



REVIEW ARTICLE

An interpretative review on a catastrophic pathogen *Bipolaris oryzae* causing rice brown spot disease

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Abstract

Bipolaris oryzae, (Telomorph: *Cochliobolus miyabianus*) the pathogen responsible for rice brown spot disease, had a significant historical impact, notably contributing to the Bengal famine of 1943, which resulted in reduced rice yields and approximately 3 million deaths from starvation. As a polycyclic pathogen, *B. oryzae* spreads through seeds and airborne conidia (anamorphic stage), causing secondary infections in both nurseries and fields. Seed-borne infections worsen disease severity, while airborne conidia accelerate disease spread. *B. oryzae* shows variability in colony characteristics influenced by growth medium, geography and environmental conditions. Its morphological variability, including a range of conidial sizes, shapes and colors, increases its resilience and ensures its survival across diverse environments. Additionally, the pathogen's molecular variability allows it to adapt and overcome plant resistance mechanisms. *B. oryzae* produces host-specific toxins, such as cochliobolin and ophiobolin, which disrupt plant defense mechanisms and inhibit growth, particularly affecting roots, coleoptiles and leaves. Due to its broad adaptability to different climates, it remains a persistent and resilient threat in rice-growing regions worldwide. Epidemiological studies offer valuable insights into the pathogen's initiation, survival and distribution. This review highlights the importance of understanding the pathogen's variability, toxicity and mechanisms of disease spread, all of which complicate control efforts. Effective integrated management strategies are essential to mitigate the devastating impact of rice brown spot disease on global rice production.

Keywords: *Bipolaris oryzae*; epidemiology; integrated disease management; pathogen variability; rice brown spot; toxicity

Introduction

Rice (*Oryza sativa* L.) is a vital staple crop, providing essential calories and nutrients to more than half of the global population. It plays a particularly crucial role in Asia, where most rice cultivation and consumption occur (1). India is a major player in the global rice market, contributing approximately 40 % of worldwide rice exports, reaching over 150 countries. Often referred to as the "grain of life" (2), rice is central to food security. Rice cultivation, though crucial, encounters a variety of challenges, including both biotic and abiotic factors. One of the most severe threats is rice brown

spot (RBS), a disease caused by the fungal pathogen *Bipolaris oryzae*, which is also known as sesame leaf spot or Helminthosporiosis. RBS impacts rice at every growth stage, from seed to grain, making it one of the most significant challenges to rice production (3). Historically, RBS has caused significant crop losses, including two major epidemics in India: one in 1918-1919 in the Krishna-Godavari delta and another in 1942, which affected both India and Bangladesh. The latter epidemic led to yield losses of 50-90 % and is linked to the Great Bengal Famine, resulting in an estimated 2 million deaths due to food shortages (4).

The pathogen *B. oryzae* produces toxins that spread via contaminated seeds and airborne spores. As a polycyclic pathogen, it can complete multiple infection cycles within a single growing season, contributing to its persistence and spread (5). Its high variability and adaptability make it a challenging pathogen for rice growers, complicating disease management efforts (6).

First documented in Indonesia in 1900 (7), RBS has since become a widespread issue worldwide. In India, the disease is prevalent across several states, including Assam, West Bengal, Bihar, Chhattisgarh, Jharkhand, Madhya Pradesh, Odisha, Andhra Pradesh, Tamil Nadu and Karnataka (5). It is especially common in regions where susceptible rice varieties are grown, with high incidence rates recorded in these areas (8). Surveys have shown that RBS severity peaks during critical crop stages, emphasizing the need for timely and targeted management strategies.

Effective management of RBS requires a multifaceted approach, including the development of resistant rice varieties, judicious use of fungicides and the adoption of Integrated Disease Management (IDM) strategies. Ongoing global research is essential to further our understanding of the pathogen's biology and epidemiology, identify sustainable control measures and ensure food security in rice-dependent regions. This review underscores the importance of managing RBS to meet the growing global demand for rice and mitigate its economic and social impacts.

Occurrence of rice brown spot disease

Rice brown spot (RBS) disease poses a significant global challenge to rice cultivation. Initially documented in Indonesia in 1900 (7), it has since spread to numerous regions, severely impacting rice production worldwide. The disease affects major rice-growing areas, including Southeast Asia, Africa and the Americas. In Uganda, seed infection rates range from 3 % to 94 % (9), while Morocco reports a 31 % infection rate (10). Thailand experienced notable losses in 2005 due to multiple forms of infection (11).

In Brazil, the presence of *B. oryzae* in seed-borne inoculum has exacerbated disease severity, particularly before flowering (12). Similarly, in Paraguay, a 2014-2015 survey reported an average disease incidence of 30-40 % (13). Higher disease severity has also been observed in Pakistan's Sheikhpura district (14), while in Kenya, RBS is endemic, especially affecting low-input agricultural systems and stressed crops (15). The disease remains widespread in major rice-growing regions such as Southeast Asia, Africa, Russia, Saudi Arabia and the Americas (16).

In India, RBS was first documented in Tamil Nadu in 1919 and has since been reported in multiple states (5, 7). Severe yield losses of up to 90 % have been recorded in Madhya Pradesh (17), while in Karnataka, the highest disease severity was observed in Mandya taluk (18). In Panagar village, Madhya Pradesh, disease prevalence ranged from 3 % to 25 % (19). In Jammu and Kashmir, a 2018-2019 survey reported incidence rates ranging from 32.65 % to 74.51 % (20). In Tamil Nadu, a 2019-2020 survey found severity rates as high as 35.89 % in Nagapattinam district (21). Additionally, RBS reported 35 % infection in

Sirgazli, Mayiladhurai district (22). Cuddalore and Vellore districts exhibited the highest disease severity, with nearly 35 % incidence.

The pathogen *B. oryzae* infects rice plants at all stages of growth, leading to a wide range of characteristic symptoms. These include leaf spots, reduced tiller number, stunted root and shoot growth, grain chaffiness, stalk rot and grain discoloration (24). Infected plants exhibit distinct oval or eye-shaped lesions on the leaf blades. Smaller lesions are dark brown, while larger lesions transition from dark brown at the edges to pale yellow or dirty white in the centre (7). As the disease progresses, lesions may merge and develop a chlorotic halo (25), eventually causing the affected leaves to brown and dry out.

B. oryzae infects various parts of the rice plant, including foliage and parts of the inflorescence (7). Symptoms on the foliage are most pronounced, with lesions appearing on the coleoptile, leaf blades, leaf sheaths and glumes. The leaf spots vary in size and shape, typically brown with a gray or whitish centre, often oval or cylindrical, resembling sesame seeds and surrounded by a yellow halo in the early stages. Young spots are small, circular and may appear dark brown or purplish (13). The pathogen is also responsible for grain discoloration in rice (26), with infected seeds producing diseased seedlings that show discoloration and shrivelling (27). Black spots develop on glumes and spread, causing severe discoloration and shrinkage of seeds from infected plants (19) (Fig. 1-3).

A distinctive symptom produced by the pathogen is a light reddish-brown lesion with a gray centre, surrounded by a dark to reddish-brown margin and a bright yellow halo (23). In addition to its visible effects, *B. oryzae* significantly impacts the plant's physiological processes, including carbon assimilation, transpiration and ionic composition (28). The infection leads to increased susceptibility over time, exacerbating disease severity. This affects leaf physiology by damaging cells down to the membrane level, resulting in elevated levels of malondialdehyde (MDA) and electrolyte leakage (EL), along with reduced transpiration, photosynthesis, stomatal conductance, mesophyll potential and light harvesting capacity (29).

Pathogen: *Bipolaris oryzae*

Rice Brown Spot (RBS), caused by the fungal pathogen *B. oryzae*, is a major threat to rice production worldwide. The disease spreads primarily through contaminated seeds and airborne spores. *B. oryzae* is a polycyclic pathogen, producing enormous asexual conidia capable of initiating secondary infections in both nursery and main fields, which contributes to significant yield losses (30). Notably, the pathogen's airborne spores exhibit a circadian rhythm in their dispersal, enhancing their persistence and facilitating the wide geographical spread of the disease across rice-growing regions.

Taxonomically, *B. oryzae* has undergone several reclassifications over time. It was initially described in 1900 as *Helminthosporium oryzae* by Breda de Haan. In 1966, it was reclassified as *Drechslera oryzae* by Subramanian and Jain, placing it within the *Drechslera* genus. However, the



Fig. 1. Severe occurrence of rice brown spot disease at field.



Fig. 2. Panicle infection.



Fig. 3. Grain infection.

currently accepted binomial name, *Bipolaris oryzae* (Breda de Haan) Shoemaker, was proposed in 1959 and is now the standard nomenclature. The sexual stage of *B. oryzae*, initially identified as *Ophiobolus miyabeanus* by Ito and Kuribayashi in 1927, was later placed in the genus *Cochliobolus* by Drechsler in 1934. This stage is now classified as *Cochliobolus miyabeanus* (Ito and Kuribayashi) Drechsler ex Dastur. The sexual morph of *B. oryzae*, known as *Cochliobolus miyabianus*, is not commonly found in nature but is occasionally induced under laboratory conditions. Since this pathogen infects through its asexual conidia, it is referred to as *B. oryzae* rather than

C. miyabianus. These taxonomic revisions reflect ongoing efforts to clarify the genetic diversity and ecological impact of this pathogen in agricultural systems.

Morpho cultural variability of *B. oryzae*

B. oryzae exhibits considerable diversity in its morphological and cultural characteristics as evidenced by various studies. Earlier studies (1, 13, 20, 23, 31) have highlighted substantial variations among isolates, including differences in size, color, conidial structure and modes of infection. The sporophores of *B. oryzae* are described as robust and upright, geniculate at the base and emerging in clusters of 3-5 conidia through stomata (32). *B. oryzae* populations is classified 52 isolates based on their mycelium color (blackish, grey, white), growth texture (fluffy or cottony) and spore dimensions (length from 5.34 to 7.48 μm , width from 4.10 to 5.51 μm), reflecting the phenotypic diversity.

The mycelial characteristics of *B. oryzae* have been extensively studied, revealing septate structures ranging in color from grey to dark greenish gray, with both inter- and intra-cellular growth patterns (13) (Fig. 4). This mycelium typically develops as light brown to black and displays branched structures, indicating its adaptability and complexity in colonizing and infecting rice tissues (21). The study by Nayak and Hiremath (33) provided further insights into morphological diversity, categorizing isolates based on colony characteristics, mycelial growth patterns, spore germination rates and detailed spore dimensions (length,



Fig. 4. *B.oryzae* vegetative structure (Mycelium).

width, number of septa), emphasizing the diversity and potential implications for pathogenicity and adaptation strategies. Another expanded classification of *B. oryzae* isolates was made into distinct groups based on mycelium color and growth patterns, including classifications such as black mycelium with fluffy growth and various shades of grey with cottony or suppressed growth. This systematic approach aids in understanding the range of morphological variations within the species and their relevance to disease epidemiology and management. The colony morphology, mycelial characteristics (including color and texture), sporulation behavior and conidial traits of *B. oryzae* isolates were independently detailed in previous literature (22). These studies collectively underscore the diversity and adaptability critical for developing effective disease management strategies and conducting genetic studies in this pathogenic fungus.

Conidial variability of *B. oryzae*

B. oryzae exhibits considerable variability in its sporulation and morphological characteristics, which are influenced by both the growth medium and geographical location. There are high levels of sporulation of *B. oryzae* was reported on potato dextrose agar (PDA) and malt extract agar after 96 hrs of incubation at 28 °C in previous investigations (1, 3). *B. oryzae* isolates can produce black-colored, fluffy growth with significantly higher conidial production (35). It was found that sporulation was particularly abundant when cultured on rice polish agar medium in the earlier scientific studies (34).

Microscopic analysis reveals that *B. oryzae* conidia are typically fusiform or obclavate, (Fig. 5) widest at the middle and tapering towards both ends, with a minute papilla-like hilum and 6-14 distosepta. The conidia range in size from 63 to 153 µm in length and 13 to 22 µm in width (36). They are often curved and pale to mid-golden brown in color, with 5 to 6 septa and a visible hilum. Notably, there is considerable size variation among isolates, which may be linked to differences in the environmental conditions or geographical location of the isolates (1, 3, 31, 33, 34).



Fig. 5. Mature conidia.

A defining feature of *B. oryzae* is the bipolar germination (Fig. 6) of its conidia, a characteristic that is essential for its taxonomic classification (35). The fungus produces conidiophores that can be either solitary or grouped, with structures that are either straight or flexuous and range in color from pale to medium brown. These conidiophores are the sites of conidia production. Interestingly, the dimensions of the conidiophores vary significantly across different geographical regions. For example, conidiophores in Japan measure 68-688 x 7.6-20 µm, while those from India range from 70-175 x 5.6-7 µm. Chinese specimens show conidiophore sizes of 99-345 x 7-11 µm and those from the USA range from 150-600 x 4-8 µm. The conidia themselves exhibit a distinct morphology, appearing club-shaped to cylindrical, with a curved form and a light to golden brown color. Typically, they contain 6-13 transverse septa (13).

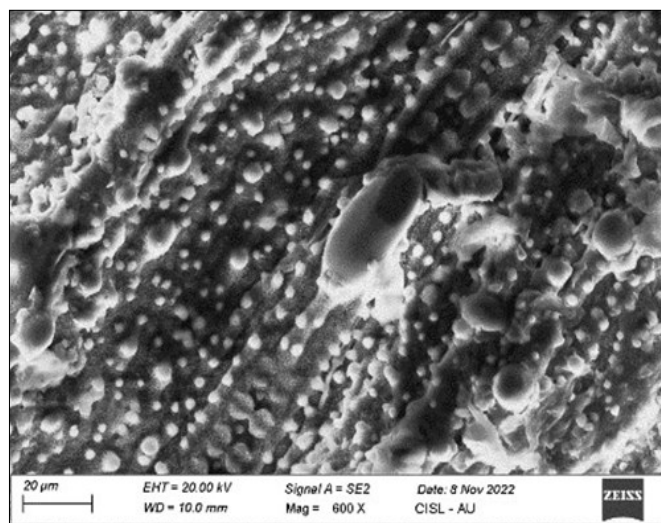


Fig. 6. SEM image of *B. oryzae* bipolar germinating conidia.

Molecular variability of *B. oryzae*

Recent advancements in DNA sequencing and phylogenetic analysis techniques have greatly enhanced our understanding of the genetic variability within *B. oryzae* populations. Significant contributions were made in their populations by employing variable number tandem repeat (VNTR) analysis, which categorized 152 *B. oryzae* samples into 12 distinct genetic groups, revealing substantial genetic diversity within the pathogen (37). Similarly, 36 isolates of *B. oryzae* from different regions of India were examined using various molecular markers, including universal rice primers (URPs), random amplified polymorphic DNA (RAPD) and inter-simple sequence repeats (ISSR). Their study highlighted significant regional genetic differences among the *B. oryzae* populations (38).

UPGMA clustering was employed to analyse genetic variations among *B. oryzae* isolates, observing variability levels ranging from 50 % to 91.6 % (39). Their analysis classified the isolates into two primary genetic clusters, each containing several subgroups based on ITS sequencing. REP-PCR (repetitive element sequence-based PCR) technique was executed to assess genetic diversity, producing dendrograms that illustrate the genotypic relationships among different *B. oryzae* isolates in another study (40). Further investigations have used the ITS1 and ITS4 primers to classify *B. oryzae* isolates.

Nayak and Hiremath (33) clustered ten isolates into distinct phylogenetic groups based on a 600 bp DNA amplicon. Identification of 570 bp fragment in five isolates and 500 bp gene product in another *B. oryzae* isolates (41, 42). More recently, characterization of 77 isolates of *B. maydis* was also carried out using ribosomal markers and protein-coding genes, revealing detailed genetic relationships (43). The brown spot isolates were grouped into two major clusters based on phylogenetic analysis (44). The study revealed a high degree of genetic and morphological variability among the isolates collected from the Cauvery Delta region of Tamil Nadu (44).

Epidemiology

Extensive studies have been conducted on the life cycle and spread of *B. oryzae* in rice crop (7). The pathogen's sporulation process is influenced by alternating periods of light and darkness, with near-ultraviolet radiation promoting growth, while blue light suppresses it. *B. oryzae* thrives at temperatures between 27 °C and 30 °C, with conidial germination occurring most effectively in the 25 °C to 30 °C range (7). Remarkably, the conidia exhibit broad adaptability to varying pH levels, germinating in environments with pH values ranging from 2.6 to 10.9. However, they prefer slightly alkaline conditions with a pH between 6.8 and 7.0 (45).

It was found that the incidence and severity of brown spot were higher under lowland flooded conditions compared to upland areas in Cameroon (46). As a necrotrophic pathogen, *B. oryzae* spreads rapidly under continuous rain, cloudy weather and high daytime temperatures. For successful establishment, the host leaf must remain wet for 8 to 24 hrs. Conidial formation occurs between 5 °C and 38 °C, with optimal conditions around 25 °C (1).

The severity of RBS disease, measured by the Percent Disease Index (PDI), across two seasons: Kharif (April–July 2019) and Rabi (August–December 2019) was studied in Thiruvallur District, Tamil Nadu (13°7'48"N, 79°46'30"E) (47). Their findings revealed a higher PDI during the Rabi season (PDI = 46.35) compared to the Kharif season (PDI = 26.36). In both seasons, PDI increased in the second month of crop growth, which coincided with the transplanting age.

The incidence of RBS disease (8) showed significant variation in relation to annual rainfall, with higher disease incidence observed at 410.5 mm of rainfall compared to 502 mm. Despite ongoing efforts, *B. oryzae* remains challenging to control, partly due to its preference for environments with specific conditions, such as water scarcity and imbalances in plant mineral nutrition. The disease is particularly prevalent in nutrient-deficient soils, especially those with low pH and poor nutritional profiles, where it can reach epidemic levels (48).

There was a positive correlation between disease intensity and the levels of nitrogen (N), phosphorus (P) and manganese (Mn) in rice plants, while negative correlations were observed with calcium (Ca), magnesium (Mg), potassium (K), as well as the ratios of K/N and Fe/Mn (49). Deficiencies in nitrogen or potassium were linked to increased disease intensity (48). *B. oryzae* particularly thrives in environments with limited water availability and nutritional imbalances, especially nitrogen deficiency (50).

Toxin analysis of *B. oryzae*

The production and characterization of toxins by *B. Oryza* have been the focus of extensive research, revealing a variety of biologically active compounds. The 14C toxin produced by *B. oryzae* was first identified (51) through ethanol extraction of culture filtrates followed by thin-layer chromatography. Copper oxychloride was found to fully neutralize the toxin produced by *B. oryzae* (52). Further research identified two key compounds associated with this pathogen: cochliobolin and ophiobolin. Cochliobolin was isolated from culture filtrates, while ophiobolin was extracted from infected rice leaves. Both compounds were shown to inhibit rice plant growth, particularly affecting root, coleoptile and leaf development (7). Studies of host-specific toxins secreted by *B. oryzae* have provided deeper insights into their mechanism of action. These toxins elicit the characteristic symptoms of brown spot disease by disrupting the plant's defense mechanisms, notably reducing phenolic content and inhibiting the activity of phenylalanine-ammonia lyase in the host plant (24).

A total of six toxins from the Ophiobolin family were identified as being produced by *B. oryzae* in the earlier studies (53). Among these, ophiobolin A and ophiobolin B were particularly noted for their role in the infection process, aiding in the germination of fungal spores on the surface of rice leaves.

Recent advancements in high-performance liquid chromatography (HPLC) have refined the identification and characterization of *B. oryzae* toxins. A high-purity peak in HPLC analysis of a compound namely 'bipolaroxin' was discovered from *B. sorokiniana* in HPLC analysis and its was studied using Proton NMR or hydrogen-1 NMR) H-NMR studies (54). A potent bioactive molecule, ophiobolin A, isolated from *B. oryzae* liquid cultures has significant toxic effects (7). The HPLC analysis on six *B. oryzae* isolates, revealing a consistent peak corresponding to a toxin, which facilitated further investigation into its toxicological properties in the past scientific investigation (34). The significant toxicity of ophiobolin A, a secondary metabolite secreted by *B. oryzae* was also discovered from preceding literatures (55). Another compound namely, maydisone, an oxime polyketide isolated from *B. maydis* exhibited potent inhibitory effects against glucosidase (56). Ten ophiobolin-type sesterterpenes were identified from the endophytic fungus *Bipolaris* species TJ403-B1, with bipolarotoxin D demonstrating toxicity against other microbes, as revealed by detailed NMR studies (57).

Seed-borne infection of Rice Brown Spot disease

Seed-borne fungal pathogens pose significant challenges to global seed production, affecting various stages of plant development, from pre-emergence to post-emergence. These pathogens impact seedling vigor, germination rates and overall plant morphology (58). Research conducted in various regions has highlighted the prevalence of different fungal species in rice seeds.

B. oryzae was the most prevalent pathogen among six major fungal species isolated from 290 seed samples of 24 rice varieties, accounting for 58.62 % of the samples

collected from different districts of Tamil Nadu (59). Pantha and Yadav (2016) conducted a study in Hardinath, Dhanusha, Nepal, in 2014 to assess the infestation level of *Bipolaris oryzae* and identify seed-borne fungi using the standard blotter method. The predominant fungal species recovered included *B. oryzae*, *Pyricularia oryzae*, *Ustilaginoidea virens*, *Aspergillus flavus*, *Aspergillus niger*, *Curvularia oryzae*, *Rhizopus oryzae* and species of *Alternaria*, *Cercospora* and *Penicillium*. All tested rice genotypes were infected with these fungi, though the frequency of fungal association varied, ranging from 12 % to 96 % (60). Eight fungal genera were identified from 287 rice seed samples that are collected from different locations of Tamil Nadu (61). *B. oryzae* was found in 58.89 % of the samples. Three seed health testing methods were done on hybrid rice varieties and detected twelve pathogens, with *B. oryzae* and *Fusarium moniliforme* was identified as the most common species across all tested varieties (62). In a comprehensive study conducted in Burkina Faso, (63) analyzed 151 rice seed samples from various genotypes and locations, isolating thirty-seven fungal species across nineteen genera. *B. oryzae* was the most frequently isolated species, found in 84.1 % of the samples, followed by *Alternaria padwickii* (66.2 %), *Curvularia lunata* (51 %), *Fusarium moniliforme* (33.1 %), *Microdochium oryzae* (30.5 %) and *Pyricularia oryzae* (13.5 %). These fungal pathogens primarily persist and spread through conidia and mycelia on seeds and crop residues, causing significant damage during the seedling stage and leading to reduced rice yields (7).

Airborne infection of Rice Brown Spot disease

The environmental factors such as relative humidity, precipitation, wind speed during the kharif season and temperature in the rabi season significantly influenced the airspora percentage contribution of the *B. oryzae* pathogen, as determined by step-down regression analysis (64). Their study also observed distinct intra-diurnal patterns, with the highest airspora percentage contribution of *B. oryzae* occurring between 12 noon and 1 p.m. (55.64 %) during the rabi crop. In contrast, during the kharif crop, two peaks were noted: one at 10-11 a.m. (19.56 %) and another at 12 noon-1 p.m. (19.09 %).

The survival and dispersal of *B. oryzae* are most pronounced during the cooler seasons, although spores of the pathogen are present in the air year-round as secondary inoculum (65). A forecasting model was developed (66) that correlates airborne fungal spores of the *B. oryzae* pathogen with meteorological factors. Both rice production and the occurrence of brown spot (BS) were influenced by soil and climatic parameters (67). Rainfall ($R = 0.38$) and relative humidity ($R = 0.64$) were key factors contributing to BS occurrence and yield reduction. Additionally, wind speed ($R = 0.62$) and maximum air temperature ($R = 0.63$) were identified as major determinants affecting rice yields (67).

B. oryzae conidia was comprised 20.7 % of the total conidia from 20 different fungal species found in the aerospora (47). Their study revealed that pathogenic conidia were present in harvested rice fields during both the dry and wet seasons, although their numbers gradually declined over time. This decline suggests that the conidia

may serve as a potential source of infection for subsequent growing seasons.

In the infection process, noting that *B. oryzae* spores germinate and enter the coleoptile, releasing new spores as the rice plant grows. These new spores lead to secondary infections, causing the characteristic leaf spots. Over time, these spores can infect the leaves, panicles and eventually the grains, completing the pathogen's life cycle and facilitating its continued spread (68).

Management of Rice Brown Spot disease

Varietal reaction of different rice cultivars to Rice Brown Spot disease

The management of rice brown spot disease (RBS) involves a multifaceted approach that includes genetic diversity assessments and field evaluations of rice cultivars. Almost 24 rice varieties were assessed for their resistance to rice brown spot disease under natural conditions, using PDI and AUDPC values as key parameters for evaluation (69). AUDPC values are used to quantify the rate of disease progression over specific time intervals, such as weekly or fortnightly periods, while PDI values represent the disease severity at the time of observation. The relationship between AUDPC and PDI is directly proportional, meaning that as the PDI values increase, the AUDPC values also increase, reflecting greater disease severity and progression. Among these, BPT5204 exhibited the highest susceptibility, with AUDPC (Area under disease progress curve) values of 240.94 in 2022 and 238.85 in 2023, along with PDI (Percent disease index) values of 34.54 and 34.85, respectively. In contrast, Karuppukavuni demonstrated exceptional resistance, showing the lowest AUDPC values of 13.75 and 12.38, with PDI values of 4.21 and 5.28, respectively.

The significant impact of environmental factors and varietal susceptibility on RBS severity, revealing marked variations in disease incidence among different rice varieties (70). In Nepal, extensive screenings were conducted and identifying *HJ-G1* and *HJ-G2* were identified as moderately resistant to RBS, emphasizing the importance of genetic diversity in developing disease resistance strategies (4). Nepalese rice varieties were categorizing into resistant, tolerant and susceptible groups, with genotypes like Radha-4 and Kabeli demonstrating resistance to RBS (6).

There are 50 rice genotypes were evaluated and identified 11 sources of resistance to RBS, with moderate resistance being the most prevalent trait among the tested varieties (18). The role of biochemical defenses, noting that enzyme activities were associated with reduced RBS severity in varieties like PARC-7, compared to more susceptible strains (71). Twenty rice genotypes were screened for finding their resistance to RBS and identified Kathe Jhinuwa, Radha-4 and Sabitri as resistant varieties, in contrast to the susceptible ones.

Additional insights were provided into genetic resilience to identify the genotypes such as Gharib Siyah Reihani and Tarom Jolodar that consistently exhibited low infection rates throughout their growth stages (73). Previous research has further validated these findings with the genotype NR 2181-465-1-1-1-1, noting its effectiveness in reducing disease severity and lowering total AUDPC under field conditions (74).

Disease management through biocontrol agents

Chemical residues in the soil can suppress soil organisms, thereby disrupting the ecological balance and leading to soil degradation and reduced productivity. Similarly, chemical residues in the atmosphere can interfere with plant pollination, resulting in sterility and diminished reproductive success in plants. The irreversible consequences of the uncontrolled application of chemicals, such as pesticides and fungicides (16), pose significant risks to agricultural sustainability. In contrast, biocontrol strategies are increasingly recognized as viable alternatives for promoting sustainable agriculture. These methods offer environmentally benign alternatives to chemical pesticides while enhancing soil physical properties and supporting the chemical and biological integrity of the soil ecosystem. The use of biocontrol agents was an effective strategy for crop protection, utilizing both direct mechanisms like hyper parasitism and indirect methods that enhance plant defences (75).

Bacillus species are Gram-positive bacteria renowned for their persistent antagonistic activity against a wide array of plant pathogens. Due to their thick cell wall, characteristic of gram-positive bacteria, they are stable and resistant to environmental changes within their micro environment. These bacteria release their antagonistic compounds in a gradual manner, with an initial slow release followed by an increasing rate over time. This sustained release enhances their overall effectiveness, contributing significantly to disease management. BS 5 was identified as the most potent strain, with a 76.66 % inhibition of mycelial growth against 40 *Bacillus* strains in the in vitro bioactivity studies (76). This strain was found to possess nine antibiotic genes, including bacillomycin, bacilysin and iturin. The efficacy of the endophytic fungus *Trichoderma harzianum* KUFA0406 in controlling brown spot disease, was reported with a significant reduction of 39.23 % and 29.64 % when applied as fresh and dry formulations, respectively (77).

Disease management through botanicals (Plant based biopesticides)

In recent years, agricultural scientists have increasingly explored plant-derived compounds as eco-friendly alternatives to chemical fungicides. This trend is driven by the growing demand for sustainable agricultural practices that effectively control fungal diseases while minimizing environmental impact. *Azadirachta indica* (neem) is particularly notable for its broad-spectrum antifungal properties. The efficacy of 100 % aqueous neem extract was (78) demonstrated in inhibiting spore germination across various fungal species, establishing its potential as a versatile fungicide. Neem oil was found effective against *Helminthosporium oryzae*, a fungal pathogen that threatens rice crops, both in controlled experiments and field conditions (1). *Allium sativum* (garlic) extracts have also shown promising antifungal properties.

Aqueous garlic extract also inhibited *Fusarium equiseti* spore germination in previous experiments, suggesting its potential as a natural fungicide (78). Field evidence of garlic's effectiveness in reducing *Botrytis oryzae*-induced stalk rot in rice was also provided in the earlier scientific studies (32) and demonstrated its broad-spectrum

activity against *Botrytis oryzae* mycelial growth (18). *Calotropis procera* has been investigated for its biocontrol potential against seed-borne fungi. Ethanol extracts of *C. procera* leaf and latex showed a strong antifungal activity against common seed-borne fungi (79). The impact of *C. procera* extracts on the mycelial growth and sporulation of *Botrytis oryzae* isolates was also discovered in previous studies suggesting its potential as a biocontrol agent (80). Additionally, *Lawsonia inermis* and its derivatives have shown promising results against *Botrytis oryzae* (81).

Chemical management of Rice Brown Spot

The fungicide Armure 30EC (82) significantly reduced disease severity and increased grain yield. Rovral and Tall were found to be effective against brown spot during both the Boro and Aman seasons (83). High efficacy of propiconazole and hexaconazole was reported in controlling this disease (32). The effectiveness of a combination of Zineb + hexaconazole in reducing disease severity and increasing yield was also investigated in earlier experiments (84). The fungicides such as hexaconazole and propiconazole were also effectively controlled brown spot disease and boosted yield (85).

Propiconazole was found as the most effective fungicide in the Jammu sub-tropics, achieving 97 % inhibition at a concentration of 250 ppm (86). Other fungicides like Ridomil and Dithane M-45 were also effective at 50 ppm against *B. oryzae* (87). It was also reported that Difenconazole 25 % EC at a concentration of 200 ppm was the most effective in inhibiting fungal mycelial growth of *Bipolaris oryzae* (88). Mancozeb and Thiophanate methyl were effective at higher doses for inhibiting *B. oryzae* growth (89). The complete inhibition of *B. oryzae* was observed at concentrations of 1000 and 1200 ppm of ICF 310 (Mancozeb 68 % + Hexaconazole 4 %) (90).

Tilt and Proud were also found as the most effective fungicides against multiple rice diseases (91). Propiconazole was highly effective in reducing disease severity and increasing yield (92) and provides the highest disease reduction in field experiments (93). The combination of propiconazole and thiophanate methyl reduced disease incidence more effectively than solo applications (94). Finally, Difenconazole 25 % EC or Tebuconazole 25.9 % EC was recommended for effective in brown spot management and improved rice yield under field conditions (95).

Efficacy of integrated management of rice brown spot disease

Integrated Disease Management (IDM) is a comprehensive approach to managing plant diseases by combining multiple control strategies in a coordinated manner. The goal of IDM is to reduce disease incidence and severity while minimizing both environmental and economic impacts. It typically includes components such as prevention, cultural practices, resistant varieties, botanicals and biological control, chemical management, monitoring and early detection of diseases and forewarning of disease outbreaks.

Presently, the need for an integrated approach to disease management (31) was emphasized and demonstrated that administering two rounds of sprays with neem cake extract, *N. oleander* leaf extract and *T. viride* (Tv2) to rice plants at the initial onset of disease and again 15 days later

significantly reduced the incidence of brown spot by 70 %, 53 % and 48 %, respectively. In an *in vitro* study conducted by Lamsal, the efficacy of various chemical, botanical and biological treatments were assessed against brown spot disease in rice in Chitwan, Nepal (96). The findings indicated that seed treatment and foliar spray with neem oil-based products such as Nico-neem and locally available botanicals like Simali were effective for eco-friendly management of the disease, comparable to the chemical treatment Hinosan.

Conclusion

Rice brown spot disease, caused by *B. oryzae*, is a significant challenge to global rice production, causing notable reductions in both yield and quality across various regions. Its complexity arises from the wide range of morphological, cultural and molecular variability, in addition to its remarkable ability to adapt to various environmental stresses. These factors contribute to the difficulty in controlling the disease, which spreads through both seedborne and airborne transmission. As a result, managing this disease requires comprehensive strategies that address both modes of transmission.

Recent advances in molecular diagnostics and toxin analysis provide promising opportunities to enhance the understanding of *B. oryzae* at the genetic level. These technological advancements are pivotal for the development of more targeted and effective control measures. Moreover, the discovery of resistance genes in several traditional rice varieties presents a potential avenue for breeding rice cultivars with improved resistance, thus contributing to better disease management.

Integrated disease management (IDM) practices, including crop rotation, proper field sanitation and the use of resistant varieties, are crucial for reducing the spread and impact of the disease. The use of eco-friendly fungicides and biocontrol agents further complements these efforts by minimizing reliance on chemical treatments and enhancing sustainability. While seedborne transmission can be controlled using various methods, focusing on airborne transmission is essential for long-term disease management. Strengthening forewarning systems and improving our understanding of airborne inoculum pressure are vital for proactive control.

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Authors' contributions

SS served as the primary research candidate, overseeing the study's execution and contributing significantly to its development. SMS conducted the meteorological analysis, providing critical insights into weather-related factors affecting the study. APS was responsible for drafting the weather parameters, ensuring that environmental conditions were accurately documented and analyzed. SK took charge of formatting the manuscript, refining its structure and ensuring consistency in presentation.

SV contributed to the research by drafting the section on resistance breeding, detailing strategies to enhance plant resilience against diseases. TR focused on the botanicals disease management aspect, outlining the role of plant-based treatments in controlling plant pathogens. MV worked on the biocontrol management section, emphasizing the use of beneficial organisms for disease suppression.

SM was responsible for drafting the molecular diagnosis section, highlighting advanced diagnostic techniques used for pathogen identification. RB meticulously compiled and formatted the references, ensuring proper citation of relevant literature. RK played a dual role, drafting the phylogenetic studies section, which involved analyzing genetic relationships and also participating in the sequence alignment process.

JS contributed by drafting the manuscript, integrating various sections into a cohesive document. PB and KS played key roles in the overall study design and coordination, ensuring the research followed a structured approach and met its objectives effectively.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

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