



Review Article

Rice Blast (*Pyricularia oryzae*) Disease in Indonesia

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Received 01 November 2024; Accepted 09 November 2024; Published 30 December 2024

Editor: Amjad Ali

Abstract

Blast disease in Indonesia has widely spread and caused damage to rice production. It was reported in 2022 that around 32434 Ha area of paddy rice field had been attacked by blast disease. Blast attacks at vegetative and generative stages can cause plant death and Crop failure. Blast disease was first discovered in upland rice fields which has spread widely and caused damage to lowland rice. Blast attacks tend to increase every year, especially in irrigated rice fields. Indonesia's most widespread blast attack area, with a very high level of damage, is the province of West Java. A few years ago, the intensity of blast attacks fluctuated. Blast attacks occurred in 33 provinces in Indonesia. Several factors influence the intensity of blast attacks in Indonesia. High doses of N fertilizer, rice varieties, frequently use of pesticide and weed control techniques had been known as factors that could increase blast attacks on rice. Integrated rice blast disease-control techniques in Indonesia are a combination of several techniques. It works to minimize the impact and prevent disease.

Keywords: Blast-resistant varieties; DNA marker; Gene resistance; MAS

Introduction

Rice blast is a disease that attacks rice plants. It is caused by the fungus *Pyricularia oryzae*. The fungus *P. oryzae* can infect plants at all stages of growth, and if younger plants are infected, it may cause crop failure. Infection in plants in the vegetative stage is usually in the part of the leaf called the leaf blast, and in the generative stage, in addition to infecting the leaves, it also infects panicle neck known as neck blast.

The symptoms of rice blast are seen on leaves, stems, panicle necks, panicles and even on the grain. Symptoms that appear on the leaves are rhombus-shaped spots with pointed ends; this is a specific symptom of rice blast disease. The color at the center of the spot is generally gray or whitish and the edges are brown or reddish-brown. The specific symptom of neck blast is the rotting of the tip of the panicle stalk which causes the grain to become hollow. Symptoms of rice blast found in grain are small, round spots with the rice blast-distinctive color (TeBeest *et al.* 2007).

Three provinces with most widespread blast attack area in Indonesia, are the province of West Java, followed by Central Java and East Java. Compared to other regions over the last ten years these three provinces fell on a very

high level of damage (PPID Data 2023). Sukabumi, Subang, Karawang and Indramayu have become endemic areas of blast disease for many years. Blast attacks in irrigated rice fields tend to increase every year. The objectives and scope of writing this article are: (1) the developmental status of blast disease in Indonesia, (2) blast-disease control and (3) prospects and challenges for developing blast-resistant rice in Indonesia.

Rice blast in Indonesia

The fungus *P. Oryzae*

The fungus *P. oryzae* belongs to the Magnaporthaceae family which has elliptical conidia with one end pointed and the other rounded and is characterized by having two walls or three chambers. *P. oryzae* conidia are generally formed and released at night when the humidity exceeds 90–92% (Miah *et al.* 2017), although it can also occur during the day such as after it rains. The released conidia are very explosive due to the osmotic pressure of the cells under the conidia. In addition, after being released, the conidia are very easily carried by the wind, thus it is easily dispersed.

To cite this paper: Fitriah N, S Rahmawati, D Astuti, AN Nurhasanah, A Rachmat, VE Windiastri, D Widyajayantie, CF Pantouw (2025). Rice blast (*Pyricularia oryzae*) disease in Indonesia. *Intl J Agric Biol* 33:330308. <https://doi.org/10.17957/IJAB/15.2284>

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Conidia that attach to the surface of the host will immediately penetrate the cuticle. The younger the surface of the plant, the more easily it is penetrated by this fungus. Conidia will germinate and, in the presence of chemical signals and changes in conditions, both temperature (25–28°C) and acidity, will induce the formation of appressoria. The appressoria will penetrate the cuticle and form penetrating hyphae that form a haustorium that will enter the host plant cell. The infection begins with the pathogen taking nutrients from the host plant cells. It continues with the pathogen invasion where the pathogen begins to develop and ends with the colonization process with the regeneration of pathogen that occurs within the host plant, both intercellular and intracellular. Symptoms will start to appear when the invasion process occurs and proceeds to the death of the host cell. The life cycle of the fungus *P. oryzae* is shown in Fig. 1.

Status of blast disease in Indonesia

Rice blast can be found in almost all rice production centers in Indonesia. Initially, this disease was only found in upland rice, but nowadays rice blast disease also attacks rice plants in irrigated rice fields in lowlands throughout Indonesia (Suganda *et al.* 2016). Ten years ago, blast disease had become the top disease that attacked rice production in Indonesia, as presented in Fig. 2. (PPID data 2023).

The intensity of blast attacks in Indonesia in the last 10 years (2013–2022) has fluctuated, where blast attacks occurred in 33 provinces with varying degree of damage. Particularly in endemic areas, the intensity of attacks was relatively high. Data on the incidence of blast attacks in Indonesia during 2013–2022 are shown in Fig. 3 (PPID data 2023). Blast-disease attacks in the last years have decreased, due to climatic changes. Hot temperature conditions will influence the development of blast fungi so that the distribution and incidence of blast attacks decrease.

Blast disease endemic areas, in particular, are Lampung, South Sumatra, Jambi, West Sumatra, Central Sulawesi, Southeast Sulawesi, and West Java, namely Sukabumi (Lestari *et al.* 2016). Panicle neck blasts are particularly common in lowland rice in West Java, namely Sukabumi and Kuningan, Lampung (Tulang Bawang and Central Lampung) and Bali in Tabanan (Santoso and Anggiani 2009).

Several factors influence the intensity of blast attacks in Indonesia, namely, high doses of N fertilizer. The intensity of N fertilizer use and plant age significantly correlate with increasing the severity of blast disease, a one-time increase in the dose of N fertilizer can increase the severity of blast disease by 8.47%, and increasing plant age every day increases the severity of the disease by 0.31% (Zulaika *et al.* 2018). The rice varieties, frequency of pesticide use and weed control techniques contribute to increasing blast disease development (Andriyani and Wiyono 2021). Moreover, water deficiency in the plant can increase blast attacks on rice; these cause the silicon levels in the plant to

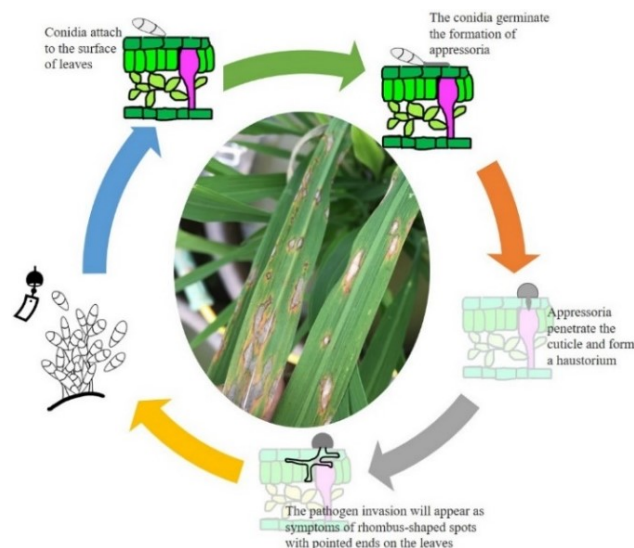


Fig. 1: The infection cycle of the fungus *P. oryzae* (Adapted from Wilson and Talbot 2009)

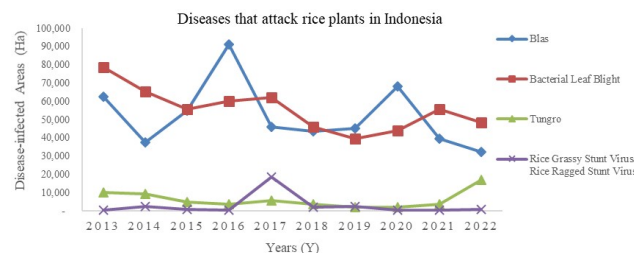


Fig. 2: Major Diseases affecting rice production in Indonesia



Fig. 3: The blast incidence in Indonesia during 2013 to 2022

decrease. Silicon affects the thickness and hardness of plant cell walls; thus, low silicon levels will make plants more susceptible to penetration by this fungus. Besides that, *P. oryzae* has high genetic diversity, so it quickly produces new races that can change their virulence properties in a short time (Sudir *et al.* 2014). Moreover, *P. oryzae* is known as an airborne and seed-borne fungus. Some abiotic conditions, such as temperature, precipitation rate, reasonably high relative humidity, and low sunlight radiation support the transmission and dispersion of this fungus (Miah *et al.* 2017).

Pyricularia races in Indonesia

P. oryzae can cross-breed between haploid hyphae of

Table 1: Composition and distribution of the *P. oryzae* race on the island of Java

Race	Region
101, 033, 001,003,011, 013, 041, 043, 051, 053, 061, 073,131, 203, 213, 221, 253, 313, 351, 353	West Java
001,003, 011, 013, 043, 073, 101, 103, 111, 113, 121, 133, 151, 153, 161, 203, 211, 213, 233, 253, 301, 311, 363	Center Java
001,003, 011, 013, 043, 053, 101, 103, 113, 121, 143, 153, 253, 273, 303, 313, 321, 333	East Java

different genetics and has a high mutation rate, allowing segregation and recombination between other races to produce new races (Santoso *et al.* 2007). *P. oryzae* races are easy to change to adapt to environmental pressures. This condition not only leads to a high level of virulence but also leads to break rice resistance immediately. Research on monitoring the types of *P. oryzae* races in Indonesia has been carried out for a long time, but complete data on all identified blast races have not been published. There are four dominant pathogenic races of *P. oryzae* in Indonesia: races 033, 073, 133 and 173. *Pyricularia* races 133 and 173 had higher virulence levels than races 033 and 073 against local rice varieties (Santoso *et al.* 2020). The composition and distribution of the blast pathogen race in several areas on the island of Java has been reported by Anggiani *et al.* (2013) and Sudir *et al.* (2014). The results of identifying the *Pyricularia* race are summarized in Table 1. The blast race that dominant in those three regions are 101, 001, 003, 041, 033, 053, 013, 073, 013, 153, 113, 151 and 273. Meanwhile, there were 26 blast races population identified in Lampung provinces during 2000 - 2004, where seven races of them, *i.e.*: 001, 023, 033, 073, 101, 133 and 173 always existed in every growing season. Race 013 was found in 2000, 2001 and 2003 growing seasons (Santoso and Anggiani, 2009). Another report on the composition and distribution of the blast pathogen race was conducted in West Papua by Santoso *et al.* (2019). Thirty-four *Pyricularia* isolates were isolated from the infected plant from Prafi, Masni, Sidey and Oransbari Districts. These isolates were classified into nine race groups, namely race 211, 213, 241, 251, 253, 313, 333, 353 and 373, and the dominated races were 333 and 373 (Santoso *et al.* 2019).

Monitoring pathogenic races is generally carried out by using a set of differential varieties in which each array has a gene that can distinguish the pathogenicity of the tested isolates. Indonesian blast differential rice plants, namely Asahan, Cisokan, IR64, Krueng Aceh, Cisadane, Cisanggarung and Kencana Bali. The *Pyricularia* race naming system uses the method developed by Mogi *et al.* (1991). Differential varieties resistance reaction data against *Pyricularia* isolates were analyzed and identified to determine the *Pyricularia* race numbers. The severity of blast attack is formulated as the blast race number and indicating the susceptible or compatible reaction of a rice variety (Santoso *et al.* 2019).

Rice blast control in Indonesia

Strategies to control and prevent rice blast disease are needed and important. Various conventional rice blast

disease-control techniques have been widely applied to overcome the challenge of the increasing distribution of rice blast disease. In general, techniques for integrated rice blast disease-control are divided based on the cultivation system, chemical agent application, biological agent utilization, and combination of several techniques (Sudir *et al.* 2014).

Cultivation System

Initially, the rice blast disease was prevented using a plant cultivation system approach. Seed selection, spacing, irrigation, fertilization and post-harvest were all carried out with consideration and supervision. These were done to overcome, minimize the impact, and prevent the disease.

Seed selection

Rice seeds to be planted must be disease-free. In endemic areas of the disease, it is necessary to treat seeds with fungicide or bactericidal soaked. Selection of healthy seeds also means reducing the initial inoculum of disease-causing pathogens, especially seed-borne pathogens (Nuryanto 2018).

Inoculant prevention

Rice plants infected by rice blast disease must be destroyed. Eradication can be done at the end of the planting season by burning or composting. Extraction of fermented straw compost from rice plants has a potential to reduce the incidence of panicle neck blast by 71–87% (Suwandi *et al.* 2016).

Planting resistant varieties

Blast disease control with rice varieties that have durable and polygenic resistance is one way to deal with blast pathogen that has many races and is very dynamic (Yuliani and Maryana 2014). The lower the intensity of blast disease in a rice variety, the higher the resistance level of the rice variety to blast disease (Yulianto 2017). The use of resistant varieties also means avoiding environmental pollution due to the use of pesticides in rice cultivation (Nuryanto 2018).

Crop rotation of resistant varieties and fertilization

Alternating resistant varieties and applying fertilizer to plant needs can effectively control blast disease in irrigated rice fields (Prayudi 2008). This method is more sustainable because it protects the environment from the adverse effects of fungicides. In addition, rotation can be done by planting crops other than rice such as legumes: peanuts, soybeans and others.

Irrigation control

It is very important to manage the rice field irrigation system. A high-humidity environment for plant growth is created by irrigated the rice field. In endemic areas of the disease, the initial inoculum is generally found in soil, weeds, rice seed, and crop residues. Early inoculums supported by long periods of wetness in plant tissues can accelerate disease development. The humidity of the plant growth environment can be reduced by adjusting the irrigation method (Nuryanto 2018). When rice is under drought stress, it is more susceptible to rice blast disease. Therefore, irrigating dry rice fields may reduce the severity of attacks. The beginning of the rainy season could also be the right time for planting to mitigate drought in upland rice fields (Pooja and Katoch 2014).

Nutrient monitoring

The regulation of nutrients is important in controlling rice blast disease. Adding organic matter to rice fields increases the population of soil organisms, fertility, and soil pH. The organic matter should be decomposed because the high temperature formed during composting causes aerobic conditions to 60°C. It can kill insect eggs and pathogens carried by diseased plant residues in the previous season (Nuryanto 2018). Nutrients are usually provided in the form of fertilizer. Silicon is one of the nutritional elements stored in rice leaves. The accumulation of silicon in rice seed shoots provides a defense mechanism, allowing rice to be more resistant to rice blast disease (Rijal and Devkota 2020).

Use of chemical agents

The lack of knowledge about biological and environmentally-friendly control leads the farmer to choose chemical agents that are practical and rapid in controlling blast disease. Farmers in Indonesia commonly use insecticides with active ingredients, namely thianectosam, deltamethrin, dimehipo, fipronil and cypermethrin. At the same time, only 15% of farmers use a fungicide with the main active ingredient, difenoconazole (Andriyani and Wiyono 2021). Several fungicides that are effective in suppressing the development of *Pyricularia* fungus are bonomyl 50WP, mencozeb 80%, cerbandazim 50%, isoprotiolan 40% and tricyclazole 20%. Spraying with fungicide should be done twice at the maximum tillering stage of the rice plant and the beginning of flowering (Halijah 2019). It is important to study the effect of specific insecticide's active reagents based on the severity of blast diseases to select specific active reagents for blast disease control.

Blasticidin S, kasugamycin, iprobenphos (IBP), edifenphos (EDDP), isoprothiolane, ferimzone and metominostrobin were chemical agents commonly applied

to control rice blast disease (Yamaguchi 2004). However, some chemical agents such as carpropamid are no longer effective in controlling rice blast disease because they gave rise to pathogenic strains that are more resistant (Takagaki *et al.* 2004).

The effect of excessive use of chemical fungicides is the increased emergence of resistant pathogenic populations. The use of glyphosate herbicides is significantly increasing the severity of blast disease (Andriyani and Wiyono 2021). Besides that, pesticide residues are dangerous for humans and the environment; organochlorine, organophosphate and carbamate insecticide residues were identified in rice plants, soil and water in rice fields in rice production centers in Central Java (Ardiwinata and Nursyamsi 2012).

Use of biological agents

The advantages of using biological agents in controlling rice blast disease are reducing environmental pollution, safe for humans and livestock, durable, and cheaper than using chemical agents. In addition, the use of biological agents prevents pest and plant disease resistance (Muslim 2019). Optimization of rice blast control with biological agents in rice plants needs to be done systematically from the soil processing phase, nursery, and fertilization, to spraying during the vegetative phase (Kusumawati and Istiqomah 2020).

The development of rice blast disease control using biological agents faces a challenge, namely the limited data on risk analysis regarding the use of biological agents for its commercialization. Some frequently used biological agents are endophytic fungi, bacteria, and yeasts. Endophytic fungi such as *Trichoderma* sp. can reduce the intensity of rice blast disease attacks by more than 85% in leaf and panicle neck rice blast (Sopialena *et al.* 2021) and can antagonize *P. oryzae* very well (Fatimah *et al.* 2020). Plant Growth Promoting Rhizobacteria (PGPR) is a group of rhizosphere bacteria that can aggressively colonize root areas and are beneficial to plants. Examples include the *Bacillus* sp. and *Pseudomonas* sp. groups (Kumar *et al.* 2015). The bacteria in PGPR can produce antimicrobial compounds, fixate nitrogen, and mobilize phosphate which can increase plant resistance and produce growth regulators that can induce plant roots, allowing plants to grow optimally. A good plant root system will increase root absorption of existing nutrients (Etminani and Harighi 2018; Kusumawati and Istiqomah 2020). Some examples include *Pseudomonas fluorescens* and *Bacillus thuringiensis*, bacteria that produce plant growth hormones such as IAA that can bind nitrogen, thus improving the growth of rice plants. Producers of biological agents from the yeast group, *Cryptococcus* sp., *Candida* sp. and *Rhodotorula* sp. can inhibit the *P. oryzae* fungus growth by producing volatile compounds, hyperparasitism and producing chitinase enzymes (Maknunah and Sinaga 2018).

The integrated method

At present, plant disease management is required to consider environmental sustainability. Reducing the use of chemicals in agriculture can be achieved by optimizing integrated disease management strategies such as the utilization of biological agents, cultivation systems and using the minimum doses of chemicals. Rice disease control with an environmental perspective has the opportunity to suppress disease development. This approach can be carried out by selectively managing the cultivation components, namely selecting resistant varieties, healthy seeds, perfect tillage, organic matter, simultaneous planting at the right time, balanced fertilization and crop irrigation arrangements. This method effectively reduces production costs by up to 60% and reduces the rate of loss of rice yields by up to 30% (Nuryanto 2018). Balgude and Gaikwand (2019) proved that the integration of seed treatment methods (using the biological agent *Pseudomonas fluorescens*), cultivation control methods (applying husk ash/addition of silica to the soil), and fungicide spraying can be used to treat rice blast on leaves, leaf necks, and nodules so that rice plants can still produce and be harvested. The principle of integrated disease management combined with the latest technology can be used as a more efficient and effective disease management strategy (Hamid and Ghazanfar 2022). The RiceTalk project (Chen *et al.* 2019) succeeded in combining the Internet of Things (IoT) and artificial intelligence (AI) to detect rice blast disease in rice plants. RiceTalk utilizes precise data from micro weather stations where rice is grown to predict environmental conditions for the emergence and development of blast inoculants. Through the ability to predict the emergence of rice blast disease, it is possible to quickly stop the rice blast disease before it spreads. Detailed predictions can also be used to determine disease management strategies suited to rice blast disease prediction (Chen *et al.* 2019).

Breeding Rice Blast-resistant Varieties

Conventional breeding

Using resistant varieties is an inexpensive and environmentally-friendly approach to controlling rice blast disease in Indonesia. The rice blast-resistant varieties are developed out through a breeding approach. Breeding of blast-resistant rice is important in increasing the numbers of rice blast-resistant varieties. In the last five decades, many rice blast-resistant rice plants have been developed with high production rates through conventional breeding (Ashkani *et al.* 2015). Various rice blast-resistant varieties had been released in Indonesia from 2010–2020. They are Inpari 11, Inpari 12, Inpari 31, Inpari 32 HDB, Inpari 33, Inpari 34 Salin Agritan, Inpari 36 Lanrang, Inpari 37 Lanrang, Inpari UNSOED 79 Agritan, Inpari 38 Tadah Hujan Agritan, Inpari 39 Tadah Hujan Agritan, Inpari 40

Tadah Hujan Agritan, Inpari 41 Tadah Hujan Agritan, Inpari 42 Agritan GSR, Inpari 43 Agritan GSR, Tarabas, Mustaban Agritan, Siliwangi Agritan, Cakrabuana Agritan, Baroma, Pamelen, Pamera, Paketih, Jeliteng, Inpari IR Nutri Zinc, Inpari 46 GSR TDH, Cisaat, Inpari Arumba, Inpari 48 Blas, Inpari Gemah, Hipa 18, Hipa 19, Hipa 20, Hipa 21, Inpago 7, Inpago 10, Inpago 11 Agritan, Rindang 1 Agritan, Rindang 2 Agritan, Luhur 1, Luhur 2, Inpara 7, Inpara 10 BLB and Purwa (Sasmita *et al.* 2020).

The development of resistant varieties begins with screening for lines that have rice blast resistance genes which will later serve as donors. The backcross (BC) method is commonly used in rice breeding, specifically in the development of rice blast-resistant varieties (Divya *et al.* 2014; Lee *et al.* 2015; Ellur *et al.* 2016; Khan *et al.* 2018). This method can be used to improve varieties that already have good agronomic and adaptable characteristics but have one or more less-desirable characteristics (Syukur *et al.* 2015).

Conventional breeding for resistance to rice blast faces several challenges, including the laborious selection process (phenotype selection). It requires several generations of crosses, it requires disease resistance testing, and it is less accurate because it is influenced by environmental conditions (Ashkani *et al.* 2015). Marker-assisted selection (MAS) based breeding is a solution to common problems in conventional breeding, namely increasing selection efficiency and accuracy.

Prospects of developing blast-resistant rice

MAS breeding is based on the principle of genetic linkage, in which DNA markers detect the presence of allelic variations of genes. Marker-assisted selection (MAS) is a combination between molecular genetics and phenotypic selection based on gene-linked markers that control resistance traits in the plant genome (Ashkani *et al.* 2015). According to Syukur *et al.* (2015), when the molecular markers linked to the desired genes are identified, these markers will reduce the population size and time required in plant breeding programs for each selection cycle.

MABS approach in the genetic improvement of superior varieties for rice blast resistance

Five advantages of MAS-based breeding are: (1) this method is more accurate where the difference in the value of the repetition of this method is minimal or there is no difference, (2) the sample required is only DNA, (3) uses the PCR procedure for marker testing and identification, (4) the results obtained are based on the polymorphic data of the DNA bands produced, and (5) in terms of cost it is more efficient than the conventional one which requires more time and funds (Mackill and Ni 2001; Mohler and Singrun 2004).

The integration of MAS into conventional breeding is better than just being a substitute, especially in rice breeding, because it makes a major contribution to increasing rice

Table 2: The donor parents of blast resistance in Indonesia

Donor	References
Tetep, Tadukan, Carreon, Klemas, Genjah Lampung, Seratus malam, Sirendah, Sibuah, Batang ombilin, Hawara bunar, Silitonga and Risliawati Punggur, Limboto, Banyuasin, Batanghari, Celebes, Banjar rodok, Raden intan, Manglar, Mujair putih, Ketan kunir, O. nivara, (2013); Hairmansis <i>et al.</i> O. rufipogon, O. longiglumis, Asahan, Gampai, Cenggong, Progol, IRBLta2-Re, IRBLkp60, IRBL6, Lagas, Arias, Cartuna, (2015); Chaniago (2019)	
Dular, Gadis Langsat, Kebo, Bandang, Sigadis, Jawa Wangi Sleman, Marahmay, Takong, Ampek Panjang, Benoraja, Siawak, Ase Balucung, Ase Bukne, Pare Lottong, Pare Pulu, Jadu, Kapas, Sayap, Kail, Keriting, Muli, Kujam Cina, Gampai, Jogja, Padi Banten, Popot, Tasik, Kualan, Sutera, Bonti, Ibu, Padi Pulut Cantung, Nipon Datang, Cempo Dele, Cere Salak, Melati, Matung, Siredep, Sengkumang, Selak, Revolusi, Lemo, Deli, Ketan, Lumbu, Cempo Putih, Matung and Sengkumang	

production and maintaining food security in the future (Hasan *et al.* 2015). Genetic improvement of superior rice blast-resistant varieties using the MAS approach, which was done by combining breeding techniques, backcrossing, and DNA markers (genotype selection), resulted in a more precise selection and faster yield of rice blast-resistant germplasm in the BC2 and BC3 generations. Selection of the donor parent segment (rice blast resistance) and repeat parent was carried out by genotype and phenotype to get Ciherang (a high yielding variety (HYV) of rice in Indonesia) with the *Pita-2* gene (Fitriah *et al.* 2019) so that the development of new varieties (BC2 and BC3) was faster as it skipped several BC generations. This approach is called Marker Assisted-Backcrossing Selection (MABS).

In general, MABS consists of foreground, recombinant, and background selections (Holland 2004). Presently, the application of MABS in cereals, specifically in rice, has been widely carried out. This method has become increasingly popular in the last ten years. The advantage of the MABS technique approach is that it can be applied to varieties that have been well-received by farmers so that a character is improved (for example disease resistance), the variety still has much potential to be liked by both farmers and the community. It provides an opportunity for existing popular varieties to be improved genetically (adding new traits) using the MABS approach.

The success of the MABS technique on several "mega-variety" rice strains continues to develop into a successful approach (Singh *et al.* 2020). Currently, the application of MABS in rice breeding in Indonesia has been carried out for several characteristics such as flood-tolerance with the development of the Ciherang-Sub1 and PSB Rc18-Sub1 varieties (Septiningsih *et al.* 2014), resistance to bacterial leaf blight (BLB) through Xa gene-pyramiding (*Xa7*, *xa5*, *Xa21* and *Xa4*) in the Ciherang and Inpari 13 varieties (Fatimah *et al.* 2015) and agronomic characterization and background selection of drought and flooding-tolerant BC3F1 Inpari 30 x Cabacu rice lines using SSR markers (Lubba *et al.* 2020). The MABS approach specifically for rice blast resistance characteristics includes the characteristics of the donor parent segment in the population of advanced cross-linked Way Rarem x Oryzica Llanos-5 (Enggarini *et al.* 2012), the development of the rice blast-resistant Situpatenggang essential variety with four genes for rice blast resistance: *Pii*, *Pita*, *Pikp* and *Pia* (Yuriyah *et al.* 2019) and blast-resistance gene introgression from the monogenic blast line IRBLta2-Re to the Ciherang variety (Fitriah *et al.* 2019). The

application of MABS techniques in Indonesia is not yet optimal because it requires large funds for its implementation. Especially for genotype selection, molecular analysis tools and materials are expensive. Research and innovation of cost-effective MABS-based rice breeding need to be developed so that future breeding activities will use MABS more efficiently in developing new superior varieties or improving genetic traits.

Information regarding rice-blast resistance genes

Sources of rice blast-resistance genes can come from local varieties (germplasm) or rice blast-differential rice collections of the International Rice Research Institute (IRRI). IRRI has developed 26 monogenic rice blast lines. Rice blast-resistance genes are mostly found in chromosome 11 followed by chromosome 12. The rice blast resistance donors in Indonesia are shown in Table 2.

The availability of molecular markers to identify target genes/loci, recombination, and donor and recipient segments in MABS-based breeding is critical. High and low costs for DNA markers are the mainstay for determining the desired phenotype (Hasan *et al.* 2021). Several types of DNA markers include sequence tagged site (STS), sequence characterized amplified region (SCAR), restriction fragment length polymorphisms (RFLP), single nucleotide polymorphism (SNP) and simple sequence repeats (SSR) associated with genes or quantitative trait locus (QTL) (Collard and Mackill 2007; Miah *et al.* 2013). A review of molecular markers for rice blast-resistance genes from chromosomes 1–12, published by Koide *et al.* (2009), is constructive for MAS breeding in rice, especially for blast resistance varieties.

Potential development of blast resistance genes

Recognition of pathogens by resistant plants is controlled by plant resistance genes and avirulent genes possessed by pathogens through signal transduction pathways that will activate the plant defence system (Baker *et al.* 1997). Generally, blast resistance is limited to one particular race and only lasts a few seasons (Prabawa *et al.* 2015). The rice resistance to blast disease is very complex, influenced by hundreds of genes spread across 12 chromosomes with complex interaction pathways (Bagnaresi *et al.* 2012). Genes that affect blast disease resistance were intensively studied to find genes that have a broad spectrum and are

durable. These genes are generally grouped into four main groups, namely: (1) resistance gene (R), (2) signal transduction of hormone, (3) pathogenesis-related gene (PR) and (4) other resistance-related genes.

The R gene has been intensively studied related to *P. oryzae*, which causes blast disease; the R gene encodes the R protein. Protein R is a protein produced by plants and functions to recognize specific effectors of disease-causing agents, then creates a secondary immune response known as effector-triggered immunity (ETI) (Pieterse *et al.* 2009; Ezzat *et al.* 2014), the AVR gene of the pathogen encodes this effector. More than 40 AVR genes of *P. oryzae* have been identified, and 14 genes have been cloned (Ning *et al.* 2020; Devanna *et al.* 2022). The R protein is only adequate for specific effectors by a mechanism known as the "gene for gene" model. Protein R itself is a reasonably large protein family in plants. Currently, there are more than 100 R genes that have been identified and mapped, which are scattered on the rice chromosome No. 3, 6, 9, 11 and 12. The rest are scattered on other chromosomes, with 64% R genes on chromosomes 6, 11 and 12 (Kalia and Rator 2019; Ning *et al.* 2020; Devanna *et al.* 2022). Ten of the R gene on chromosome 6 are success mapped, namely: *Pi8*, *Pi9*, *Pi26(t)*, *Pi27(t)*, *Pi40*, *Piz*, *Pi-2*, *Piz-t*, *Pigm(t)* and *Pi59(t)* (Koide *et al.* 2013), Nine genes have been mapped to the R-gene cluster at the telomeric end of chromosome 11, seven of which are *Pi-k*, *Pi-ks*, *Pi -kp*, *Pi-km*, *Pi-kh*, *Pi-kl*, and *Pi-l*, show to be an allele of the *Pi-k* locus (Zhai *et al.* 2011; Hua *et al.* 2012; Singh *et al.* 2015). There are nine blast-specific genes on chromosome 12, namely: *Pi12*, *Pita*, *Pita2*, *Pi39*, *Pi42*, *Pi24*, *Pi20*, *PiGD3*, and *Pi157* have been mapped to the R gene cluster (Bryan *et al.* 2000; Liu *et al.* 2004; Li *et al.* 2008; Kumar *et al.* 2010).

R proteins are grouped into eight classes based on the arrangement of their functional domains, namely: NBS-LRR-TIR, NBS-LRR-CC, LRR-TRD, LRR-TRD-Kinase, TRD-CC, LRR-TRD-PEST-ECS, TIR-NBS-LRR-NLS-WRKY, and enzymatic R protein (it does not contain NBS or LRR) (Gururani *et al.* 2012). The NB-LRR group is the largest in the R gene group. Of these, 38 R genes have been successfully cloned, and most of them are effective for leaf blast (Ning *et al.* 2020; Devanna *et al.* 2022). Only a few (*Pb1*, *Pi25* and *Pi64*) are practical for leaf and neck blasts (Ning *et al.* 2020; Devanna *et al.* 2022; Yu *et al.* 2022). The problem that needs observing is that no genes are known to function and have been characterized in detail for their involvement type of blast. Most blast studies have focused on leaf blasts compared to neck blasts. It is important to note that none of the genes related to neck blasts have been extensively studied or known to function in that specific type of blast. Most of the research on blasts has been conducted on leaf blasts instead of neck blasts. The neck blast's resistance mechanism is different from that of the leaf blast (Liu *et al.* 2016).

A pyramidal approach of two or more genes is highly

recommended to obtain resistance to leaf blast and neck blast. The pyramid of resistance genes using a molecular breeding approach has been widely carried out. However, other obstacles, such as yield reduction, could also potentially emerge due to this strategy. Other studies have shown the possibility of a decrease or loss of the effectiveness of the resistance gene due to the alleged influence of other genes in the host or parent used. Therefore, it is necessary to characterize the genes in prospective parents before the breeding program.

Conclusion

Rice blast is potentially destructive and causes loss of yield. The latest information regarding blast disease is vital in Indonesia's efforts to control blast disease. Resistant varieties are the most effective, economical, and practical way to do this. Developing broad-spectrum and long-lasting blast-resistant rice is both a challenge and a dream for researchers to reduce yield losses due to blast disease in rice plants. The development of blast-resistant rice in Indonesia and the world is still constrained by several problems, namely: (1) comprehensive data and details of critical genes for blast resistance are not yet available, (2) genetic background data is not yet available. Technological developments in genetic engineering and genome editing provide more significant opportunities for developing broad-spectrum and durable blast-resistant rice. These technologies can be used alone or both and can also be combined with molecular markers together.

Acknowledgment

We would like to thank the Ministry of Agriculture of the Republic of Indonesia for providing information about the occurrence of rice blast disease in Indonesia through the Public Information Disclosure (PPID) system.

Author Contribution

All authors collaborate actively in developing this article. Each author contributed valuable insights and feedback that significantly influenced the article's content.

Conflicts of Interest

The authors declare no conflicts of interest related to this publication.

Data Availability

The information presented in this article is readily available.

Ethics Approval

Ethics approval was not necessary for our review article

since it analyzes existing literature rather than involving original research with human participants.

Funding Source

The Disease-Resistant Plant Engineering Research Group, Genetic Engineering Research Center, BRIN funded this article independently.

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