carboxin and the contact fungicide thiram provides broad-spectrum protection against seed-borne pathogens. Seed treatment with this formulation has been reported to reduce seedling mortality by approximately 85% while effectively preventing root colonization by *C. lunata* (Paulikienė et al., 2025).

Carbendazim

Carbendazim is a systemic benzimidazole fungicide with broad-spectrum antifungal activity. Seed soaking in a 0.2% carbendazim solution for approximately 12 h has been shown to eliminate internally seed-borne fungal mycelia present within the glumes and substantially reduce primary inoculum (Palaki, 2015; Namdeo Aiwale et al., 2025).

B. Foliar application: protection of the photosynthetic canopy

Foliar fungicide application is particularly important during the booting and heading stages of rice development, when protection of the flag leaf and developing panicle is essential for maintaining grain filling and yield.

Triazoles (Propiconazole and Tebuconazole)

Triazole fungicides inhibit ergosterol biosynthesis by targeting the C14-demethylase enzyme, thereby disrupting fungal cell membrane formation. Their systemic, acropetal movement provides protection to newly emerging tissues. Tebuconazole (250 EC) has been reported to reduce *C. lunata* leaf spot severity by 60-75% under field conditions (Obeng et al., 2021).

Strobilurins (Azoxystrobin)

Azoxystrobin belongs to the quinone outside inhibitor (QoI) group and suppresses fungal respiration by inhibiting electron transport within the mitochondrial cytochrome bc₁ complex. In addition to its antifungal activity, azoxystrobin delays leaf senescence through a physiological “greening effect”, thereby prolonging photosynthetic activity and improving grain filling, ultimately reducing yield losses associated with *C. lunata* infection (Palaki, 2015).

Fungicide mixtures

Combination fungicides provide broader-spectrum disease control and reduce the risk of resistance development. Mixtures containing azoxystrobin and difenoconazole have demonstrated superior efficacy against the rice grain discoloration complex caused by *C. lunata* and associated fungal pathogens. These

formulations are widely recommended for integrated disease management in major rice-growing regions of Pakistan and India owing to their complementary modes of action and consistently high field performance (Obeng et al., 2021; Vishwakarma et al. 2025).

Conclusion

The epidemiological transition of *C. lunata* from a secondary saprophytic colonizer to a major necrotrophic pathogen of *Oryza sativa* represents a compelling example of climate-driven fungal adaptation. Its remarkable genetic plasticity, broad host range, and inherent thermotolerance have enabled the pathogen to thrive under the increasingly erratic environmental conditions associated with global climate change. Evidence from Pakistan’s rice-wheat production system demonstrates that *C. lunata* is no longer confined to foliar infections but has emerged as a major component of the grain discoloration complex (GDC), significantly reducing seed viability, grain quality, and the milling performance of premium cultivars such as Basmati rice. Current evidence further indicates that reliance on single-component chemical control is unlikely to provide sustainable disease suppression and may accelerate the emergence of fungicide-resistant populations. Consequently, durable management of this polycyclic pathogen requires a comprehensive integrated disease management strategy that combines optimized cultural practices, balanced nutrient management, resistant cultivars, microbiome-based biological control, and the judicious use of fungicides.

Research gaps and implications

Despite increasing recognition of *C. lunata* as an economically important pathogen, several fundamental knowledge gaps remain. The molecular basis of pathogenicity and host adaptation is still poorly understood. Although virulence-associated factors, including polyketide synthases, phytotoxins, and cell wall-degrading enzymes, have been identified, comprehensive characterization of effector repertoires, toxin biosynthetic pathways, and host invasion mechanisms remains limited. Elucidating the molecular interactions between the pathogen and its hosts will be essential for developing targeted disease management strategies and durable host resistance.

Current breeding programs primarily emphasize broad-spectrum disease resistance; however, the genetic

architecture underlying durable resistance to *C. lunata* has not been comprehensively characterized. The identification and validation of resistance genes, quantitative trait loci (QTLs), and genomic regions associated with reduced susceptibility across diverse rice germplasm remain significant research priorities.

Long-term epidemiological datasets encompassing seasonal disease dynamics, environmental variables, pathogen population structure, and disease incidence across diverse agroecological regions are also lacking. Most existing studies are restricted to single-season or location-specific surveys, limiting the accuracy of disease forecasting models and region-specific risk assessments. Furthermore, despite substantial advances in rapid diagnostics and high-throughput phenotyping for other plant diseases, validated field-deployable diagnostic tools for *C. lunata* remain unavailable. The development of sensitive, rapid, and cost-effective diagnostic platforms capable of distinguishing *C. lunata* from other grain discoloration pathogens and detecting latent infections before symptom expression would substantially improve disease surveillance and optimize intervention timing.

Limitations of eco-friendly management strategies

Although eco-friendly disease management approaches have shown considerable promise, several challenges limit their large-scale adoption.

1. Although botanical extracts and microbial biocontrol agents exhibit strong antifungal activity under controlled laboratory conditions, their performance under field conditions remains inconsistent. Environmental variability, including fluctuations in temperature, ultraviolet radiation, rainfall, and soil heterogeneity, often reduces their efficacy, creating a substantial gap between laboratory success and field performance.
2. Biological control agents and plant-derived formulations generally exhibit limited persistence under field conditions. Exposure to solar radiation, desiccation, fluctuating environmental conditions, and microbial competition significantly reduces their survival and biological activity. Consequently, these products often require repeated applications compared with conventional fungicides.
3. The chemical composition of botanical extracts varies considerably depending on plant genotype, growth conditions, harvesting stage, and extraction methodology. Such variability leads to inconsistent antifungal efficacy against *C. lunata*, thereby reducing reproducibility,

limiting commercial scalability, and complicating regulatory approval. Standardized extraction protocols and rigorous quality control measures remain essential prerequisites for commercialization.

4. Eco-friendly interventions primarily rely on indirect mechanisms, including competitive exclusion, antibiosis, hyperparasitism, and induced systemic resistance (ISR). These biological processes generally require more time to suppress pathogen development than the direct fungitoxic activity of synthetic fungicides, particularly during severe disease outbreaks.

5. Many biological control agents exhibit strain- or pathogen-specific activity. Given the extensive genetic diversity and pathogenic variability of *C. lunata*, individual microbial antagonists may not provide effective control against all pathogenic populations. This limitation highlights the need to develop multi-strain microbial consortia and complementary integrated biological management strategies.

6. Large-scale production of microbial biocontrol agents while maintaining viability, shelf life, formulation stability, and field efficacy remains technically challenging. Constraints related to formulation technology, storage, transportation, commercialization, regulatory approval, and limited farmer awareness, particularly in developing countries, continue to impede widespread adoption. Addressing these challenges will be essential for translating promising laboratory findings into practical field applications.

Future prospects

Future management of *C. lunata* should transition from single-component interventions toward integrated, technology-driven disease management systems. Advances in microbiome engineering provide opportunities to develop synthetic microbial consortia with enhanced ecological stability, synergistic interactions, and broader-spectrum pathogen suppression. Such engineered microbial communities may establish more effectively within plant-associated niches and provide durable disease protection.

Simultaneously, genomics-, transcriptomics-, proteomics-, and metabolomics-based investigations will play a pivotal role in identifying virulence determinants, antifungal targets, and host resistance mechanisms. Integrating multi-omics approaches will facilitate precision breeding, molecular marker development, and the design of targeted biological interventions for durable resistance.

Nanotechnology also offers considerable potential for improving the efficacy of environmentally friendly disease management. Nano-encapsulation of botanical compounds and microbial bioformulations can enhance formulation stability, prolong field persistence, improve controlled release, and increase bioavailability, thereby overcoming several limitations associated with conventional biological products.

In parallel, artificial intelligence (AI)-based disease forecasting, remote sensing, digital phenotyping, and precision agriculture technologies are expected to revolutionize disease surveillance by enabling early detection, real-time risk assessment, and timely management interventions. Integrating these digital technologies with IDM programs will substantially improve disease prediction accuracy and management efficiency. Finally, successful implementation of sustainable disease management will require stronger collaboration among researchers, breeders, extension agencies, policymakers, and farmers. Standardized bioformulation protocols, supportive regulatory frameworks, farmer-centered extension services, and region-specific management recommendations will be essential for bridging the gap between research and practical application. Collectively, these multidisciplinary approaches will contribute to the development of resilient, environmentally sustainable, and climate-smart strategies for managing *C. lunata* and safeguarding global rice production under changing climatic conditions.

Author Contributions

All authors contributed to the literature search, data collection, organization, and compilation of relevant information. They collaboratively prepared the initial draft, critically reviewed the manuscript, incorporated necessary revisions, and contributed to the improvement and refinement of the final version. All authors read and approved the final manuscript.

Research Funding

This research did not receive any grant from funding agencies.

Conflict of Interest

The authors declare no conflict of interest.

Sustainable Development Goals Targeted

SDG 2: Zero Hunger

SDG 12: Responsible Consumption and Production

SDG 15: Life on Land

Policy Addressed

This review supports policies promoting integrated disease management, certified disease-free seed systems, phytosanitary surveillance, and climate-resilient crop protection. It advocates strengthened molecular diagnostics, biosecurity, sustainable pesticide use, biological control, and farmer extension programs to reduce disease losses, improve grain quality, safeguard rice exports, and enhance national food security.

References

- Abubakar, M., Koul, B., Sharma, Y., 2026. Plant-based fungicides: a sustainable alternative to synthetic fungicides in vegetable production. *Phytochemistry Reviews* 25(2), 1681-1749.
- Ackaah, F.M., Nyaku, S.T., Darkwa, E., 2023. Seed-borne fungi associated with diverse rice varieties cultivated in the Western North region of Ghana. *International Journal of Microbiology* 2023, 1-12.
- Adomako, J., Larbi-Koranteng, S., Bukari, T.A., Danso, Y., 2025. Pathogenic variability among *Curvularia* species causing brown leaf spot disease of rice. *Journal of Plant Pathology* 107(1), 243-249.
- Ahmed, M., Tariq, M., Shahid, M., Khan, S., 2022. Current status of grain discoloration disease of rice in Pakistan and its management. *Clinic Search Journal of Agricultural Science* 3(2).
- Ali, I., Abro, M.A., Syed, R.N., 2023. Isolation of rhizospheric bacteria from soil and their antifungal activity against *Helminthosporium oryzae*, the causal agent of brown spot of rice. *Journal of Microbiological Sciences* 2(1), 14-20.
- Ali, M., 2020. Rice sector of Pakistan. Trade Development Authority of Pakistan, Islamabad, Pakistan. <https://tdap.gov.pk/wp-content/uploads/2022/03/1.2-Pakistan-rice-sector-report-2020.pdf>
- Andriani, V., Ajiningrum, P.S., Hanifah, R.P., 2025. Antagonistic activity of *Pseudomonas fluorescens* against *Curvularia* sp. causing leaf spot disease in maize. *STIGMA: Jurnal Matematika dan Ilmu Pengetahuan Alam Unipa* 18(1), 21-28.
- Araujo Magano, D., Ricardo Carvalho, I., Gonzalez da Silva, J.A., Eduarda Arnold, L., Schwederke Stibe, G.A., de Oliveira Krahn, C., Folleto, E., dos Santos Schwingel, G., 2025. First record of *Curvularia* sp.

- in canary grass (*Phalaris canariensis*) cultivation in Ijuí, RS, Brazil. GeSec: Revista de Gestao e Secretariado 16(1), e4639-e4639.
- Ariyawansa, H.A., Thambugala, K.M., Manamgoda, D.S., Jayawardena, R., Camporesi, E., Boonmee, S., Wanasinghe, D.N., Phookamsak, R., Hongsan, S., Singtripop, C., 2015. Towards a natural classification and backbone tree for Pleosporaceae. Fungal Diversity 71, 85-139.
- Ashfaq, M., Mubashar, U., Haider, M.S., Ali, M., Ali, A., Sajjad, M., 2017. Grain discoloration: An emerging threat to rice crop in Pakistan. Journal of Animal and Plant Sciences 27(3).
- Ashwini, J.H., Hiremath, S., Muttappagol, M., Nandan, M., Bharath, M., Shankarappa, K.S., Lakshminarayana Reddy, C.N., 2025. Screening of potential endophytes against fungal pathogens, *Curvularia lunata*, *Bipolaris oryzae* and *Pyricularia setariae* using in vitro and computational approaches. Journal of Phytopathology 173(2), e70050.
- Asif, S., Nisar, M., Ullah, S., Naeem, M., 2025. Reviewing the impact of seed-borne mycoflora on mycotoxin accumulation: A threat to lentil genetic resources. Toxicon, 108290.
- Barnwal, M.K., Kotasthane, A., Magculia, N., Mukherjee, P.K., Savary, S., Sharma, A.K., et al., 2013. A review on crop losses, epidemiology and disease management of rice brown spot to identify research priorities and knowledge gaps. European Journal of Plant Pathology 136, 443-457.
- Belete, T., Boyraz, N., 2019. Biotechnological tools for detection, identification and management of plant diseases. African Journal of Biotechnology 18(29), 797-807.
- Bello, G.D., Sisterna, M., 2010. Use of plant extracts as natural fungicides in the management of seedborne diseases. In: Management of Fungal Plant Pathogens. CABI, Wallingford, United Kingdom, pp. 51-66.
- Bhardwaj, S., 2025. Integrated disease management: Combining biological, cultural, and chemical approaches. Contemporary Issues in Plant Pathology: Research and Perspectives p, 34.
- Bhuyan, G.V., Deka, N., Bhagabati, A.K., 2024. Rice farming in Assam (India): Ecology, tradition, and transformation. Springer Nature 189-207.
- Carrell, A.A., Lawrence, T.J., Cabugao, K.G.M., Carper, D.L., Pelletier, D.A., Jawdy, S., et al., 2020. *Sphagnum* peat moss thermotolerance is modulated by the microbiome. bioRxiv. <https://doi.org/10.1101/2020.08.21.259184>
- Chen, B., Chen, Y., Chen, H., Liang, Z., Chen, J., Wu, R., Zhang, T., Zhou, G., Yang, X., 2023. Identification, characterization and prevalence in southern China of a new iflavirus in the leafhopper *Recilia dorsalis* (Hemiptera: Cicadellidae). Virus Research 323, 199005.
- Cheng, J., Li, X., Mi, Y., Hu, Y., Cui, L., 2025. First report of *Curvularia dactylocteniiicola* causing *Curvularia* leaf spot of maize in China. Plant Disease. Advance Online Publication.
- Cucu, M.A., Choudhary, R., Trkulja, V., Garg, S., Matić, S., 2025. Utilizing environmentally friendly techniques for the sustainable control of plant pathogens: A review. Agronomy 15(7), 1551.
- Detmann, K.C., Araújo, W.L., Williams, T.C., DaMatta, F.M., 2024. Silicon-mediated resistance in rice against foliar and grain pathogens: A physiological perspective. Plant Physiology and Biochemistry 196, 107-118.
- Disanayaka, D.M.S.A., Ferdinandez, H.S., Yapa, P.N., Wijesinghe, M.M., Manamgoda, D.S., 2025. First report of *Curvularia chiangmaiensis* on *Oryza rufipogon* (wild *Oryza* spp.) in Sri Lanka.
- Dutta, P., Deb, L., Pandey, A.K., 2022. *Trichoderma*-From lab bench to field application: Looking back over 50 years. Frontiers in Agronomy 4, 932839.
- Ehsan, S., Qureshi, A., Chaudhary, N., Ali, A., Niaz, A., Javed, H., Ijaz, F., Anwar, S.A., 2023. Effect of fluorescent-producing rhizobacteria on cereal growth through siderophore exertion. Journal of Applied Research in Plant Sciences 4(02), 601-611.
- EPBDT, 2025. Economic Policy and Business Development Think Tank. Pakistan, s rice sector: Economic policy and business development report. <https://epbdt.org.pk/wp-content/uploads/2025/03/rice.pdf>
- FAO, 2024. Food and Agriculture Organization. GIEWS country brief: The Islamic Republic of Pakistan.
- FAO, 2025. OECD-FAO Agricultural Outlook 2025-2034. OECD Publishing.
- Ferdinandez, H.S., Adhikari, T., Mew, T.W., 2021a. First report of *Curvularia lunata* as a causal agent of grain discoloration in rice (*Oryza sativa*) in Sri Lanka. Sri Lankan Journal of Agriculture and

- Ecosystems 3, 45-58.
- Ferdinandez, H.S., Manamgoda, D.S., Udayanga, D., Deshappriya, N., Munasinghe, M.S., Castlebury, L.A., 2021b. Molecular phylogeny and morphology reveal three novel species of *Curvularia* (Pleosporales, Pleosporaceae) associated with cereal crops and weedy grass hosts. *Mycological Progress* 20, 431-451.
- Garcia-Aroca, T., Doyle, V., Singh, R., Price, T., Collins, K., 2018. First report of *Curvularia* leaf spot of corn, caused by *Curvularia lunata*, in the United States. *Plant Health Progress* 19, 140-142.
- Gebeyaw, M., 2020. Review on: Impact of seed-borne pathogens on seed quality. *American Journal of Plant Biology* 5, 77-81.
- GOP, 2023. Government of Pakistan, Ministry of National Food Security and Research, Economic Wing, 2023. Crops area and production (district wise) 2022-3. Islamabad, Pakistan.
- Gore, B., Shishupala, S., 2025. Diversity assessment of *Curvularia* species through morphological, physiological, pathological and metabolomic analyses. *Microbiology Research Journal International* 35, 152-172.
- Guo, Z.J., Amenyogbe, M.K., Chen, S.Q., Rashad, Y.M., Deng, J.X., Luo, H., 2025. Morphological and phylogenetic analyses reveal two novel species of *Curvularia* (Pleosporales, Pleosporaceae) from southern China. *MycKeys* 120, 139.
- Haque, M.A., Rafii, M.Y., Yusoff, M.M., Ali, N.S., Yusuff, O., Datta, D.R., Anisuzzaman, M., Ikbal, M.F., 2021. Recent advances in rice varietal development for durable resistance to biotic and abiotic stresses through marker-assisted gene pyramiding. *Sustainability* 13, 10806.
- Heinrichs, E.A., Muniappan, R., 2017. IPM for tropical crops: Rice. *CABI Reviews* 12, 1-31.
- Hoang, A.T., Lam, T.T., Thi, H.T.P., Nguyen Thi, H., Pham, H.P., Doan Thi, L., Do, A.D., 2025. Identification of *Nigrospora sphaerica* and *Curvularia lunata* as causal agents of leaf spot disease in cantaloupe (*Cucumis melo*) in southern Vietnam. *Australasian Plant Pathology* 54, 1-10.
- Honger, J.K., Lamptey, J.N., Ennin, S.A., 2022. Characterisation of *Curvularia lunata*, the causal agent of brown leaf spot disease of rice in Ghana. *Agricultural and Food Science Journal of Ghana* 15, 1420-1432.
- Islam, W., Ahmed, M., 2017. Identification of different fungi associated with grain discoloration complex disease of rice and management of infested grains through fungicides. *International Journal of Scientific Research in Agricultural Sciences* 4, 30-35.
- Jatoi, G.H., Abro, M.A., Memon, S., Hussain, S., Mangi, N., Maari, S.A., 2015. Efficacy of different botanical extracts on the linear colony growth of *Helminthosporium oryzae*. *European Academic Research* 3, 8383-8397.
- Jatoi, G.H., Abro, M.A., Tariq, J.A., Memon, S., Mangi, N., Keerio, A.U.D., Qiu, D., 2016b. Screening of potential bacterial biocontrol agents against *Helminthosporium oryzae* under in vitro conditions causing brown spot of rice. *Pakistan Journal of Biotechnology* 13, 95-100.
- Jatoi, G.H., Abro, M.A., Tariq, J.A., Memon, S., Mangi, N., Kerio, A.U.D., Menga, A.S., 2016c. Efficacy of selected fungicides on the linear colony growth of *Helminthosporium oryzae* causing brown spot disease of rice. *Pakistan Journal of Biotechnology* 13, 13-17.
- Jatoi, G.H., Bhatti, A.G., Hidayatullah, S.M., Bhatti, M.U., Abro, M.A., Memon, S., 2016a. Rhizobacteria associated with rhizospheric soil and their antifungal activity against brown spot fungus (*Helminthosporium oryzae*). *Science International (Lahore)* 28, 4119-4122.
- Jatoi, G.H., Keerio, A.U., Abdulle, Y.A., Qiu, D., 2019. Effect of selected fungicides and biopesticides on the mycelial colony growth of *Helminthosporium oryzae*, the causal agent of brown spot of rice. *Acta Ecologica Sinica* 39, 456-460.
- Kamaluddeen, S., Simon, S., Lal, A.A., 2012. A new blight disease of rice caused by *Curvularia lunata* from Uttar Pradesh. *Journal of Biopesticides* 5, 112-114.
- Khan, M., Nizamani, Z.A., Pussio, G.B., Rahim, H., 2025b. Integrated study on the etiology and in vitro fungicidal management of false smut disease in rice. *Journal of Applied Research in Plant Sciences* 6, 56-62.
- Khan, M.F.A., Riaz, A., Ahsan, R., Ahmad, I., Ullah, S., Raza, A., Zakria, M., 2025a. Genetic variability among isolates of *Curvularia lunata* and *Exserohilum rostratum* causing brown leaf spot of rice from Pakistan. *Current Microbiology* 82, 436.
- Khatun, M.S., Rayhan, M.A., Aktar, P., Sikder, M.M., Alam,

- N., 2025. *Curvularia geniculatus* associated with garlic leaf blight disease: Molecular identification, mycelial growth, and biological control. Plant Tissue Culture and Biotechnology 35, 335-346.
- Khemmuk, W., Shivas, R.G., Henry, R.J., Geering, A.D., 2016. Fungi associated with foliar diseases of wild and cultivated rice (*Oryza* spp.) in northern Queensland: Khemmuk W. et al. Australasian Plant Pathology 45(3), 297-308.
- Khoo, S.S., Zakaria, L., Cheng, A., 2022a. First report of *Curvularia lunata* causing leaf spot on *Oryza sativa* in Sabah, Malaysian Borneo. Plant Disease 106, 764.
- Khoo, Y.W., Tan, H.T., Khaw, Y.S., Li, S.F., Chong, K.P., 2022b. First report of *Lasiodiplodia theobromae* causing leaf spot on *Aloe vera* var. *chinensis* in Malaysia. Plant Disease 106, 2258.
- Khunnamwong, P., Lertwattanasakul, N., Jindamorakot, S., Suwannarach, N., Matsui, K., Limtong, S., 2020. Biocontrol of rice seedling rot disease caused by *Curvularia lunata* by epiphytic yeasts. Microorganisms 8, 647.
- Kusai, N.A., Azmi, M.M.Z., Zulkifly, S., Yusof, M.T., Zainudin, N.A.I.M., 2015. Morphological and molecular characterization of *Curvularia* and related species associated with leaf spot disease of rice in Peninsular Malaysia. Rendiconti Lincei. Scienze Fisiche e Naturali 27, 205-214.
- Limonard, J., 1968. A modified blotter test for seed health. Proceedings of the International Seed Testing Association 33, 1-8.
- Limtong, S., Into, P., Attarat, P., 2020. Biocontrol of rice seedling rot disease caused by *Curvularia lunata* and *Helminthosporium oryzae* by epiphytic yeasts from plant leaves. Microorganisms 8, 647.
- Listihani, L., Selangga, D.G.W., Yuliadhi, K.A., Yuniti, I.G.A.D., Ariati, P.E.P., 2024. Molecular characterization of Rice ragged stunt virus and Rice grassy stunt virus on rice in Gianyar, Bali, Indonesia. Journal of Tropical Plant Pest Disease 24, 48-57.
- Lu, Zhixiang, Lin Shang, Shaoqing Wang, Xinhua Wang, Yaqian Li, Shunping Zhang, Jing Wang, and Jie Chen., 2025. Pathogenic roles of polyketide synthase CLPKS18 and (R)-(-)-mellein from *Curvularia lunata* in maize leaf spot. Journal of Fungi 11, 627.
- Maharjan, E., Jain, D., Wong, M. Y., Adhikari, R., Joshi, D. R., 2025. *In vitro* antagonistic effects of *Bacillus* species against phytopathogenic fungi. Nepal Journal of Biotechnology 13, 35-44.
- Majeed, R. A., Shahid, A. A., Ashfaq, M., Saleem, M. Z., Haider, M. S., 2016. First report of *Curvularia lunata* causing brown leaf spots of rice in Punjab, Pakistan. Plant Disease 100, 219.
- Manzar, Nazia, Abhijeet Shankar Kashyap, Avantika Maurya, Mahendra Vikram Singh Rajawat, Pawan Kumar Sharma, Alok Kumar Srivastava, Manish Roy, Anil Kumar Saxena, and Harsh Vardhan Singh., 2022. Multi-gene phylogenetic approach for identification and diversity analysis of *Bipolaris maydis* and *Curvularia lunata* isolates causing foliar blight of *Zea mays*. Journal of Fungi 8, 802.
- Miah, G., Rafii, M.Y., Ismail, M.R., Sahebi, M., Hashemi, F.S.G., Yusuff, O., Usman, M.G., 2017. Blast disease intimidation towards rice cultivation: A review of pathogen and strategies to control. Journal of Animal and Plant Sciences 27, 1058-1066.
- MoF, 2025. Pakistan Economic Survey 2024-25: Chapter 2 - Agriculture. Ministry of Finance, Pakistan.
- Muhammad, N., Ansar, W., Bashir, T., & Khan, H. R. (2026). *Bacillus*-derived antimicrobial peptides as alternatives to antibiotics in poultry: mechanisms, applications, and future prospects-a review. Archives of Microbiology, 208(8), 399.
- Naik, J.H., Pal, J., Amaresan, N., 2025. *Curvularia*. In: Compendium of Phytopathogenic Microbes in Agro-Ecology. Vol. 1. Fungi. Springer Nature Switzerland, Cham, pp. 199-.
- Namdeo Aiwaile, H., Sarnobat, D.H., Dhavale, M.C., 2025. Integrated pest and disease management (IPDM). In: Plant Health and Disease Management: A Modern Approach, p. 156.
- Naqvi, S.A.H., 2019. Bacterial leaf blight of rice: An overview of epidemiology and management with special reference to the Indian sub-continent. Pakistan Journal of Agricultural Research 32, 359.
- Nawaz, A., Tariq, J. A., Lodhi, A. M., Memon, R. M., 2020. Studies on characteristics of *Xanthomonas oryzae* isolates associated with rice crop. Journal of Applied Research in Plant Sciences 1, 30-35.
- Németh, M. Z., Kovács, G. M., 2025. A comprehensive guide to loop-mediated isothermal amplification, an emerging diagnostic tool for plant pathogenic fungi. Frontiers in Plant Science 16, 1568657.
- Notomi, T., Mori, Y., Tomita, N., Kanda, H., 2015. Loop-mediated isothermal amplification (LAMP):

- Principle, features, and future prospects. Journal of Microbiology 53, 1-5.
- Obeng, J., Adams, B., Azupio, S., Obeng, O. A., 2021. *In vitro* evaluation of commercial fungicide Othello® (Azoxystrobin and Difenconazole) against *Cocos nucifera* and *Elaeis guineensis* foliar pathogens. Sustainable Agriculture Research 10, 13-20.
- Ojha, S., Rana, P., Tiwari, R., 2025. A comprehensive review: The role of herbs in management of fungal infection. Current Clinical and Medical Education 3, 54-65.
- Palaki, V., 2015. Curvularia leaf spot of maize and its integrated management. M.Sc. (Agriculture) Thesis. University of Agricultural Sciences, Dharwad, Karnataka, India, pp. 60-81.
- Pandey, S., Singh, R. K., Singh, A. K., 2019. Sustainable rice production systems in Asia: Issues and challenges. Agriculture, Ecosystems and Environment 269, 71-80.
- Pankhurst, C.E., McDonald, H.J., Hawke, B.G., Kirkby, C.A., 2002. Effect of tillage and stubble management on chemical and microbiological properties and the development of suppression towards cereal root disease in soils from two sites in NSW, Australia. Soil Biology and Biochemistry 34, 833-840.
- Paulikienė, S., Benesevičius, D., Benesevičienė, K., Ūksas, T., 2025. Seed treatment: Importance, application, impact, and opportunities for increasing sustainability. Agronomy 15, 1689.
- Persaud, R., Khan, A., Isaac, W., Ganpat, W., Saravanakumar, D., 2019. Plant extracts, bioagents and new generation fungicides in the control of rice sheath blight in Guyana. Crop Protection 119, 30-37.
- Pramesh, D., Kirana, K., Prasannakumar, M.K., 2024. Characterization of fungal pathogens associated with brown spot disease of rice. Journal of Applied Biology and Biotechnology 12, 162-171.
- Ramírez-Olier, J., Trujillo-Salazar, J., Osorio-Echeverri, V., Jaramillo-Ciro, M., Botero-Botero, L., 2019. In vitro antagonism of *Trichoderma asperellum* against *Colletotrichum gloeosporioides*, *Curvularia lunata*, and *Fusarium oxysporum*. Revista UIS Ingenierías 18, 159-165.
- Rao, S.S., Kumar, M.R., Madhusudhan, P., Reddy, B.R., 2021. Comparative efficacy of different plant extracts on mycelial growth of *Curvularia lunata* (Wakker) Boedijn causing rice grain discoloration in vitro. The Pharma Innovation Journal 10, 1151-1155.
- Rashid, M.M., 2001. Detection of *Curvularia* species on Boro rice seeds of Dinajpur. Journal of Biological Sciences 1, 591-592.
- Riegler, A.N., Grayson, J.W., Greenway, J.W., Woodworth, B.A., McCarty, T.P., Pappas, P.G., Leal, S.M.Jr., 2025. Histopathologic insights into *Curvularia*-induced chronic granulomatous fungal sinusitis: A guide for surgical pathologists. Modern Pathology 100898.
- Santos, P.R., Lima, C.S., Adami, A.K., Rodrigues, J., Juliatti, F.C., 2018. Morphological and molecular characterization of *Curvularia lunata* pathogenic to forage grass. Bragantia 77, 326-332.
- Sarma, B., Kashtoh, H., Lama Tamang, T., Bhattacharyya, P.N., Mohanta, Y.K., Baek, K.H., 2023. Abiotic stress in rice: Visiting the physiological response and its tolerance mechanisms. Plants 12, 3948.
- Sepe, M., Daud, I.D., Gassa, A., Firdaus, 2020. Infectivity of *Beauveria bassiana* (Balsamo) against *Tribolium castaneum* (Coleoptera: Tenebrionidae). Journal of Applied Research in Plant Sciences 1, 53-58.
- Shaheen, S.S., Fatima, H., Khan, M., 2017. Technical efficiency analysis of rice production in Pakistan under dry and puddle conditions: A case study of selected districts of Punjab province, Pakistan. Sarhad Journal of Agriculture 33, 447-458.
- Sopialena, S., Sahid, A., Suryadi, A., Aditya, N., 2025. The effect of climate on the development of brown spot disease (*Curvularia oryzae*) in rice plants. BIO Web of Conferences 206, 06006.
- Tann, H., Soyong, K., 2017. Biological control of brown leaf spot disease caused by *Curvularia lunata* and field application method on rice variety IR66 in Cambodia. AGRIVITA Journal of Agricultural Science 39, 32-41.
- TDAP, 2024. Trade Development Authority of Pakistan. Rice export performance and quality standards.
- Tennant, P., Gubba, A., Roye, M., Fermin, G., 2018. Viruses as pathogens: Plant viruses. In: Tennant, P., Fermin, G., Foster, J.E. (Eds.), *Viruses*. Academic Press, Cambridge, MA, USA, pp. 135-156.
- USDA, 2024. Foreign Agricultural Service. World agricultural production: Rice production by country 2024/2025.
- Varshini, S., Ajaydesouza, V., Raja, J., 2025. Multifaceted investigation of *Curvularia lunata* in rice: Isolation, identification and grain spot disease pathogenicity. Plant Archives 25, 1-8.
- Vishwakarma, S.K., Manzar, N., Kashyap, A.S., 2025. A

- systematic approach for the detection and management of rice brown spot disease. In: Detection, Diagnosis and Management of Air-Borne Diseases in Agricultural Crops. Springer Nature Singapore, Singapore, pp. 317-339.
- Wang, S., Lu, Z., Lang, B., Wang, X., Li, Y., Chen, J., 2022. *Curvularia lunata* and *Curvularia* leaf spot of maize in China. ACS Omega 7, 47462-47470.
- Wolfe, D.W., Ziska, L., Petzoldt, C., Seaman, A., Chase, L., Hayhoe, K., 2008. Projected change in climate thresholds in the Northeastern U.S.: Implications for crops, pests, livestock, and farmers. Mitigation and Adaptation Strategies for Global Change 13, 555-575.
- Wu, W., Zhang, Y., Jiao, G., Wei, X., 2024. Progress in understanding and enhancing rice tolerance to biotic and abiotic stresses. Plants 13, 3206.
- Xuan, T.H., Gergon, E.B., 2018. Strategies for the management of rice pathogenic fungi. In: Fungi, pp. 396-431.
- Yu, J., 2025. Chemical composition of essential oils and their potential applications in postharvest storage of cereal grains. Molecules 30, 683.
- Zhou, X., El-Sappah, A.H., Khaskhoussi, A., Huang, Q., Atif, A.M., Elhamid, M.A.A., Tahri, W., 2025. Nanoparticles: A promising tool against environmental stress in plants. Frontiers in Plant Science 15, 1509047.

Publisher's note: EScience Press remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.



Open Access: This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license and indicate if changes were made. The images or other third-party material in this article are included in the article's Creative Commons license, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons license and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this license, visit <http://creativecommons.org/licenses/by/4.0/>.