

## Integrated pest management programme for cereal blast fungus *Magnaporthe oryzae*<sup>1</sup>

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### Abstract

*Magnaporthe oryzae*, the causal agent of blast diseases, is a destructive filamentous fungus that infects many plants including most economically important food crops, rice, wheat, pearl millet and finger millet. *M. oryzae* has numerous pathotypes because of its high host-specificity in the field. The *Oryza* pathotype (*MoO*) of *M. oryzae* is the most devastating pathogen of rice, which causing 10-30% yield loss in the world. On the other hand, the *Triticum* pathotype (*MoT*) causes blast disease in wheat, which is now a serious threat to wheat production in some South American countries, Bangladesh and in Zambia. Because of low fungicide efficacy against the blast diseases and lack of availability of resistant varieties, control of rice and wheat blast diseases is difficult. Therefore, an integrated management programme should be adopted to control these two diseases in the field. Here, we introduced and summarized the classification, geographical distribution, host range, disease

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symptoms, biology and ecology, economic impact, and integrated pest management (IPM) programme of both rice and wheat blast diseases.

**Keywords:** rice blast, wheat blast, *Magnaporthe oryzae*, integrated pest management

## 1. Introduction

Integrated Pest Management (IPM) is the implementation of diverse methods of pest controls, paired with monitoring to reduce unnecessary pesticide applications (USDA, <https://nifa.usda.gov/program/integrated-pest-management-program-ipm>). The goal of IPM in agriculture is to reduce the levels of pests below the level at which they would cause economic injury to crops by an ecosystem approach that combines various management strategies and practices to minimize the use of pesticides. Although IPM may include the use of pesticides, the primary components of IPM clearly separate it from typical pest control practices that rely exclusively on trapping and poisoning. Those five components are inspection/monitoring, identification, establishment of threshold levels, implementation of two or more control measures, measurement and evaluation ([https://www.cdc.gov/nceh/ehs/Docs/Factsheets/What\\_Is\\_Integrated\\_Pest\\_Management.pdf](https://www.cdc.gov/nceh/ehs/Docs/Factsheets/What_Is_Integrated_Pest_Management.pdf)).

The filamentous ascomycete fungus *Magnaporthe oryzae* (*Mo*: anamorph *Pyricularia oryzae*) infects more than 50 species of grasses including the most economically important food crops, rice, wheat, maize, pearl millet and finger millet, and causes blast diseases (Igarashi *et al.* 1986; Couch and Kohn 2002; Talbot 2003; Sesma and Osbourn 2004; Dean *et al.* 2005; Wilson and Talbot 2009; Islam *et al.* 2016; Pordel *et al.* 2021). However, a high degree of host-specificity exists among and within various lineages or pathotypes of *M. oryzae* (Kato *et al.* 2000; Klaubauf *et al.* 2014; Gladieux *et al.* 2018). Among them, rice blast caused by the *Oryza* pathotype (*MoO*) of *M. oryzae* is a causal organism of the most destructive blast disease in rice. It causes 10-30% yield loss in the rice-growing countries and poses threat to food and nutritional security of the ever-increasing

population of the world (Mutiga *et al.* 2021). It is estimated to destroy enough rice to feed more than 60 million people in every year. The fungus is a serious threat to rice production in 85 countries (Scardaci *et al.* 2003). Due to the ability of rapid mutation and development of resistance to chemical fungicides and overcome of the resistance of rice varieties against this notorious fungus, durable management of rice blast is a challenging research subject since long (Wang and Valent 2017).

The *Triticum* pathotype of *M. oryzae* (*MoT*) causes blast disease in wheat, which is now a serious threat to wheat production in some South American countries (such as Brazil, Bolivia, Argentina and Paraguay) (Igarashi *et al.* 1986; Islam *et al.* 2020), Bangladesh (Islam *et al.* 2016) in Asia and Zambia in Africa (Tembo *et al.* 2020). The wheat blast disease was first discovered in Paraná state of Brazil in 1985 and then gradually spread to neighboring wheat growing countries. It is a fearsome disease of wheat which causes yield loss up to 100% (Islam *et al.* 2016). It is now a threat to wheat production in about 3 million hectares of wheat growing areas in South America, nearly one million hectares in Bangladesh (Islam *et al.* 2020) and wheat-growing areas in Zambia (Tembo *et al.* 2020). Application of fungicides to control this disease is unreliable (Castroagudin *et al.* 2015) and the resistant varieties are not durable. At conducive environmental conditions (18-30°C and >80% RH, relative humidity) during ear emergence or grain filling, this disease can become an epidemic and devastate wheat crop within a week (Islam *et al.* 2019). In 2016, the first epidemic outbreak of wheat blast in Bangladesh destroyed more than 15,000 hectares of wheat in eight districts (Islam *et al.* 2016). Using field pathogenomics and open data sharing approaches, the causal organism of wheat blast in Bangladesh was determined as a lineage of South American *M. oryzae* (Islam *et al.* 2016). The recent Zambian wheat blast was also caused by the same *Triticum* lineage of *M. oryzae* (*MoT*) (Tembo *et al.* 2020). Considering the seedborne and windborne natures of the *MoT*, scientists fear that wheat blast fungus may further spread to the neighboring South Asian and African wheat-growing countries (Islam *et al.* 2020). Therefore, wheat blast is now a formidable foe of global wheat production. It clearly poses a serious threat to food and nutritional security of South

America, Asia and Africa (<https://www.cabi.org/isc/datasheet/121970>). It is worthy to mention that China and India are the first and second largest wheat producing countries in the world, respectively. Therefore, novel approaches are needed to combat this wheat killer before it becomes catastrophic by introducing this disease in the major wheat-growing countries (Islam *et al.* 2020; Mutiga *et al.* 2021). Although a large body of literature is available, effective management of blast disease in major cereal food crops is still a highly challenging task (Islam *et al.* 2020; Mutiga *et al.* 2021). IPM may be a plausible approach to manage the blast diseases in rice and wheat. This report introduces and summarizes the classification, geographical distribution, host range, disease symptoms, biology and ecology, economic impact, and IPM programme of both rice and wheat blast diseases.

## **2. Classification, geographical distribution, and host range of the pathogens**

Rice and wheat blast fungus each have several scientific names and share the same taxonomic tree from domain to genus. The only difference is that they are distinct pathotypes of *M. oryzae* (Table 1). Rice blast is widespread in the 85 rice-growing countries of the world. On the other hand, wheat blast disease is a big problem in Brazil, Bolivia, Paraguay, Argentina, Bangladesh and Zambia (Table 2) (Islam *et al.* 2020; Tembo *et al.* 2020). *M. oryzae* has a broad host range at the species level, including rice (primary), wheat, maize, barley, millet and more than 50 species of Poaceae and some members of dicotyledonous plants (Asuyama 1965; Ou 1972; Talbot 2003; Zhang *et al.* 2016; Pordel *et al.* 2021). *M. oryzae* has several host-specific pathotypes such as *Oryza* (*MoO*), *Triticum* (*MoT*), *Lolium* (*MoL*) etc. (Gladieux *et al.* 2018). The *MoT* has a moderate host range including wheat (primary), barley, triticale and oats (Urashima *et al.* 2004; Kohli *et al.* 2011; Saharan *et al.* 2016).

**Table 1. Classification of rice and wheat blast fungus**

Pathogen	Preferred Scientific Name	Other Scientific Names	Disease	Taxonomic tree							
				Domain	Kingdom	Phylum	Class	Order	Family	Genus	Species
Rice blast fungus	<i>Magnaporthe oryzae</i> Oryza (MoO)	<i>Pyricularia grisea</i> , <i>M. grisea</i> , <i>P. oryzae</i> Oryza	Rice blast	Eukaryotes	Fungi	Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	<i>Magnaporthe</i>	<i>M. oryzae</i> Oryza
Wheat blast fungus	<i>M. oryzae</i> Triticum (MoT)	<i>P. oryzae</i> Triticum, <i>M. oryzae</i> Triticum	Wheat blast	Eukaryotes	Fungi	Ascomycota	Sordariomycetes	Magnaporthales	Magnaporthaceae	<i>Magnaporthe</i>	<i>M. oryzae</i> Triticum

**Table 2. Distribution of wheat blast disease across the world**

Continent/Country/Region	Distribution	Last reported	Origin	First reported	Invasive	Reference	Notes
<b>Asia</b>							
Bangladesh	Present: widespread	2020	Introduced	2016	Yes	Islam <i>et al.</i> 2016, 2020; Malaker <i>et al.</i> 2016	First recorded in the districts of Kushtia, Meherpur, Chuadanga, Pabna, Jessore, Jhenaidah, Bhola and Barisal. The fungus gradually spread to total 20 districts (out of 64) of Bangladesh.
<b>North America</b>							
USA	Infection occurred in only one spike in an experimental farm in Kentucky, USA which	-	Host shift from <i>M. oryzae</i> <i>Lolium</i>	2011	No	Farman <i>et al.</i> 2017	A gray leaf spot on annual & perennial ryegrass caused by wheat blast pathogen was recorded in 2002.

	was successfully contained.						
<b>South America</b>							
Brazil	Present: all the wheat growing regions in Brazil	2020	Host shift from a local <i>M. oryzae</i> strain	1985	Yes	Igarashi <i>et al.</i> 1986	
Bolivia	Present: widespread	2020	Introduced	1996	Yes	Barea and Toledo 1996	Santa Cruz
Paraguay	Present: widespread	2020	Introduced	2002	Yes	Viedma and Morel 2002	Alto Parana, Itapua, Caaguazu, Caazapa, Canindeyu and Guaira
Argentina	Present: widespread	2020	Introduced	2007	Yes	Cabrera and Gutiérrez 2007	Chaco, Corrientes, Formosa and Buenos aires
<b>Africa</b>							
Zambia	Present: widespread	2020	Unknown	2019	Yes	Tembo <i>et al.</i> 2020	

### 3. Disease symptoms at different growth stages of the host plants

Both *MoO* and *MoT* cause disease on all above-ground parts of the rice and wheat plants. *MoO* can also cause disease on rice roots in the laboratory studies (Valent 2004). Typical rice blast lesions are diamond shaped, but the most diagnostic symptom is the eye-shaped lesions on the leaves (TeBeest *et al.* 2007) (Fig. 1-A). The first visible symptom of wheat blast on the leaf is water-soaked and diamond-shaped lesions (Fig. 2-G). Under favorable conditions, lesions of both diseases can merge together and rapidly enlarge to several centimeters in length, eventually killing the leaf, and ultimately resulting in plant death. However, wheat blast is predominantly a head disease, while rice blast mainly causes leaf and neck diseases in the field (Islam *et al.* 2020; Mutiga *et al.* 2021).

The symptoms of rice blast on leaves were varied according to the environmental conditions, the age of the plant, and the levels of resistance of the rice cultivars. Initial lesions appear dark green or grey with brown borders; while older lesions are light tan with necrotic borders (Wang *et al.* 2013). On resistant cultivars, lesions induced by *MoO* often remain small in size (1-2 mm) and brown to dark brown in color (TeBeest *et al.* 2007).

The *MoO* often infects neck of rice, resulting in rotten neck or neck blast, which makes the seeds unable to fill normally and even the whole panicle falls down. It can also infect the panicles, and the lesions can be found on the panicle branches, spikes, and spikelets with gray-brown discolorations (TeBeest *et al.* 2007) (Fig. 1-B).



Similar to the Fusarium scab, the most obvious symptoms of wheat blast also appear in the head, and the head is partially or completely bleached (Fig. 2). The affected spike usually has no grain or shriveled grain depending on the stage of flowering/grain filling of the wheat plant (Goulart *et al.* 2007, Islam *et al.* 2016, Surovy *et al.* 2020, Islam *et al.* 2020). Gray marks on the bleached head indicate the formation of fungal spores on the infection point(s) (Islam *et al.* 2016, Islam *et al.* 2020) (Fig. 2-A and B). The white patchy symptoms could be clearly seen at a reasonable distance from the field during the early period of infection (Islam *et al.* 2020).





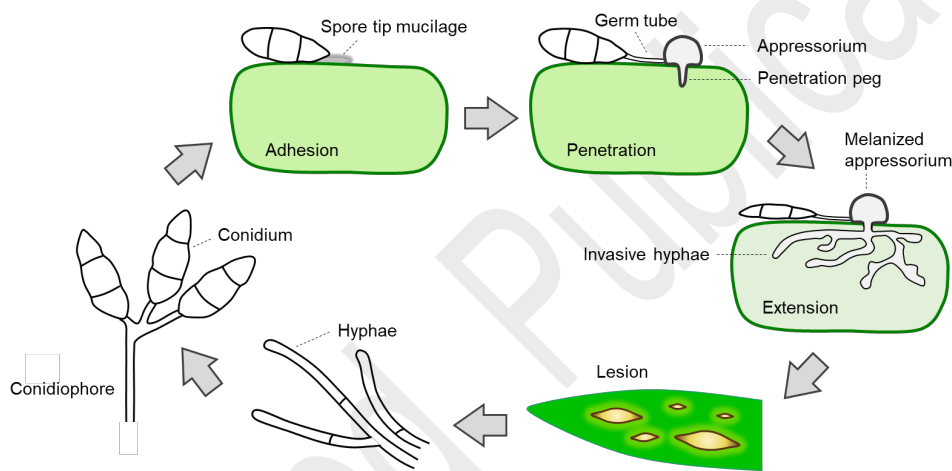
**Fig. 2** Symptoms of blast disease in different parts of wheat plants. (A) Partial to completely bleached (right to left) wheat spikes collected from a blast-affected farmer's field in Meherpur district of Bangladesh. Arrow indicates the point of infection. (B) Completely bleached wheat spikes with traces of grey from blast sporulation at the neck (arrow) of the spike. (C) Complete or partial bleaching of wheat spikes in a blast-devastated field. (D) Normal colour of uninfected wheat grains. (E) Severely shrivelled or wrinkled and discoloured wheat grains affected by the wheat blast. (F) Three shrivelled grains (whitish colour, arrow) and a normal (green)-coloured uninfected grain just below the infection point in a spike. (G) Typical eye-shaped lesion (arrow) with grey centre. (H) Brown coloured lesions with grey centres (arrows) of the infected stems of wheat.

#### 4. Biology and ecology of the pathogen

Foliar infection of *MoO* is initiated by attachment of a three-celled pyriform conidium to the rice leaf cuticle, and formed a dome-shaped structure called an appressorium at the germ tube tip once sensing the hard and hydrophobic signals of rice leaves (Talbot 2003, Ebbole 2007). The mature appressorium generates huge turgor that forces invasive nail through rice epidermis into the interior of plant cells, resulting in the disease lesions that are symptomatic of rice blast disease. The fungus can release a large number of spores from the diseased spot under high humidity conditions, and spread to neighboring rice plants through wind or dew splashing (Ou 1985; de Jong *et al.* 1997; Talbot 2003) (Fig. 3). The pathotype of wheat blast disease appears to follow the similar disease cycle of rice blast (Tufan *et al.* 2009; Chakraborty *et al.* 2021).

There are many factors that affect the occurrence of rice and wheat blast diseases, the most important of which is meteorological factors (Goodman *et al.* 2005; Dixit *et al.* 2020; Islam *et al.*

2019). Rainy and humid weather conditions with favourable temperature can promote the occurrence and development of rice and wheat blast. Global climate change may affect the distribution and development rate of pathogens, thus changing the resistance, growth and metabolism of the plants (Coakley *et al.* 1999; Bevitori *et al.* 2014; Islam *et al.* 2019, Islam *et al.* 2020; Kohli *et al.* 2011; Liu *et al.* 2019; Zhang *et al.* 2014). According to the climate analogue analysis, Mottaleb *et al.* (2018) warned that out of 40.9 million ha of total wheat-producing land in India, Bangladesh, and Pakistan, more than 17% of the area (6.9 million ha) is vulnerable to wheat blast (Mottaleb *et al.* 2019).



**Fig. 3** Life cycle of the rice blast fungus *M. oryzae* *Oryza*. The rice blast fungus causes lesions on rice plants through asexual spores and initiates a new disease cycle within 7 days.

## 5. Economic impact

Rice blast is an economically important disease in all major rice-growing countries because of its severe destruction, which annually leads to the loss of enough rice to feed 60 million people (Pennisi 2010). Several epiphytotics of the disease have been recorded in different parts of the world resulting in serious losses in yield in history. It is the only rice disease that has ever caused serious losses in yield in Korea, and caused more than 65% loss in yield in the hills. Rice blast disease represents a significant threat to rice production worldwide in a long term.

The economic importance of wheat blast derives from the fact that the fungus can reduce yield and grain quality (Goulart *et al.* 2007; Islam *et al.* 2016; Surovy *et al.* 2020). A 5-10% loss in wheat production due to a potential outbreak of wheat blast in Bangladesh, India and Pakistan would reduce wheat production by 886-1771 thousand tons worth of USD 132-264 millions in a single year (Mottaleb *et al.* 2018). In Brazil, reported yield losses on susceptible cultivars ranges from 10 to 100% (Goulart *et al.* 1992; Goulart and Paiva 2000). Due to introduction of wheat blast disease, the wheat cultivation area and total production of wheat in Bangladesh significantly reduced which has lead the country among the top 5 wheat importing nation in the world (Islam *et al.* 2020).

## **6. Components of the IPM programme for rice and wheat blast**

### **1) Detection and inspection**

In order to achieve a rapid, accurate and early detection of rice diseases, several research methods have been developed. The first commonly used method is DNA-based polymerase chain reaction (PCR) analysis. This method has the advantages of strong performance, high sensitivity, and easy operation. At present, PCR analysis of rice fungal diseases mainly uses PCR and DNA sequencers to detect *MoO* spores indoors (Gupta *et al.* 2020).

The second commonly used method is a conventional spectroscopic detection method. Spectroscopy has a wide range of applications in rice disease detection. On the one hand, spectroscopy can provide image information in different spectral bands of the target to be measured and does not require high spatial resolution of the image (Vaks *et al.* 2017). On the other hand, spectroscopic methods need to build complex models, but those models are not universal. Spectral technology has high requirements for instruments and equipment, and it is prone to giving false-positive results (Zhu *et al.* 2018). In general, spectroscopic detection has the advantages of high accuracy, fast response, and intuitive observation results, which can quickly and safely detect crop diseases.

Whole genome analysis was used to identify DNA markers that differentiate *MoT* isolates from other host-specific pathotypes including *MoL* isolates (Pieck *et al.* 2017). A PCR-based diagnostic assay using the marker of MoT3 shows specificity and sensitivity in laboratory studies and is now being developed as a tool for detecting the wheat blast pathogen in the field and in wheat seed or grain lots from affected areas (Pieck *et al.* 2017). However, Gupta *et al.* (2019) found that MoT3 primer also amplifies DNA of rice blast isolates and suggested for development of a highly specific molecular diagnostic tool for the detection of *MoT* for monitoring and surveillance of the worrisome wheat blast disease. Recently, a rapid, specific and convenient diagnostic method was developed for wheat blast pathogen, *M. oryzae Triticum* pathotype using genome-specific primers and Cas12a-mediated technology (Kang *et al.* 2021). This simple method can easily be adapted by plant pathologists, quarantine specialists, and agriculture extension workers to rapidly detect *MoT* in infected plants, seed lots, and alternate hosts.

## 2) Prevention and control

The successful management of rice blast and wheat blast results from a comprehensive series of recommendations that employ several different management strategies, including resistant cultivars, traditional chemical pesticides and biopesticides (Chakraborty *et al.* 2020a, b, 2021; Mutiga *et al.* 2021). Currently, the most effective means of controlling rice blast disease is by the deployment of high-yielding rice cultivars carrying single dominant disease resistance (*R*) gene. This was achieved via a gene-for-gene interaction model, in which *R* gene recognizing a single corresponding dominant avirulence (*AVR*) gene in a particular pathogen strain (Table 3) (Liu and Wang, 2016; Skamnioti and Gurr 2009). However, because *M. oryzae* races are easy to shift under selection pressure to escape host recognition, single-locus resistance is short-lived and often lasting for only 2-4 years, which particularly occurs in large acreages of genetically uniform rice cultivars (Bonman *et al.* 1992). Based on this finding, another effective mean is to monitor the variation of *AVR* gene in the field

population, which are informative for the release and rotation of blast-resistant rice cultivars, and could also be a component of the IPM programme (Table 4) (Fernandez and Orth 2018). Additionally, planting diversified cultivars with different *R* genes or the multiline varieties consisting of blast resistant isogenic loci in the same area, and the adjusted fertilizer application, like appropriately reducing nitrogen and increasing phosphorus and potassium fertilizers after heading can also enhance rice resistance to blast disease.

**Table 3. Cloned rice blast resistance genes and finely mapped rice blast resistance genes from wild rice relatives**

<i>R</i> gene	Origin	Structural information	Resistance	Selected references
<i>Pi-b</i>	indica	NBS-LRR	Broad-spectrum to Japanese blast isolates	Wang <i>et al.</i> 1999
<i>Pi-ta<sup>c</sup></i>	indica	NBS-LRR	Race-specific resistance to US blast isolates until 2004 Arkansas blast outbreak	Bryan <i>et al.</i> 2000
<i>Pi9</i>	<i>Oryza minuta</i>	NBS-LRR member of multi-gene family (9 genes), high amino acid identity to <i>Pi2</i> and <i>Piz-t</i>	Broad-spectrum to SE Asia blast isolates; low level resistance in S. Korea isolates	Qu <i>et al.</i> 2006
<i>Pi2 (Piz-5)</i>	indica	NBS-LRR see <i>Pi9</i> and <i>Piz-t</i> 9 genes	Broad-spectrum to some Philippine isolates but different range from <i>Piz-t</i>	Zhou <i>et al.</i> 2006
<i>Piz-t</i>	indica	NBS-LRR see <i>Pi9</i> and <i>Pi2</i> 9 genes, 8 aa difference between <i>Piz-t</i> and <i>Pi2</i>	Broad-spectrum to some Philippine isolates but different range from <i>Pi2</i>	Zhou <i>et al.</i> 2006
<i>Pi-d2</i>	indica	Receptor-like kinase, mannose binding lectin and serine threonine kinase domain, single gene	Tested only against limited number of Chinese isolates	Chen <i>et al.</i> 2006
<i>Pi33<sup>2</sup></i>	indica and <i>O. rufipogon</i>	Finely mapped NBS-LRR but RPM1-like	Tested only against limited number of isolates	Berruyer <i>et al.</i> 2003
<i>Pii</i>	japonica	70 AA secreted protein	Tested only against limited number of Japanese isolates	Yoshida <i>et al.</i> 2009
<i>Pi36</i>	indica	NBS-LRR Single gene	Unknown	Liu <i>et al.</i> 2007
<i>Pi37</i>	japonica	NBS-LRR 4 genes	Unknown	Lin <i>et al.</i> 2007
<i>Pi50</i>	japonica	NBS-LRR 12 genes	Broad-spectrum	Su <i>et al.</i> 2015
<i>Pi64</i>	japonica	NBS-LRR	Broad-spectrum	Ma <i>et al.</i> 2015
<i>Pikm</i>	japonica	NBS-LRR	Tested only against limited number of isolates	Yoshida <i>et al.</i> 2009; Ashikawa <i>et al.</i> 2008
<i>Pit</i>	japonica	NBS-LRR	Tested only against limited number of isolates	Hayashi <i>et al.</i> 2009
<i>Pi5</i>	japonica	NBS-LRR	Tested only against limited number of Korean isolates	Lee <i>et al.</i> 2009
<i>Pid3</i>	indica	NBS-LRR	Tested only against	Shang <i>et al.</i> 2009

<i>Pid3-A4</i>	<i>Oryza rufipogon</i>	NBS-LRR	limited number of isolates Tested only against	Lv <i>et al.</i> 2013
<i>Pi54</i>	Tetep	NBS-LRR	limited number of isolates Broad-spectrum to India and US isolates	Costanzo <i>et al.</i> 2010
<i>Pish</i>	japonica	NBS-LRR	Tested only against	Takahashi <i>et al.</i> 2010
<i>Pikp</i>	japonica	NBS-LRR	limited number of isolates Tested only against	Yoshida <i>et al.</i> 2009; Yuan <i>et al.</i> 2011
<i>Pi25</i>	japonica	NBS-LRR	limited number of isolates Tested only against	Chen <i>et al.</i> 2011
<i>Pi1</i>	C101LAC	NBS-LRR	Broad-spectrum	Hua <i>et al.</i> 2012
<i>Pi-CO39(t)<sup>c</sup></i>	indica and japonica	Locus carries multiple NBS-LRR-like genes, flanked by serpins	Unknown	Chauhan <i>et al.</i> 2002
<i>Pi40</i>	<i>O. australiensis</i>	Finely mapped, nests within 6 NBSLRs: single gene	Broad-spectrum to Korean and Philippine blast isolates	Jeung <i>et al.</i> 2007
<i>Pik<sup>h</sup></i>	indica	NBS-LRR 6 genes	Broad-spectrum to NW Himalayan blast isolates	Sharma <i>et al.</i> 2005
<i>pi21</i>	japonica	Novel protein with heavy-metal binding and proline-rich domains	Partial R gene but specific	Fukuoka <i>et al.</i> 2007
<i>Pigm</i>	GM4	NBS-LRR 2 genes	Broad-spectrum	Deng <i>et al.</i> 2017

**Table 4 Identified avirulence genes in *Magnaporthe oryzae* *Oryza***

AVR gene	ID number	Function	Cognate R gene in rice	Reference
<i>AVR-Pita</i>	AF207841	Zinc metalloprotease	<i>Pita</i>	Khang <i>et al.</i> 2021; Orbach <i>et al.</i> 2000; Chuma <i>et al.</i> 2011; Jia <i>et al.</i> 2000
<i>AVR-Piz-t</i>	HE578813	Target rice U3 ubiquitin ligase; reduces Flg22 and chitin induced ROS production	<i>Piz-t</i>	Park <i>et al.</i> 2012
<i>AVR-CO39</i>	AF463528	Interacts with RGA4/RGA5	<i>CO39</i>	Ribot <i>et al.</i> 2013; Cesari <i>et al.</i> 2013
<i>AVR-Pia</i>	AB498873	-	<i>Pia</i>	Yoshida <i>et al.</i> 2009
<i>AVR-Pii</i>	AB498874	C2H2 zinc-finger motif	<i>Pii</i>	Yoshida <i>et al.</i> 2009
<i>AVR-Pik/km/kp</i>	AB498875-AB498879	-	<i>Pik</i>	Yoshida <i>et al.</i> 2009
<i>AVR-Pib</i>	KM887844	-	<i>Pib</i>	Zhang <i>et al.</i> 2015
<i>AvrPi9</i>	MGG_12655	-	<i>Pi9</i>	Wu <i>et al.</i> 2015
<i>PWL1</i>	AB480169	-	-	Kang <i>et al.</i> 1995
<i>PWL2</i>	MGG_04301	-	-	Khang <i>et al.</i> 2010; Kang <i>et al.</i> 1995; Sweigard <i>et al.</i> 1995; Giraldo <i>et al.</i> 2013
<i>ACE1</i>	AJ704622	Polyketide synthase-peptide synthetase	<i>Pi33</i>	Böhnert <i>et al.</i> 2004
<i>AVRPi54</i>	MGG_01947	-	<i>Pi54</i>	Ray <i>et al.</i> 2016

Fungicide application is another useful strategy to control rice blast disease. Its efficacy is determined by the chemical structure of compound, timing and method of application. The levels of

disease, efficiency of forecasting systems and the rate of emergence of fungicide resistant strains are all important for the control efficiency. The most commonly used rice blast fungicides in global markets are as follows: Probenazole in Oryzemat<sup>TM</sup>, Meiji Seika, Tricyclazole in Segard<sup>TM</sup>, DowAgrosciences, Azoxystrobin in Quadris<sup>TM</sup>, Syngenta, Isoprothiolane in Fuji-One<sup>TM</sup>, Nihon Nohyaku and Propiconazole in Tilt<sup>TM</sup>, Syngenta (Skamnioti and Gurr 2009). Additionally, several herbicides (metazachlor, cafenstrole and diallate) were reported as effective drugs for control of the rice blast disease by preventing septin ring assembly in appressorium and host penetration (He *et al.* 2020). In recent years, more and more studies are focused on the development of targeting chemicals or compounds which inhibit the activity of key proteins of the pathogens. For example, one lead compound (lead 25) which binds to the docking site of a key enzyme (trehalose-6-phosphate synthase, Tps1) responsible for trehalose synthesis and pathogenicity, is indicated the potential to be used as an inhibitor of Tps1 for the control of *M. oryzae*-mediated rice blast disease (Xue *et al.* 2014). The biopolymer, chitosan is a potent biofungicide against rice blast, which requires the cell integrity pathway, disrupts plasma membrane function and inhibits septin-mediated rice plant infection (Lopez-Moya *et al.* 2021).

Biological control of rice blast disease is desirable, low-cost and more environmentally benign than fungicide application. Control of rice blast by microbial agents and their derivative have intensively been investigated (Chakraborty *et al.* 2021). For example, using avirulent isolates of *M. oryzae* (Ashizawa *et al.* 2005), the wheat and barley fungal pathogen *Bipolaris sorokiniana* (Manandhar *et al.* 1998), the fungus *Exserohilum monoceras* (Tsukamoto *et al.* 1999) and the rice phylloplane fungal isolate MKP5111B (Ohtaka *et al.* 2008) have been effectively suppressed. Besides, antagonistic bacterial strains of *Pseudomonas fluorescens*, *Bacillus polymyxa* (Karthikeyan *et al.* 2008), *B. licheniformis* (Tendulkar *et al.* 2007) and *Streptomyces* sp. PM5 (Prabavathy *et al.* 2006) are reported to be useful to control rice blast disease (Chakraborty *et al.* 2021). Promise of endophytic *Bacillus* spp. in biocontrol of wheat blast has also been demonstrated in both greenhouse

and field conditions by Dutta *et al.* (2018) and Islam *et al.* (unpublished). However, the effectiveness of biological control of wheat blast has not been proven in the large-scale and long-term field experiments (Chakraborty *et al.* 2021). Therefore, an integrated management program should be implemented to avoid overuse of a single control method and fight against genetic resistance. For example, eliminating crop residue could reduce the occurrence of overwintering and limit infection in the subsequent seasons (Scardaci *et al.* 2003).

Similar to rice blast control, breeding of blast-resistant wheat varieties is an environment-friendly method to control wheat blast, but resistance sources for breeding durable blast resistant variety are very limited (Table 5). To date, only 10 genes and a chromosomal segment have been identified as the resistance sources to wheat blast fungus, and majority of these genes are not effective in protecting wheat plant from blast fungus at higher temperature (Table 5) (Islam *et al.* 2020). Introgression of *Rmg8* and *RmgGR119* genes into the elite wheat varieties (including variety having 2NS translocation) of Bangladesh are in progress in Institute of Biotechnology and Genetic Engineering (IBGE) of Bangabandhu Sheikh Mujibur Rahman Agricultural University (Islam *et al.* unpublished personal communication). Additionally, planting diversified cultivars with different *R* genes or the multiline varieties consisting of blast resistant isogenic loci in the same area, and the adjusted fertilizer application can also contribute to blast disease resistance.

**Table 5 Resistant genes identified in wheat against blast fungus**

Resistant gene	Wheat source	Reference
<i>RmgTd(t)</i>	<i>Triticum dicoccum</i> KU109 (Tat 4)	Takabayashi <i>et al.</i> 2002
<i>Rmg1(Rwt4)</i>	Common wheat, Norin 4 (hexaploid)	Takabayashi <i>et al.</i> 2002
<i>Rmg2</i>	Common wheat, Thatcher	Zhan <i>et al.</i> 2008
<i>Rmg3</i>	Common wheat, Thatcher	Zhan <i>et al.</i> 2008
<i>Rmg4</i>	Common wheat, Norin 4	Nga <i>et al.</i> 2009
<i>Rmg5</i>	Common wheat, Red Egyptian	Nga <i>et al.</i> 2009
<i>Rmg6(Rwt3)</i>	Common wheat, Norin 4	Vy <i>et al.</i> 2014
<i>Rmg7</i>	<i>Triticum dicoccum</i> (tetraploid wheat), KU112 (St17), 120 (St24), KU122 (St25)	Tagle <i>et al.</i> 2015
<i>Rmg8</i>	Common wheat, S-615	Anh <i>et al.</i> 2015 ; Anh <i>et al.</i> 2018
<i>RmgGR119</i>	Albanian wheat accession GR119	Wang <i>et al.</i> 2018
2NS translocation	Chromosomal segment from <i>Aegilops ventricosa</i>	Cruz <i>et al.</i> 2016



Fungicides are effective to wheat blast control by reducing the *MoT* sporulation (Bockus *et al.* 2015) and eradicating *MoT* primary inoculum via an effective seed treatment (Toledo 2015). The only fungicide labelled for seed treatment against wheat blast in Brazil is the demethylation inhibitor (DMI) difenoconazole. The eradicator fungicide dimethyldithiocarbamate thiram, which is labelled for the control of other seed-borne wheat pathogens, is also effective against *MoT* (Bockus *et al.* 2015). In Brazil, 28 fungicides were labelled for the management of wheat blast, including 11 triazoles and seven mixtures of quinone outside inhibitors (QoIs) and triazoles (Ministério da Agricultura Pecuária e Abastecimento - MAPA, 2017). Besides, strengthening of quarantine and seed trading laws will provide the best course of action to prevent the further spread of wheat blast (Valent *et al.* 2013; Mezzalama, 2016; Sadat and Choi 2017; Singh 2017; Islam 2020). To prevent further spread of wheat blast through grain trading, recently developed rapid diagnostic method (Kang *et al.* 2021) should be deployed at all plant quarantine offices worldwide.

Some plant probiotic *Bacillus* spp. isolated from rice and wheat grains significantly controlled wheat blast disease in the greenhouse and field conditions in Bangladesh (Dutta *et al.* 2018; Islam *et al.* 2020). These bacteria suppressed wheat blast fungus through antibiosis and induced systemic resistance in the wheat plants (Dutta *et al.* 2018). Besides, some non-cytotoxic linear lipopeptide isolated from a marine *Bacillus subtilis* strain 109GGC020 (Chakraborty *et al.* 2020a), and oligomycins and staurosporine from *Streptomyces* spp. inhibited conidiogenesis, and germination of conidia of the *MoT* fungus both *in vitro* and *in vivo* and significantly suppressed wheat blast disease in the greenhouse and field conditions (Chakraborty *et al.* 2020b). Recently, the TiO<sub>2</sub> P25 type nanoparticles have been shown high efficacy in control of wheat blast in Bangladesh (Islam *et al.* unpublished personal communication). Until the development of a durable blast resistant variety either by classical breeding or gene editing, some novel integrated management approaches are needed to combat wheat blast fungus in the field.

## 7. Future perspectives

Blast disease remains a serious threat to rice and wheat production and global food security. Although a large number of research efforts have been given against the rice and wheat blast, many questions and approaches should be answered and established to guarantee safe production of rice and wheat. Considering the devastating nature and potential economic impacts of blast diseases in rice and wheat, we suggest following integrated approaches for the durable management of this formidable foe of the major food crops:

- (1) Cloning and breeding of broad-spectrum disease-resistance genes.
- (2) Release and rotation of blast-resistant rice cultivars according to the *AVR* genotype of the field population.
- (3) Application of microbiome-based biological control strategies.
- (4) Monitoring of pathogens in early stage and optimization of prevention and control approaches.
- (5) Application of rapid diagnostic method in plant quarantine for restricting further spread of wheat blast and also the early detection of the diseases in the fields.
- (6) Timely weather forecasting and introduce a warning to the growers.

Finally, based on the current knowledge, an integrated management programme should be practiced for reducing the crop failure due to blast diseases in rice and wheat.

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