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WHEAT BLAST: A LOOMING GLOBAL THREAT – THE URGENCY FOR PROACTIVE RESEARCH AND INTEGRATED MANAGEMENT STRATEGIES

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ABSTRACT

Despite being a critical staple crop essential to global food systems, wheat production is increasingly hindered by a wheat blast disease. This disease, caused by a unique fungal pathogen, has spread from South America to Asia and Africa. Wheat blast is characterized by distinct diamond-shaped lesions on leaves that lead to whiplike, bleached, shrunken spikes that result in loss of yield and diminished grain quality. The pathogen can spread quickly through infected seeds and airborne spores, making this disease a global pandemic. Apart from the obliteration of the productivity of the crops, wheat blasts also severely impact farmers and entire agricultural systems, mainly where wheat is their staple food. Recently, significant strides have been made toward understanding the complex relationship between the fungus and its host, resisting genes and developing better screening methods. Disease impacts can be reduced using chemical, structural and cultural practices alongside traditional breeding. Moreover, changing climate conditions, the evolution of the pathogen, and the development fungicide-resistant strains rationalize the need for more innovative and proactive approaches to research. This review sheds light on the wheat blast, biology, epidemiology, and the existing control measures while highlighting the gaps and the need for further research and coordinated efforts to avert a possible disaster at a global level regarding wheat cultivation.

Keywords: Wheat Blast, Fungal Pathogen, Food Security, Integrated Management, Resistance Breeding, Crop Protection

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1. INTRODUCTION

Wheat (*Triticum aestivum*) is a significant crop around the globe. It serves as a primary food source for over a billion people while being one of the most critical sources of dietary protein (Singh et al., 2023; Walkowiak et al., 2020). The global wheat production in 2023-24 was 793MT, showing an increase over the previous year's production of 779.6MT (Shahbandeh, 2025; Zardari et al., 2025). At the current rate of population growth around the globe, the need for food production is increasing at an extremely rapid rate, which makes wheat one of the most important crops in protecting food security today. However, wheat cultivation suffers from biotic as well as abiotic stresses. Droughts and extreme temperatures are examples of abiotic stresses, while fungal pathogens are examples of biotic stress (Umar et al., 2021). Wheat blast, which is caused by the ascomycete fungus, *Magnaporthe oryzae* pathotype Triticum (MoT), is among the most troublesome of these diseases, which can lead to significant crop loss (Surovy, 2024; Tembo et al., 2020).

Wheat blast disease was registered in 1985 in Brazil (de Campos Dianese et al., 2021). It has since spread to several South American countries, some Asian countries, and, more recently, African regions (Mahapatra et al., 2024; Tembo et al., 2020).

The disease is known for its diamond-shaped, water-soaked lesions, which cause necrosis. Later leaf and spike infection stages are characterized by eye-shaped necrotic spots and bleached spikes (Surovy, 2024). If these symptoms develop within critical crop growth stages, such as flowering, they can decrease grain quality and yield, and completely eradicate the harvest (Hossain, 2022).

The most recent studies have been directed towards the genetic resistance of wheat crops to blast infection. Several resistance genes, such as Rmg8 and RmgGR119, have been described to protect against some of the MoT isolates (Juliana et al., 2020; Yoshioka et al., 2024). The protective effectiveness of these genes is, however, undermined to some degree by environmental conditions and the pathogen's overriding virulence, which makes

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further investigations and the planning of durable resistance strategies all the more important (Hossain, 2022). The ability of wheat blast to become pandemic stems from a few converging factors: the ease with which *M. oryzae* Triticum can adapt and change genetically, the transformative effects of climate change towards certain regions, and the global exchange of agricultural products. All these phenomena indicate the growing necessity of an integrated solution to contain wheat blasts, which involves sophisticated breeding, intensive monitoring, and multilateral cooperation (Tembo et al., 2020).

With all the issues regarding this, this review attempts to analyze wheat blast by analyzing the pathogen's biology, distribution, infection processes, and the status of resistance research. We will argue for a more proactive approach to explaining why the wheat blast represents a potential global threat—capable of becoming a pandemic if not dealt with properly—by integrating recent findings and gaps in knowledge.

2. BACKGROUND AND GLOBAL DISTRIBUTION

2.1 Historical Perspective

In 1985, Brazil witnessed the introduction of wheat blast for the first time, which suggested an emergent and harmful pathogen in wheat producing regions (Masih, 2024). This new pestilential disease was first identified in the Brazilian region of Ȯbras in 1986 and was followed by rapid progression of wheat across Brazil. Wheat farmers across Brazil suffered massive cutbacks in revenue due to pestilential losses. They were closing in on employing strategies to remove this disease, losing an evident yield of wheat crops (Igarashi, 1986). These reports further indicated rapid environmental degradation, raising alarming concerns about the probable impacts of this disease (Pereira et al., 2014).

The pathogen spread across South America from Brazil, extending to Paraguay, Bolivia, and Argentina with time. Its damage was effectively (Mills et al., 2021). This showcased the potential of the pathogen in surpassing natural borders and caught the attention of Lead Researchers. The blast prompted Scholars to realize that a regional difference in meteorology and farming was an important factor in blast proliferation, therefore, the pathogen had mastered the ability to transform and adapt in varying agro-meteorological scopes (Mahapatra et al., 2024).

While the wheat blast spread across the continent, scientists noted increasing variation in the pathogen's behavior and virulence (Mills et al., 2021). This phase was characterized by intensive efforts focused on how this pathogen adapts so rapidly and evolves in its pathogenicity. All the genetic variability seen during this phase raised red flags regarding the effectiveness of any purported host resistance for the foreseeable future, emphasizing the need for alertness, continual monitoring and research into the evolutionary processes of the disease (Kwok et al., 2021).

In 2016, the incursion of wheat blast into Bangladesh marked the pathogen's first significant entry into Asia and considerably widened its geographic scope(He et al., 2025; Khan et al., 2022). Not only did this incursion disrupt local wheat production in Bangladesh, but it also warned the global agricultural community of how wheat blasts could spread beyond their initial boundaries (Islam et al., 2016).

Even more recently, incidents in Zambia amplify the pathogens' ability to penetrate new areas (Tembo et al., 2020). The history—from the first case in Brazil through the cases seen on several other continents—depicts this worrying extension and modification of the disease, which, if not contained with pre-emptive action, underscores the gravest consequences for the world (Tembo et al., 2020).

2.2. Global Distribution

The presence of wheat blasts in South America, Africa and Asia is a known fact, as cited by CABI in 2021. Tembo et al. (2020) elaborated on the disease's climate, geography, and historical spread and provided evidence on how the pathogen ecologically evolves to different regions. Among many places, Bangladesh and Zambia, which are located on opposite sides of the globe, were discovered to have the disease after it was found in Brazil.

Global wheat yields vary significantly across continents (Fig. 1). Regions such as United States, Canada, Russia, China, France, and India produce large volumes of wheat per hectare, produce large volumes of wheat per hectare, making them both economically and nutritionally dependent on stable wheat production. Should wheat blasts become established in these high-yield regions, the resultant yield losses could have far-reaching consequences for food security, underscoring the urgency for effective disease management strategies.

The spread of wheat blast can be ascribed to many factors, as cited previously. The geographical scope of Islam et al. (2016) states the primary hypothesized wheat blast natural dispersal mechanism is through wind-contained spores, thereby contributing to the disease's ability to spread over long distances. Mildew can also potentially seed itself, causing contamination and spreading the disease to new regions. Coupled with poor quarantine protocols, these attempts by the pathogen resulted in the establishment of various ecological regions shown in Table 1.

The *Magnaporthe oryzae* Triticum pathotype is mapped in a distribution map provided by the CABI invasive species database. This data can be found in the compendium of CABI (2021). Table 2 outlines additional granular

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details that assist in augmenting the distribution and invasion potential of this pathogen. In juxtaposition with Table 1, it shows more specifics concerning the global presence of this pathogen.

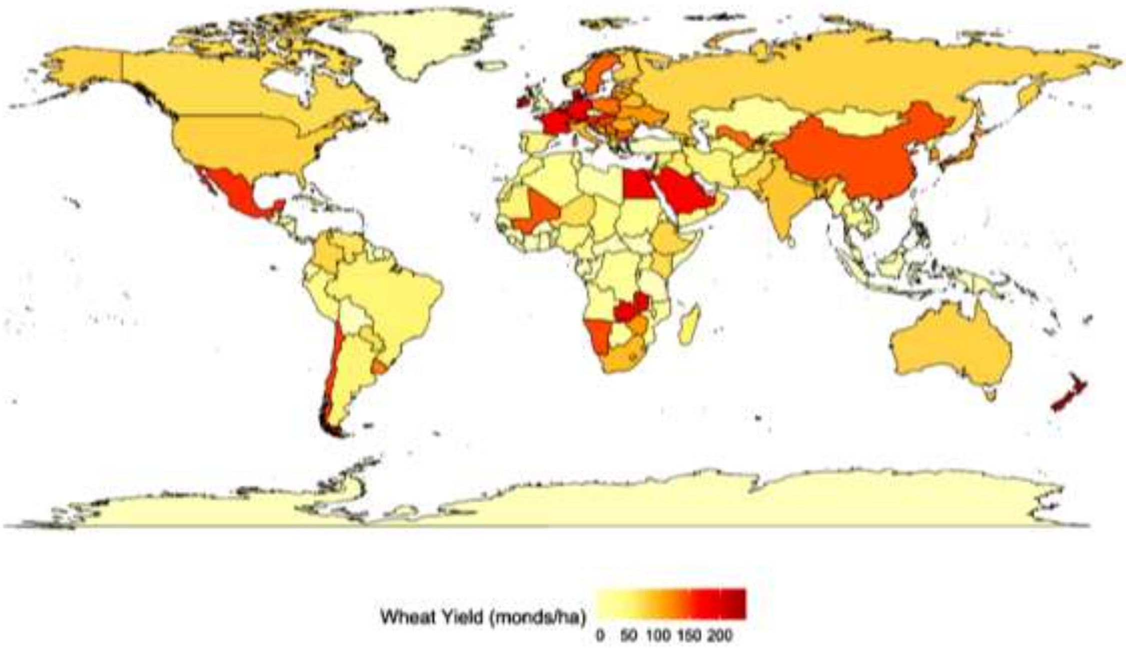

Fig. 1: Global Wheat Yield Distribution (2023). Data Source from FAOSTAT. Darker shades higher population.

Table 1: The distribution table for wheat blasts is based on information from the literature (CABI, 2021)

Country/ region	Status (present/ absent)	Source	Year reported	Reference
Bangladesh	Present, Widespread	Introduced	2016	(Islam et al., 2016)
Zambia	Present			(Tembo et al., 2020)
Paraguay	Present, Widespread	Introduced	2002	
Sao Paulo	Present			(Castroagudín et al., 2015)
Rio Grande do Sul	Present			(Castroagudín et al., 2015; Pereira et al., 2014)
Parana	Present, Widespread	Introduced	1985	(Pereira et al., 2014)
Minas Gerais	Present			(Castroagudín et al., 2015; Pereira et al., 2014)
Mato Grosso do Sul	Present			(Castroagudín et al., 2015)
Goias	Present			(Castroagudín et al., 2015)
Distrito Federal	Present			(Castroagudín et al., 2015)
Brazil	Present		1985	(Igarashi, 1986)
Bolivia	Present, Widespread	Introduced	1996	(Mills et al., 2021)
Argentina	Present, Widespread	Introduced	2007	(Pereira et al., 2014)
Kentucky	Absent, formerly present			(News.ca, n.d.)

Table 2: Datasheet based on distribution map for Magnaporthe oryzae Triticum pathotype (CABI, 2021)

Region	Latitude	Longitude	Presence	Extent	Origin
Zambia	-14.33	28.5	Present	-	-
Bangladesh	24	90	Present	Widespread	Introduced
Argentina	-34	-64	Present	Widespread	Introduced
Bolivia	-17	-65	Present	Widespread	Introduced
Brazil	-10	-55	Present	-	-
- Distrito Federal	-15.75	-47.75	Present	-	-
- Goias	-15.58	-49.64	Present	-	-
- Mato Grosso do Sul	-20.5	-55	Present	-	-
- Minas Gerais	-18	-44	Present	-	-
- Parana	-24.5	-51.33	Present	Widespread	Introduced
- Rio Grande do Sul	-30	-53.5	Present	-	-
- Sao Paulo	-22	-49	Present	-	-
Paraguay	-23.33	-58	Present	Widespread	Introduced

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The international trades and the exchange of wheat germplasm exacerbate containment difficulties. With the growth of global seed markets, the likelihood of the pathogen being moved to new, previously unexposed areas rises, which is a clear trend in the reports from numerous countries (Tembo et al., 2020). Table 1 summarizes the disease status with sources and years reported from various countries that depict wheat blasts' rapid and extensive spread. Other regions' epidemiological variation of wheat blast poses different challenges. The incidence and severity of the disease are influenced by the environmental factors of temperature, humidity, and rainfall, resulting in different regional outbreak patterns (CABI, 2021). This variability requires specific management practices considering local agro-climatic and cropping conditions (Islam et al., 2016).

Although strides have been made in understanding the spatial and temporal dimensions of its tracking, there are serious deficiencies in monitoring and control. The lack of adequate quarantine and predictive measures in many impacted areas renders agricultural systems open to unanticipated eruptions (Tembo et al., 2020). In light of the evidence for the adaptability and mobility of the pathogen, there is a dire need for global cooperation to formulate norms for self-defence surveillance and control measures to avert future global epidemics (CABI, 2021).

2.3 Economic and Food Security Implications

Wheat remains one of the most prominent cereal crops after maize and rice, a primary dietary protein source (Walkowiak et al., 2020). New outbreaks of wheat blast in different regions threaten global food security, especially for regions that depend on wheat as a subsistent staple. The damage due to blast is exceptional, resulting in infected crops having low quality grain, less nutritious value, and sometimes complete crop failure (Surovy et al., 2020). The disease control through fungicides, quarantines, and breeding resistant cultivars also add to the negative economic results (Islam et al., 2016; Singh et al., 2021). There is a consensus that the continuous spread of wheat blast calls for immediate attention for corrective countermeasures, international cooperation, and outsized management strategies.

The combined analysis of the peripheral spread and current spread of wheat blast specifically emphasizes the need for diabetes-proactive mitigatory strategies. The movement of this pathogen to newer geographical areas from its previously known areas of action is not just a regional problem. It is a global issue that requires all-encompassing knowledge about its epidemiology and methods to protect food and wheat security worldwide. Regarding global population data, Fig. 2 shows that Asia and parts of Africa have the highest population density which coincide with vital wheat growing regions. Any disruption in wheat production in these regions, either by wheat blast or other factors, causes food security issues in heavily populated areas. It is therefore important to ensure stable wheat yields in these parts to sustain the protein and caloric requirements of billions.

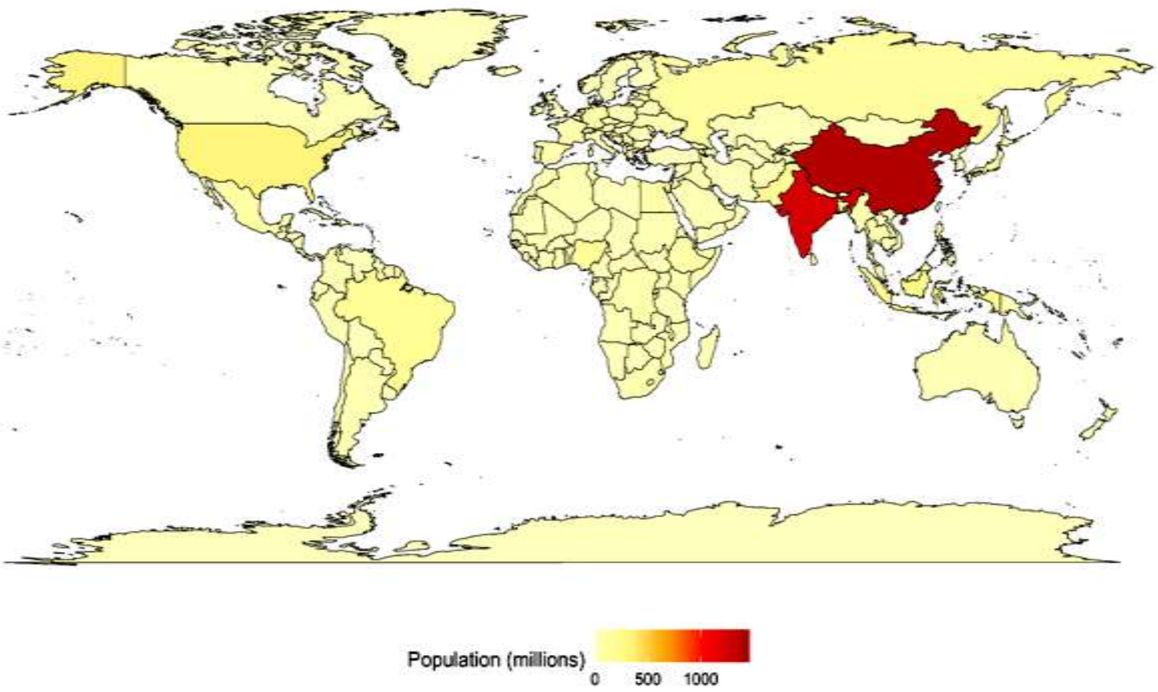

Fig. 2: Global Population Distribution (2023). Data Source from FAOSTAT. Darker shades higher population.

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3. TAXONOMY AND BIOLOGY OF THE PATHOGEN

3.1. Taxonomic Classification

Wheat Blast disease is due to the *Magnaporthe oryzae* pathogen, which is part of the 'Fungi' kingdom, and whose class, order and family are as follows: 'Sordariomycetes', 'Magnaporthales' and 'Pyriculariaceae' respectively (Chakraborty et al., 2021; Klaubauf et al., 2014). For some time, the pathogen was known by yet another synonym, Pyricularia graminis-tritici (Islam et al., 2016). This designation is critical because it helps integrate the wheat blast disease into other cereal destructive pathogens, like the rice blast fungus, offering its phylogenetic context and degree of host association.

3.2. Physiological Effects of Mot on Host Plant

The infection caused by *Magnaporthe oryzae* Triticum results in various physiological changes in wheat. The pathogen causes impairment to cell functioning and elicits specific observable features in different parts of the plant (Chakraborty et al., 2021). These effects consist of necrosis of stems and leaves, blight and necrotic lesions on inflorescence, fruit discoloration and abnormal shapes, and necrosis in tissues of higher plants (Table 3). Besides, affected seeds are often shrunk and their color is changed together with stems which show color changes and necrotic bark. The plant in totality is subject to dieback and death in its severest form.

Table 3: Symptoms of Wheat Blast on Different Plant Parts

Symptoms	
Plant organ/ Plant part	MoT effects
Fruit	Abnormal shape, discoloration, mummification
Inflorescence	Blight; necrosis, lesions on glumes, premature ripening
Leaves	Abnormal colors, fungal growth, necrotic areas, rot
Seeds	Discolorations, shriveled
Stems	Discoloration, discoloration of bark, necrosis

3.3. Comparison with other pathotypes

Integrated pest management effectively controls *M. oryzae* Triticum oligocllae, Multihosts species Oryzae, and *Bipolaris sorokiniana* in wheat crops (Rodrigues et al., 2020). However, the complexity of blast disease requires further research on its epidemiology and accurate characterization of its causal agents (Perello et al., 2020). Rice and wheat have very different ecosystem requirements, meaning wheat blast has little competition (Pequeno et al., 2024). Further evolutionary divergence can occur when there is little interspecific hybridization or gene flow. Thus, genetic incompatibility regions can be maintained through more substantial selection for these traits. Rapid pathogen adaptation and its ability to break resistance genes imposed by a variety APM are alarming aggressive characteristics that warrant consistent attention and research by APM plant pathologists. Effective pest management should be sought for the established races of this pathogen to target resistant lines of wheat varieties (Islam, 2024). This would guarantee that wheat yields will remain steady until more breeding solutions become available.

Special attention should be given to devising pest management strategies tailored for resistant lines of these wheat varieties until better mitigation measures are developed. Constructing a disease-resistant wheat variety will assist with wheat yield and lessen reliance on traditional methods to control pests.

4. EPIDEMIOLOGY AND DISEASE CYCLE

4.1. Infection Process and Disease Development

The initial stage of wheat blast commences with the striking of the conidia (the three-celled asexual spores of *Magnaporthe oryzae* Triticum) on vulnerable wheat plant surfaces (MESHUK, 2021). Conidia in contact for more than six hours differentiate into polarized germ tubes and subsequently undergo specialized host penetration structural cut known as appressoria (Surovy, 2024). The appressorium helps achieve the needed turgor pressure, making the invasion feasible because it captures water-soluble substances. The acquired turgor pressure is then utilized to form a penetration peg that makes a hole through the epidermal cell wall (Doehlemann et al., 2017). This allowed the fungus to reach the tissues below the body and begin the infection.

Inside the host, the pathogen can expand due to the singular formation of invasive hyphae. Most of these hyphae collapse using the constituents of plant cells encapsulated with biotrophic interfacial complex which aids in injecting effector proteins into plant cells (Surovy et al., 2023). These proteins neutralized immune responses around the host tissues during the disease's early phase, hence eliciting fast settlement (Chen et al., 2014). In 120 hours of infection, new conidia emerge, but before that, infection lesions are common in the tissue between 72-96 hours (MESHUK, 2021).

4.2. Environmental influences on disease spread

Wheat blast is no different from other diseases in terms of environmental determinants. It requires a

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temperature of 15-27 degrees Celsius and a relative humidity of over 93% (Bishnoi et al., 2021). Such circumstances are ideal for cercnidial germination, appressorium production, and improving conidia's airborne dispersal. Rainfall events help to promote the disease by allowing conidia to move from infected plants to healthy ones (Valent et al., 2021). Furthermore, the ambiguous nature of the ailment, which is both seed and dust borne, means that it can be spread relatively fast and easily throughout and under geographic regions that have favourable environmental conditions, making control harder.

4.3. Disease Cycle in the Field

The life cycle of *Magnaporthe oryzae* pathotype Triticum (MoT), the fungus responsible for wheat blast, is driven primarily by rapid asexual reproduction, enabling its efficient spread and infection of wheat crops (Joubert, 2023). his cycle commences once the three-celled conidia, which are a form of asexual spores, are placed on the plant surfaces that are susceptible to infection, generally the leaves or the spikes of wheat plants (Surovy, 2024). Ideally, temperatures from 15 to 27 degrees Celsius with a relative humidity of over 93 percent facilitate the germination of conidia with the production of polarised germ tubes within a window of six hours (Singh et al., 2021). These tubes then become specialized infection structures called appressoria. By accumulating arginine and other compatible solutes, the appressoria develops high turgor pressure and can generate a penetration peg that mechanically breaches the host's epidermal cell wall (Singh et al., 2021).

When the fungus gets inside the plant, it starts producing invasive hyphae that grow in the host tissue, obtaining nutrients while neutralizing plant defenses with effector proteins such as Avr-Pita and Avr-Pii. Notable lesions begin to appear on the affected parts of the plant after 72-96 hours post-infection (Quime et al., 2025; Wei et al., 2023). Around 120 hours later, fresh conidia are formed in these lesions and later spread through wind, water, or human actions like using tools or seeds that are contaminated, which starts new cycles of infection in new fields or plants. Although asexual reproduction is most common in field settings, under certain conditions, Magnaporthe oryzae pathotype Triticum is capable of sexual reproduction, although this is seen less often (Quime et al., 2025). This ability of the pathogen to live in infected seeds and crop residues amplifies its threat to wheat cultivation in later seasons, further facilitating its survival.

During fieldwork, the conidia deposition on the plant initiates what is referred to as the wheat blast disease cycle (Fig. 3) followed by rapid germination and host tissue penetration. First initial infections are most likely to occur on the leaves, where lesions manifest as diamond, water-soaked spots. In the advanced stage of the disease, the fungus moves to the spikes resulting in the typical bleached heads and decayed grains during severe outbursts (Surovy et al., 2020). The cycle becomes even faster with infected tissues, which produce and disseminate conidia, which are easily moved by wind, splashes of rain, or human intervention, resulting in constant infection to nearby fields and plants.

5. HOST-PATHOGEN INTERACTION AND MECHANISMS OF INFECTION

5.1. Molecular basis of infection

The highly sophisticated molecular relationship between *Magnaporthe oryzae* Triticum and the wheat crop defines the wheat blast pathogenesis. After the first penetration, the pathogen injects a set of effector proteins to alter host cellular activities. These effectors form well-characterized proteins Avr-Pita, Avr-Pii, and Avr-Piz-t, which are secreted in the early stages of infection and target the host's defense systems through suppressive means (Chen et al., 2014; Islam et al., 2022). These effectors can bind to the apoplast, for instance, chitin oligosaccharides, which prevents the plant's immune surveillance receptors from detecting the pathogen, thus blocking immune response activation.

Appressoria, which not only achieve physical penetration of host cells but also act as effector delivery ports, are specialized infection structures that facilitate delivery of these effectors (Evangelisti & Govers, 2024). Once inside the host, the invasive hyphae are enveloped by a biotrophic interfacial complex—a structure that allows the fungus to maintain a delicate balance between nutrient acquisition and evasion of host defenses (Jensen & Saunders, 2023).

5.2. Role of Effector Proteins

Effector proteins are central to the success of wheat blast infection. These molecules perform multiple functions. Pathogenic effectors play a critical role in suppressing host immune responses, enabling successful colonization of plant tissues. By directly interacting with host defense components, effectors such as Avr-Pita and Avr-Pii prevent the activation of programmed cell death and other immune responses, thereby ensuring that the pathogen can colonize living tissue (Chen et al., 2014). Apart from immune suppression, some manipulators modify host metabolism to aid pathogen development and survival. Some effectors redirect metabolic pathways of the host to allocate resources to the pathogen (Zhang et al., 2022). This modification is essential to sustaining fungal

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proliferation and growth within the tissues of the host.

Moreover, effectors may disrupt the plant's hormonal signaling and exacerbate the interference of phytohormonal effectors and defense mechanisms. Some effectors may modulate phytohormone signaling pathways such as auxins and salicylic acid, thereby making it more difficult for the plant to defend itself (Mosquera et al., 2009). This approach demonstrates the complex dynamic between host manipulation and pathogen survival and virulence.

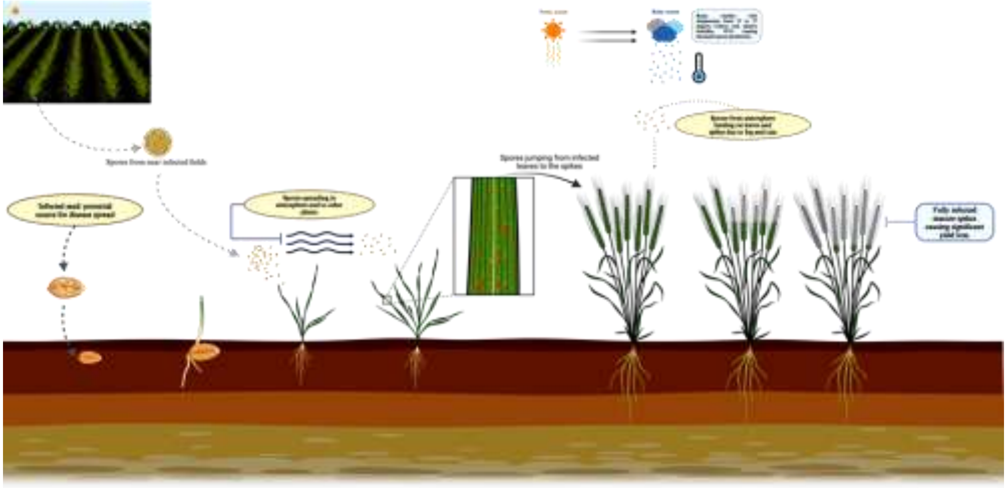

Fig. 3: Disease spread in field/ disease cycle (Created with BioRender.com).

5.3. Biochemical and Cellular Responses in Wheat

Wheat plants have evolved a range of biochemical and cellular responses to counteract pathogen invasion. As a response to pathogen-associated molecular patterns (PAMPs), wheat cells mobilize several defense mechanisms such as self-defense actions by strengthening their walls, oxidative burst (production of reactive oxygen species), and PR (pathogenesis-related) protein production. However, the swift action of MoT effectors can suppress or delay these responses, enabling the fungus to form a biotrophic association with its host (Giraldo et al., 2013; Mosquera et al., 2009).

Furthermore, the relationship between the host's resistance genes and the pathogen's avirulence (Avr) genes is gene-for-gene. In this regard, the suggested model indicates that wheat with the appropriate resistance gene will respond aggressively if a specific Avr effector is recognized (Bourras et al., 2019). Nonetheless, the currently high mutation rate and genetic variability of *M. Oryzae* Triticum lie in providing new virulent strains that would bypass these resistance strategies (Cruz et al., 2016).

5.4. The role of secondary metabolites

The wheat blast pathogenesis is enhanced through the use of secondary metabolites in addition to effector proteins. Unsurprisingly, the mycotoxin known as Tenuazonic acid has been connected to the disruption of the safeguarding strategies of the host and the facilitation of fungal invasion (Martínez-Culebras et al., 2021; Yan & Talbot, 2016). This compound not only demolishes the cellular structure of the host tissue but may also be able to inhibit the governing signals from the immune system. The combined effects of the effectors and other secondary metabolites sculpt the microenvironment conducive for rapid penetrating tissue mycosis and germination of the fungi.

5.5. Integrated Interaction Model

Succeeding infection of wheat by M. oryzae Triticum is the result of several virulence factors working in unison (Hossain, 2022). The intrusion of the host epidermis through mechanical penetration and the diffusive secretion of effector proteins and other secondary metabolites exemplifies a tactic targeted at host protective defence neutralisation (Montenegro Alonso, 2020). This complete model of host-pathogen interaction showcases the complexity of interactivity within the wheat blast disease system, which is highly intricate during the endeavour to establish sustainable resistance.

These molecular and biochemical elements of study towards the host-pathogen interface augment the understanding of wheat blast pathogenesis while marking the scope of focus for future intervention strategies (Rauwane et al., 2020). Focusing on the search for novel resistance genes and the creation of effector action blocking compounds may be essential in coping with the destruction caused by this disease.

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6. RESISTANCE IN WHEAT: GENES AND SCREENING METHODS

6.1. Identified Resistance Genes

Numerous resistance (R) genes that offer varying resistance levels to Magnaporthe oryzae Triticum have been discovered in the past twenty years. These genes comprise, but are not limited to, Rmg1, Rmg2, Rmg3, Rmg4, Rmg5, Rmg6 (known as Rwt3), Rmg7, Rmg8, RmgGR119 (Ferreira et al., 2020; He et al., 2022; Hossain, 2022). This gene group is most recognised for providing varying degrees of resistance to different pathogen isolates together with different environmental settings, Rmg8 and RmgGR119 (Horo et al., 2020; Juliana et al., 2020).

The relationship among the various wheat blast resistance (R) genes and the accompanying pathogen avirulence (AVR) genes, as illustrated in Fig. 4, associates with the defence against Magnaporthe oryzae Triticum. Major R genes such as Rmg1, Rmg2, Rmg8, and RmgGR119 are shown as highly connected nodes corresponding to the recognition of the effector AVR. As an example, Rmg8 located in hexaploid wheat (Anh et al., 2015) is linked to its corresponding effector AVR-Rmg8 illustrating the gene-for-gene relationship where the subsequent defense mechanism activated involves the pathogen being equipped with this AVR protein.

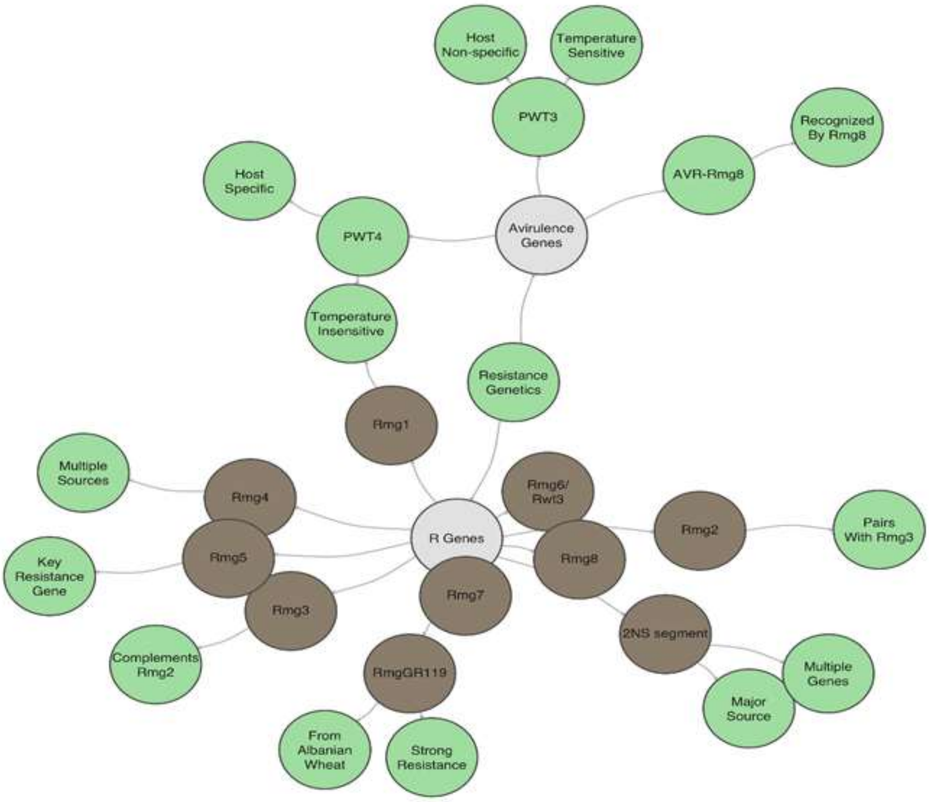

Fig. 4: Wheat Blast Resistance Gene Network.

In the network, each resistance gene is linked to its known or putative avirulence partner. Rmg1, one of the first wheat blast R genes identified in the cultivar Norin 4 (He et al., 2020) and Rmg2 and Rmg3 by Asuke et al. (2024) are included, though their effectiveness can vary. Field assessments have indicated that although Rmg2 and Rmg3 conferred some degree of seedling resistance, they were relatively ineffective at the spike (heading) stage - a shortcoming recognized in later research. In contrast, Rmg8, which was in other studies confirmed by Anh et al. (2015) is positioned as a stem node because of its strong resistance at both seedling and heading stages. The illustration indicates Rmg8 as a central node because of his extensive efficacy and direct recognition of AVR-Rmg8.

An additional important factor is RmgGR119, reported from Albanian wheat Cruz et al. (2016). This component offers very high resistance and is illustrated with an association to some presumed effector, popularly known as AVR-RmgGR119. Even though RmgGR119's effector is yet to be molecularly described, Cruz et al. (2016) have shown that several *M. oryzae* Triticum isolates possess a matching counterpart which supports the dominance of Rmg8 and RmgGR119.

These results, for example, suggest that Rmg8, by itself or in combination with RmgGR119, demonstrates intense levels of resistance during seedling and heading stages. Field and greenhouse tests show accessions with these genes markedly curtail disease development even at high temperatures that promote wheat blast (Horo et al.,

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2020). Conversely, some other R genes like Rmg2 or Rmg3 demonstrated some level of effectiveness, however, certain MoT strains could bypass their defences (Hossain, 2022).

Among the identified resistance genes, Rmg8 has garnered particular attention for its robust protection at both seedling and heading stages (Anh et al., 2015). The corresponding pathogen avirulence locus, AVR-Rmg8, shows considerable sequence diversity across different P. oryzae isolates. In Fig. 5, it was used the maximum likelihood method of phylogenetic analysis for AVR-Rmg8 alleles with MEGA X (Asuke et al., 2024). It is remarkable that the tree groups several Brazilian isolates harboring AVR-Rmg8 with some from other regions, indicating several evolutionary events. This variability emphasizes the need for constant monitoring for novel Rmg8 defensing pathogen variants. Improved knowledge of such genetic diversity also assists breeding strategies based on combining resistance genes to provide long-lasting safeguards against wheat blast. Attention has been given to several R genes for resistance to wheat blast, however, these R gene resources still need to be utilized fully. The resistance genes of wheat blast are mentioned in Table 4.

Table 4: Resistance genes for wheat blast (Bishnoi et al., 2021)

Resistance gene	Source	Chromosome	References
Rmg4	P168, Shin-chunaga, Norin 4, Norin 26, Norin 29	4A	(Chaves et al., 2022)
Rmg6 (Rwt3)	Common wheat Norin 4	1D	(Asuke et al., 2024)
Rmg5	Red Egyptian	6D	(Ferreira et al., 2020)
Rmg1	Norin 4	1D	(Asuke et al., 2021)
Rmg8	Common wheat S-615	2B	(Anh et al., 2015; Bishnoi et al., 2021)
Rmg2 and Rmg3	Thatcher	7A and 6B, respectively	(Zhan et al., 2008)
Rmg Td(t) and Rmg7	*T. dicoccum*		(Hossain, 2022)
2NS a chromosome segment	Ae. ventricosa		(Cruz et al., 2016)
RmgGR119	Albanian wheat, GR119		(Cruz et al., 2016)

Fig. 5: Phylogenetic analysis of AVR-Rmg8 avirulence gene in Pyricularia oryzae lineage Phylogenetic and molecular evolutionary analyses were conducted using MEGA version X (Asuke et al., 2024).

6.2. Aegilops Ventricosa 2NS Chromosome Segment

Apart from the conventional R genes, the 2NS translocation from Aegilops ventricosa is now regarded as an important source of resistance. That chromosome segment has been integrated into some cf-exaploid wheat subclasses and contains several presumed disease resistance genes, some of which are in the NBS-LRR family (Cruz et al., 2016; He et al., 2022). Markers Ventriup-LN2 and cslVrgal3 are usually used for the identification of the 2NS segment, but its dominant nature severely complicates the identification of heterozygous individuals (He et al., 2022). Subsequent studies have used more sophisticated approaches relying on QTL mapping to enhance the delineation of the region on chromosome 2AS associated with resistance, which was previously described approximately, estimating a 2.3 Mb region of interest containing many candidate genes responsible for the defensinism response and recognition (He et al., 2020).

6.3. Screening and Identification Techniques

The approaches for recognising and confirming the resistance genes of wheat employ classical genetics and contemporary molecular approaches. Inoue et al. (2021) identified two loci of fungi Pwt3 and Pwt4 that are components of the Avena isolate Br58 avirulence. They hypothesized that PWT1, PWT2, PWT3, and PWT4 are

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functional alleles following gene-for-gene interactions. They also reported the contrasting phenotypic nature of both genes. They concluded that PWT4 was cultivar/host specific and temperature insensitive compared to the PWT3, which is cultivar/ host non-specific but temperature sensitive, when they inoculated Norin 4 and Chinese Spring with Br58. In this experiment, Br58 was highly avirulent on the Norin 4 cultivar even at high temperature, but the same results were not observed in case of the Chinese Spring cultivar. Hence, these observations confirmed the host-specific and temperature-insensitive nature of the PWT4 (Yoshioka et al., 2024)

Asuke et al. (2023) identified the first gene exhibiting resistance in wheat cultivar Norin 4 against wheat blast and designated it Rwt4 due to its correspondence toward PWT4. Later under the rules of nomenclature this gene was named as Rmg1 (located on chromosome 1D) (synonym Rwt4) (Asuke et al., 2021).

Hossain (2022) successfully identified the first two genes in Triticum spp. Governing resistance against wheat blast fungus Triticum isolates of *M. oryzae*. They reported that both genes are equally effective in providing resistance, and each gene, Rmg2 (Resistance to *Magnaporthe grisea* 2) and Rmg3(Resistance to *Magnaporthe grisea* 3,) in isolate, condition provides, resistance which is comparable to the cultivar namely called, Thatcher which carried both of these genes (Islam et al., 2024).

To identify resistance genes, Spychała et al. (2023) studied a series of Chinese Spring substitution lines, each carrying 21 pairs of chromosomes replaced by the homologous pair from the Thatcher cultivar. These lines were inoculated with Br48 (Triticum isolates of *M. oryzae*), and two resistant lines were found out of 21, leaving 19 susceptible. The resistant lines were namely identified as CS(Tc7A) and CS(Tc6B) (CS from Chinese Spring and Tc from Thatcher). From these results, they concluded that resistance genes are located on chromosome 7A and 6B and were designated as Rmg2 (7A) and Rmg3 (6B) (Islam et al., 2024).

Phuke et al. (2022) identified two resistance genes named RmgN4 and RmgRE that showed resistance against Digitaria isolate. However, these genes differed from recently discovered genes Rmg1, 2, and 3 precisely because of their location on different chromosomes; therefore, they designated RmgN4 as Rmg4 and RmgRE as Rmg5. To identify which chromosomes, carry Rmg4, they performed monosomic analysis. They concluded that the Rmg4 gene lies on chromosome 4A from their experiment. To determine the chromosome carrying Rmg4, they inoculated the F2 population with the Dig41 isolate and incubated at 26°C, which was derived from crosses between the 21 CS (Chinese Spring) monosomics and N4 (Norin 4). Segregation ratio of resistant and susceptible seedlings in F_2 populations was 3:1 in crosses between mono-4B and N4, mono-4D and N4. However, the 12 F_2 populations from a cross between mono-4A and N4 were of 2 types, i.e., type I, where segregation of resistant and susceptible seedlings followed a 3:1 ratio. In contrast, in type II, all seedlings were resistant. 12 F_2 populations were derived when they crossed mono-4A and N4, included six populations in which the ratio of segregation of resistant and susceptible plants deviated from 3:1; and they found all the seedlings resistant in these populations (Richard, 2023).

To identify the chromosome carrying Rmg5, they developed a series of CS lines. In these lines, each of the 21 chromosome pairs was replaced by the homologous pair from RE (Red Egyptian) cultivar. Further, these lines were inoculated with Dig41 and incubated at 26°C. It was observed that the line CS/RE6D carrying chromosome 6D of RE showed high resistance. Whereas, in contrast to this, other lines were highly susceptible, indicating that the Rmg5 gene is located on chromosome 6D (Nga et al., 2009).

6.4. Challenges in Resistance Breeding

Despite significant progress, breeding for durable resistance to wheat blast remains challenging. The high genetic variability of *M. oryzae* Triticum means that resistance genes can quickly become ineffective as new virulent strains emerge. Additionally, environment unfavourably affects R gene expression and multi-location trials are extensive to confirm the resistance validation in various agro-climatic regions (Islam et al., 2022). In addition, potential epistatic interactions between resistance genes and other complications make breeding more complicated because stacking multiple genes does not always result in more than one phenotypic value (Horo et al., 2020).

These efforts also need to be complemented by global cooperation in genomic selection and more classic breeding techniques to develop wheat varieties that are resistant to the constantly emerging threat of wheat blast. As such, developing durable resistance by incorporating wild relatives of wheat, such as *Aegilops ventricosa*, into commercial cultivars is a viable option.

7. MANAGEMENT AND CONTROL STRATEGIES

7.1. Conventional Breeding and Genetic Improvement

Integrating genomics into traditional breeding practices is still crucial for developing wheat varieties with improved resistance to wheat blast. Recently, breeding efforts have been directed toward pyramiding the Rmg8 and RmgGR119 R genes with the 2NS translocation from *Aegilops ventricosa* into the elite wheat lines

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(Cruz et al., 2016; Horo et al., 2020). The process has been expedited further with the implementation of marker-assisted selection of resistance genes in large breeding populations (He et al., 2020). Alongside this, new methods of genomic selection using high throughput sequencing and phenotyping have already been incorporated into the breeding programs to aid in predicting the performance of new varieties under different conditions (Juliana et al., 2020).

7.2. Chemical Control Measures

Using fungicides is one of the most common methods of controlling wheat blast disease in the field, especially during critical disease pressure periods. Strobilurins and triazoles systemic and contact fungicides, such as Strobilurins and Triazoles, have been used to limit the disease's dissemination by inhibiting fungal growth and conidial production (Islam et al., 2024). Unfortunately, *M. oryzae* Triticum's resistant strains' rapid emergence often renders fungicide application ineffective (Tembo et al., 2020). Additionally, excessive reliance on fungicides can harm the environment by causing imbalances in natural microbial populations. The best form of chemical control is integration with other control measures.

7.3. Cultural and Agronomic Practices

Implementing proper agronomic practices can substantially reduce the incidence and severity of wheat blast. Key strategies include:

Crop rotation and field sanitation are essential strategies for managing plant pathogens and reducing disease incidence in agricultural systems. As noted by Singh et al. (2021), rotating wheat with different crop types and eliminating infected crop residues aid in reducing inoculum buildup in the field. Sanitary methods like cleaning farm tools and machines or refraining from planting infected seeds also contain the pathogen. Moreover, refraining from planting infected seeds ensures that new crops are not exposed to initial pathogen loads, contributing to overall disease suppression and improved crop health (Singh et al., 2021).

Optimized irrigation and planting practices are crucial for reducing the risk of fungal infections in crops. Changing irrigation practices to prevent excessive humidity for a long time, in conjunction with proper plant spacing, can assist in lowering canopy density and consequently reducing the microclimate favorable for the growth of fungi (Islam et al., 2022). Besides, to curtail disease progression, more planting delays during the most favorable infection periods are beneficial.

Implementing stringent seed certification procedures and using disease-free, certified seeds are fundamental strategies for managing wheat blast and preventing its spread. Due to the possibility of seed transmission of wheat blast, the implementation of stringent seed certification procedures alongside the use of disease-free, certified seeds is fundamental to a sound management plan (Surovy et al., 2020).

7.4. Integrated Disease Management (IDM)

Because wheat blast epidemiology is multifaceted, managing this disease requires an integrated disease management (IDM) strategy. IDM achieved more significant and lasting impact on disease management by combining genetic resistance, chemical control, and cultural practices. For example:

Combining resistant varieties with fungicide application is an effective strategy for managing wheat blast, as it creates a synergistic effect that reduces both initial infection and disease spread. If resistant cultivars are deployed along with fungicide applications, there tends to be a synergistic effect associated with reducing the initial infection and the disease spread (Tembo et al., 2020).

Similarly, monitoring and early warning systems play a crucial role in disease management by enabling the timely detection of outbreaks. Establishing surveillance systems and applying remote sensing instruments can help identify and respond to disease outbreaks early. Such systems are also integral in preventing outbreaks from escalating into larger public health crises (Islam et al., 2016).

Furthermore, farmer education and extension services are essential for ensuring the effective implementation of management strategies at the local level. Teaching farmers about wheat blast and its symptoms, along with appropriate management practices, assures effective implementation of control measures at the local level. (Walkowiak et al., 2020).

7.5. Future Approaches and Emerging Technologies: Looking ahead, novel technologies and approaches hold promise for further enhancing wheat blast management:

- **Biocontrol Agents and RNA Interference (RNAi):** The study of biocontrol agents, especially antagonistic microorganisms that suppress *M. oryzae* Triticum, is gaining attention. So do strategies based on RNAi that aim at important genes of the pathogen which could lessen the damage (Juliana et al., 2020).
- **CRISPR/Cas-Mediated Genome Editing:** Research on CRISPR/Cas systems has revealed genome-editing

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technologies that could improve resistance in wheat plants. Unlike traditional breeding, these methods may augment or add resistance characteristics with greater precision and speed (He et al., 2020).

- **Integration of Omics Approaches:** Advances in genomics, transcriptomics, and proteomics will provide a more comprehensive understanding of the host-pathogen interaction. This information can be used to identify novel resistance genes and design targeted interventions to disrupt the pathogen's infection mechanisms (Juliana et al., 2020).

All these revolutionary management tactics highlight the need for a comprehensive strategy in fighting wheat blast disease. As its causative agent inexorably adapts over time and extends its range, protection of wheat on a global scale and subsequently, food security will heavily depend on the integration of established and novel methods.

8. FUTURE PERSPECTIVES AND RESEARCH DIRECTIONS

8.1. Emerging Trends in Wheat Blast Research

Current developments in genomics, transcriptomics, and proteomics have started to provide insights into the host-pathogen interactions with wheat blast at its molecular base. Novel methods such as high-throughput sequencing coupled with bioinformatic analyses have identified novel effector proteins and attraction resistance candidates which in the classical approaches were not detectable (He et al., 2020; Juliana et al., 2020). Furthermore, comparative genomic analysis among different *Magnaporthe oryzae* pathotypes contributes to understanding the evolutionary changes that enable the pathogen to be polyphagous. This most recent information is expected to provide bases for more efficient intervention strategies.

8.2. Climate change and Pathogen Evolution

Understanding the impact of climate change on wheat blast epidemiology for the future is critical, especially as it is deemed one of the most pressing challenges. Increasing temperature, humidity, and rainfall variation will likely enhance pathogen development and/or spread (Islam et al., 2022). In addition, stress on wheat plants due to climate changes can make them more vulnerable to infection. In this scenario, keeping track of new virulence markers and the emergence of new pathogens is crucial. Predictive modeling for disease outbreaks using different climatic conditions, environmental data, and pathogen genomic information to predict possible changes in disease dynamics needs to be the focus of further study.

8.3. Integration of Advanced Technologies in Disease Management

The future of wheat blast management lies in the integration of innovative technologies:

- **CRISPR/Cas-Mediated Genome Editing:** The precise editing of genomes offers opportunities for both the incorporation and improvement of resistance traits in wheat. Researchers may use CRISPR/Cas systems to produce wheat lines that are more resistant to wheat blast while sidestepping some of the issues caused by traditional breeding (He et al., 2020).
- **RNA Interference (RNAi) Strategies:** The progress in RNAi technologies provides a precise means of silencing specific virulence genes of *M. oryzae* Triticum. Virus aggressiveness and disease severity would be lessened (Juliana et al., 2020).
- **Digital Agriculture and Remote Sensing:** The new developments in remote sensing, machine learning, and big data analytics are transforming disease surveillance. The body of work Islam et al. (2016) supported the idea that these intersections may give rise to proactive detection systems capable of identifying the onset of an outbreak and tracking the evolution of a disease to take necessary actions in real-time.

8.4. Interdisciplinary and International Collaboration

The encompassing propensities of wheat blast require a collaborative research initiative that transcends disciplines and global fronts. The upcoming research schema should promote partnerships among plant pathologists, breeders, climatologists, and data analysts. Sharing genomic, environmental, and field experiment information can be expedited through international consortia and open-access data platforms, thus improving the rate of invention and discovery concerning wheat blast control.

8.5. Policy and Extension Services

Strong policies, competent management and effective extension services must ensure adequate disease management. There is a need to focus on funding for research on wheat blast, and policymakers need to construct laws that will enable the quick application of new technologies. At the same time, extension services help farmers by ensuring they get information and assistance, so that new and better ways of managing the problem are implemented. As for conclusions, expected future efforts geared toward fighting the wheat blast should attempt to put together at least molecular biology methods and models with international research collaboration. Overcoming

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the impact of climate change, how pathogens are developed, and international trade will be essential in keeping wheat blast in check from being a pandemic threat that endangers food supply all over the globe.

9. CONCLUSION

Wheat blast, caused by *Magnaporthe oryzae* pathotype Triticum, constitutes a serious and increasing threat to international wheat cultivation and nutrition. Following its first detection in Brazil during 1985. This pathogen has extended its geographical spread to include important wheat-producing countries of South America, Asia, and Africa. The disease's ability to spread through both seed and air, together with lightning-fast cycle of infection and the making of virulence factors like effector proteins and secondary metabolites, amplifies the intricacy of its pathogenesis. The knowledge of taxonomy, biology and epidemiology of *M. oryzae* Triticum should be well outlined to proffer efficient management procedures. The discovery of resistance genes such as Rmg8, RmgGR119, and the resistance-conferring 2NS chromosome segment from Aegilops ventricosa offer hopeful prospects for breeding programs. On the other hand, the pathogen's elevated genetic diversity and capacity to quickly defeat resistance mechanisms necessitate constant vigilance and multiple control strategies.

Strategies that integrate conventional breeding, chemical control, cultural practices, and new intervention biotechnologies (i.e., CRISPR/Cas genome editing, RNA interference) are the most effective ways of reducing the impact of wheat blast disease. Moreover, the unchecked spread of climate change, which can make conditions increasingly conducive for pathogen invasion, calls for foresight and new approaches to address future research needs, which include predictive modeling and comprehensive interdisciplinary work. Addressing the possible development of a pandemic due to wheat blast disease makes a strong case for an anticipatory and integrated research framework. Protection of global wheat production to ensure food security for all in the presence of this dangerous pathogen will require increased international collaboration, improved surveillance systems, and hastened application of novel genetic and biotechnology approaches.

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