Transgenic Rice Live Against Bacterial Blight

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Abstract

Rice is one of the most essential staple foods for most of the countries in the world. Yield of this important crop is severely hampered worldwide by an increasing number of microbial attacks. Among these, bacterial blight (BB) caused by *Xanthomonas oryzae* pv. *oryzae* is one of the main constraints of rice production. Different management strategies are promoted to alleviate this serious problem. Conventional breeding practices are mostly utilized to develop resistant cultivars in the different parts of the world as the approaches are cost effective and environment friendly. However, the fruitful results may not be achieved due to low yield and reduced effectiveness against that pathogen. On the other hand, pathogen races are gradually changing their organization to adopt the unfavorable environment. In this present situation, the research efforts have been shifted to find out resistance genes in plants or in others, against specific pathogens. Till date around 40 genes have been detected in rice. Only few genes have been cloned successfully and tested against this devastating pathogen. However, scientists are now concerning about the durability and long-term protection by developing new molecular tools which might also help in sustainable agriculture. In this chapter, we are trying to summarize different aspects of this disease and recent researches on rice plant against this pathogen.

Keywords

Conventional breeding · Sustainable agriculture · Transgenic approaches

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1 Introduction

Rice is one of the most accepted staple crops of almost two thirds of the world and specially for developing countries like India. However, cultivation of this popular crop has been constrained due to rigorous climate change. Rice farming is still challenging due to global population expansion, extensive urbanization, and constant shifting of cultivable land to industrial park. Greater modernization promotes greater abiotic stresses to the plants like rise in temperature, prolonged drought condition, and water stress, increases harmful radiations, upholds reactive oxygen species (ROS) generation, etc. Employment of excessive amount of fertilizers ultimately reduces soil fertility. Use of harmful chemical pesticides and fungicides contaminates groundwater and also encourages pathogens to improve themselves and to develop new races. Application of non-judicious farming technology and mistreatment of high throughput up to date agricultural technologies has ultimately gifted non-cultivable lands (Delteil et al. 2010). To fulfill the rising demand of food supply throughout the world, growers have to produce more than 40% extra rice by 2030 (Khush 2005; Delteil et al. 2010). However, it will be a herculean task today due to tremendous challenging factors. In spite of other abiotic factors, bacterial and fungal pathogens cause a serious threat on rice cultivation (Delteil et al. 2010). Near about 20–30% of rice production is regularly hampered per year globally by various rice pathogens (Chattopadhyay et al. 2017). In this connection, *Xanthomonas oryzae* pv. *oryzae*, a Gram-negative bacterium and the causal organism of bacterial leaf blight of rice, causes almost more than 50% crop loss in respect to others (Ishiyama 1922; Chattopadhyay et al. 2017). Though it is mainly a seed-borne disease, all the developmental stages are susceptible to the pathogen under encouraging environmental situations (Chattopadhyay et al. 2017).

This disease outbreak occurs throughout the world and causes serious crop loss and economic suppression mainly in different parts of Western Africa and Asia. Moreover, intense wind associated with rains may amplify the epidemic of bacterial blight (Chattopadhyay et al. 2017). It basically occurs in high-yielding rice varieties grown in the monsoon season, under profound nitrogen fertilization and especially in the irrigated and rain-feed ecosystems (Laha et al. 2017). Bacterial blight epidemics were reported from different parts of India (Laha et al. 2009, 2017; Yugander et al. 2014). More than 50% crop loss was reported in different West African countries due to this major destructive disease (Basso et al. 2011; Laha et al. 2017). Singh et al. (2013) recorded the highest economic loss in the following series Pusa Basmati-1 (45%) > Haryana Shankar Dhan-1 (31%) > HKR 47 (23%) in India. Besides that, severe economic loss was also noticed in various regions of Southern China, Japan, the Philippines, Pakistan, Nepal, and South and Central American countries (Adhikari and Mew 1991; Mew et al. 1993; Khan et al. 2000; Akhtar et al. 2003; Qi 2009; Corral et al. 2013).

It was the most challenging task to control this devastating pathogen over time. The most convenient, economic, useful, and sustainable method was to generate resistant cultivars against this pathogen (Chattopadhyay et al. 2017). However, selection of wild resistant varieties was tedious, and new varieties of pathogen races were also challenging over time. Researchers sometimes utilize some abiotic and biotic inducers also, which are able to boost up the innate immunity of the plants. However, it was not so effective in this pathosystem. Nowadays, more researches move on to developing transgenic rice varieties against this pathogen. More than 40 genes have been tested till date to generate elite variety of rice (Chattopadhyay et al. 2017; Laha et al. 2017). By virtue of the advancement of molecular biology and biotechnological methods, multi-genes are incorporated within a single rice variety through gene pyramiding and marker-assisted selection techniques (Chattopadhyay et al. 2017). Consequently, whole genome editing tools like clustered regularly interspaced short palindromic repeats/CRISPR-associated protein (CRISPR/Cas9) and transcription activator-like effector nucleus (TALEN) are also utilized (Chattopadhyay et al. 2017; Laha et al. 2017).

This chapter emphasizes on the detailed outlook of the important disease and also provides information about the various strategies including molecular tools for the improvement of bacterial blight resistance of rice.

2 Geographical Distribution and Past History of Bacterial Blight

The devastating pathogen of bacterial blight disease of rice has been first identified and reported in the year of 1884 from Japan (Tagami and Mizukami 2008; Chattopadhyay et al. 2017). Later on, it was characterized properly and named as *Xanthomonas oryzae* pv. *oryzae* (Ishiyama) Swings et al. (*Xoo*) in the year 1922. Though almost all the rice-growing regions of the Caribbean island like Salvador, Mexico, Costa Rica, Honduras, and Panama were affected by this disease, it was first reported from the Mali region of West Africa (Buddenhagen et al. 1979). In South America, the affected regions include Colombia, Ecuador, Bolivia, and Venezuela (Lozano 1977; Sere et al. 2013). Louisiana and Texas from North America were most vulnerable for this pathogen (Jones et al. 1989). Furthermore, it was accounted from Australia and all the Asian countries (Ou 1985; Devadath 1992; Win et al. 2013). Srinivasan et al. (1959) reported the incidence of this disease from the state Maharashtra in India. However, its occurrence has not been established in Europe. The worldwide distribution of this disease is presented in Fig. 1.

3 Symptoms

It is a representative of typical vascular disease among others and has three discrete phases of symptoms. In the first phase of the disease, it shows pale-green to straw-colored striped water-soaked lesions with wavy margins on the tip of the isobilateral leaves which migrates longitudinally downward (Fig. 2). The leaf blight lesions may appear on both edges of the leaf and ultimately cover the whole leaf in the severe condition. Finally, it turns to whitish to grayish black due to the progression of saprophytic fungal growth. A small opaque yellowish drop containing bacterial

Fig. 1 World distribution of blast disease of rice (Laha et al. 2017)

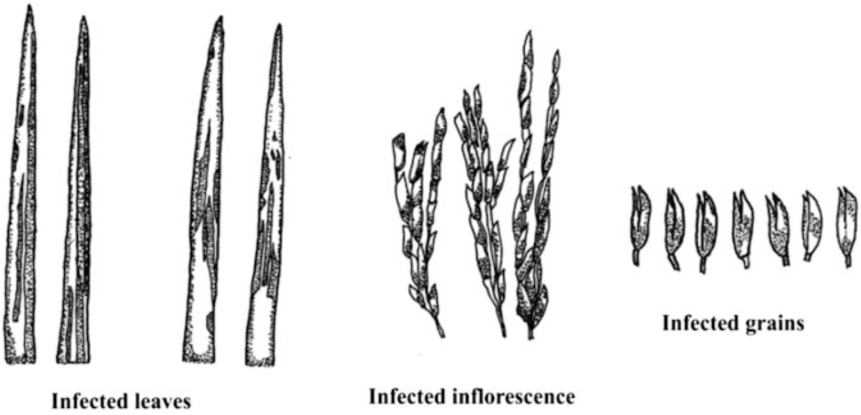

Fig. 2 Symptoms of bacterial blight disease

eluents may be observed in the humid areas at the morning, which dries up and turns into small spherical yellowish beads (Chattopadhyay et al. 2017).

In the tropical countries, kresek or wilt phase is the harshest phase of this disease. In this situation, the leaves become yellow to grayish in color and roll completely with wilting symptoms. In the acute phases, the tillers shrivel, and the affected plants ultimately die (Laha et al. 2017).

On the other hand, in the Philippines, the symptoms appear in the cluster of leaves which turns into pale yellow or whitish, and finally the affected leaves wither and dry up (Laha et al. 2017).

4 Pathogen

Xanthomonas oryzae pv. *oryzae* (Ishiyama) Swings et al. is a rod-shaped, non-spore-forming, Gram-negative, and motile uniflagellate bacterium having a single polar flagellum. It belongs to Xanthomonadaceae (family), Xanthomonadales (order), Gammaproteobacteria (class), and Proteobacteria (phylum) in the domain Bacteria. It secretes xanthomonadin (a brominated aryl polyene pigment), a typical non-diffusible yellow pigment (Laha et al. 2017).

5 Disease Cycle and Epidemiology

According to the inception of different studies on this disease carried out by different scientific organizations like the International Rice Research Institute (IRRI), Manila, Philippines, All India Coordinated Rice Improvement Project (AICRIP), the main cause of the disease is seed infection (Laha et al. 2009). However, there are few such references which indicate that the disease may not occur due to planting of those seeds. Furthermore, it was observed that the infection may occur in the self-grown plants, from the pre-infected stubble straws and also from the infected wild rice varieties. The pathogen may also survive on some wild grasses like *Panicum repens*, *Leersia hexandra*, and *Cyperus rotundus* and contaminate irrigation water which may also act as a source of primary inoculum. Cloudy humid conditions along with moderate temperature like 28–30 °C and excess use of nitrogenous fertilizer aggravate rapid growth and spreading of the disease (Ezuka and Kaku 2000) (Fig. 3).

6 Brief Overview of Disease Management Strategies Employed till Date

Various control measures including host nutrition and physical, cultural, and chemical control are employed to restrict this devastating disease. However, the best possible outcome may not be achieved due to regular modification of the pathogenic races, though improvement of plant resistance by the introduction of new gene or by regular breeding technique may be the best solution to overcome this disease.

Use of cultural control as an essential part of integrated disease management may be useful to some extent to control this disease. Removing infected plant trashes, wild rice plants, and weeds like *Leersia* sp. and *Cyperus* sp. may be quite useful to confine pathogen progress. Restriction of unnecessary pruning of plant parts and field to field irrigation may be helpful to control this disease. Not only that, use of pathogen-free certified seeds and judicious use of manures mainly nitrogen may be beneficial (Ezuka and Kaku 2000; Laha et al. 2009, 2017).

After disease inception, the use of different chemicals may act as SOS to control this destructive disease, though chemicals which are utilized in the field may not be eco-friendly. Till date various chemicals like chloramphenicol, cellomate, Sankel, streptomycin, phenazine, etc. have been used in the field (Laha et al. 2017).

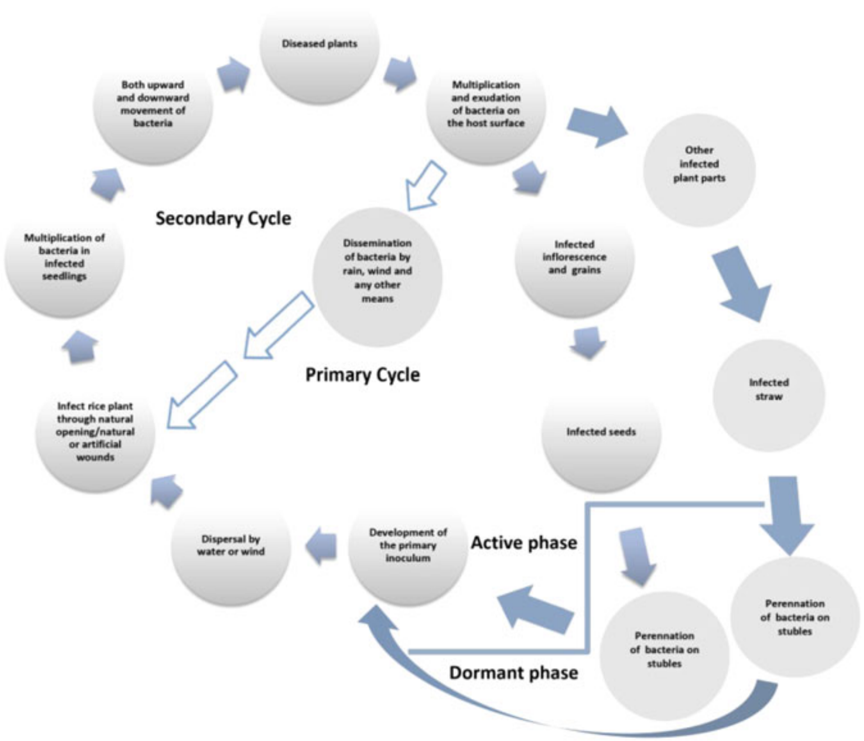

Fig. 3 Disease cycle of bacterial blight (causal organism: *Xanthomonas oryzae* pv. *oryzae*)

However, satisfactory results may not be achieved and sometimes more than one chemical was required to control this pathogen and the remnants of which may cause serious health hazards (Srivastava 1972; Laha et al. 2017). Seed soaking with various chemicals like Agrimycin 100, streptomycin, Terramycin, chlortetracycline hydrochloride, Ceresan, etc. at variable proportions along with hot water treatment may diminish the pathogen inoculum from seeds (Laha et al. 2017). Srivastava (1972) reported that TF-130 and ATDA (2-amino-1,3,4-thiadiazole) were most efficient against this pathogen in Japan and adjoining countries. Agrimycin 100 and Fytolan (copper oxychloride) in a specific proportion (50:500) may be useful to check secondary infection (Singh et al. 1980). According to Laha et al. (2009), 12.5 kg/ha Klorocin application 10 days after transplanting may give useful results. The highest disease control by the application of chemicals was achieved by applying Streptocycline (200 mg/l), copper oxychloride (2.5 g/l), and 2,4-D ethyl ester (1.0 ml/l) in combination (Singh et al. 2012b; Laha et al. 2017).

Crop improvement by conventional breeding methods may also help to combat against this disease. In the year 1969, two bacterial blight rice varieties named IR 20 and IR 22 were developed from IRRI, mostly on the basis of the major resistance genes like *Xa4* (Khush et al. 1989; Laha et al. 2017). However, those high-yielding varieties (HYVs) showed different degrees of susceptibility in different countries against this pathogen, which may be due to the development of more virulent new pathogenic races (Laha et al. 2017). Consequently, new resistance genes like *Xa5* and *Xa7* have been incorporated by plant researchers (Khush et al. 1989; Laha et al. 2017). Gradually other bacterial blight resistance-related new genes were discovered from wild rice varieties like *Xa21*, obtained from *Oryza longistaminata* (Khush et al. 1990; Laha et al. 2017). Till date more than 35 genes including *Xa23*, *Xa27*, *Xa30(t)/Xa38*, and *Xa33* have been identified from various sources and customized for marker-assisted selection breeding (Sundaram et al. 2014; Kim et al. 2015; Laha et al. 2017). Nowadays, to achieve the highest durable resistance against this destructive pathogen, amalgamation of different genes into a single rice cultivar was taking place by using the process of marker-assisted selection breeding (Laha et al. 2017). By using this technique, various rice varieties were obtained which are listed in Table 1.

Researches on host resistance against this pathogen are not so wide in Africa as in Asia. According to available reports, NERICA 4, NERICA 8, and NERICA 14 varieties showed modest level of bacterial blight resistance (Banito et al. 2012). However, few accessions of *O. glaberrima* from Mali showed high degree of resistance against this pathogen race A3 (Djedatin et al. 2011; Laha et al. 2017).

7 Why Modify the Employment of Bacterial Blight Resistance Genes?

It is well-known that the effective genes present in the elite clones of different rice varieties are evenly distributed all across the vast geographic areas. Sometimes they interact with the existing pathogen community of local inhabitants. Very often, long-term contact with efficient pathogen may cause an epidemic outbreak, which is mainly due to the loss of durability of the resistance genes (Dossa et al. 2015). A detailed understanding of pathogen physiology, host metabolism, and disease epidemiology and consequently knowledge of interdisciplinary approaches are very much necessary to control the pathogen dynamics. Studies on suppressive environments and effective genes through effector biological programs may employ a new arena in the field of integrated disease management. The outcome of those experiments should be properly informed to the forerunner of the cultivation.

Near about 40 genes were identified for bacterial blight of rice mostly from the wild and cultivable varieties (Khan et al. 2014; Zhang et al. 2014; Dossa et al. 2015). In Asia, the resistance genes like *Xa 4*, *Xa 5*, *Xa 13*, and *Xa 21* are mostly used for breeding purposes (Khan et al. 2014). Interestingly, the bacterial blight pathogen uses transcription activator-like (TAL) effectors to colonize the host system. In the large deployment of disease resistance against this pathogen and in contrast to the other pathosystems, *Xa* genes can be further classified into sub-categories (Boch et al. 2014; Dossa et al. 2015). The roles of different *Xa* genes are discussed in Table 2.

Table 1 Different commercialized rice varieties obtained by breeding

S. no.	Name of the rice varieties	Genes involved	Country	References
1.	Samba Mahsuri	*Xa21*, *Xa13*, and *Xa5*	India	Laha et al. (2009)
2.	PR106	*Xa5*, *Xa13*, and *Xa21*	India	Singh et al. (2001)
3.	Type 3 Basmati	*Xa21*, *Xa13*, *sd-1*	India	Rajpurohit et al. (2011)
4.	Lalat and Tapaswini	*Xa21*, *Xa13*, *Xa5*, and *Xa4*	India	Sundaram et al. (2014)
5.	PAU 201	*Xa38*, *Xa13*, *Xa21*	India	Sundaram et al. (2014)
6.	*O. rufipogon*	*Xa39(t)*	India	Sundaram et al. (2014)
7.	Mahsuri	*Xa4*, *Xa5*, *Xa13*, and *Xa21*	India	Guvvala et al. (2013)
8.	Swarna and IR64	*Xa21*, *Xa13*, and *Xa5*	India	Sundaram et al. (2014)
9.	Pusa Basmati-1	*Xa21* and *Xa13*	India	Singh et al. (2012a), Sundaram et al. (2014)
10.	Angke	*Xa4* and *Xa5*	Indonesia	Laha et al. (2017)
11.	Konde	*Xa4* and *Xa7*	Indonesia	Laha et al. (2017)
12.	NSIC Rc142 (Tubigan 7)	*Xa4* and *Xa21*	Philippines	Laha et al. (2017)
13.	NSIC Rc154 (Tubigan 11)	*Xa4* and *Xa21*	Philippines	Laha et al. (2017)
14.	RD6	*Xa5/Blast R*	Thailand	Pinta et al. (2013)
15.	Zhonghui 8006, Zhonghui 218, Guodao 1, Guodao 3, Guodao 6, and II You 8006	*Xa21*	China	Verdier et al. (2012), Rao et al. (2014), Laha et al. (2017)
16.	Minghui 63 (a restorer line)	*Xa21*	China	Chen et al. (2000)
17.	Minghui 63	*Xa7* and *Xa21*	China	Zhang et al. (2006)

Table 2 List of R genes of various rice cultivars securing resistance toward *Xanthomonas oryzae* pv. *oryzae*

Source material	Gene	Ch No.	Nature of resistance	References
Oryza sativa sp. *japonica* (cv. Kogyoku)	*Xa1*	4L	Resistant to Japanese race 1 (race specific dominant)	Yoshimura et al. (1998), Chattopadhyay et al. (2017)
Oryza sativa sp. *indica* (cv. Tetep)	*Xa2*	4L	Resistance to Japanese race 2 (race specific dominant)	He et al. (2006), Chattopadhyay et al. (2017)
Oryza sativa sp. *japonica* (cv. Wase Aikoku 3)	*Xa3/ Xa6/ Xa26*	11	Highly resistant to Philippine races 1, 2, 3, 4, 5, and 9	Xiang et al. (2006), Hur et al. (2013), Chattopadhyay et al. (2017)
Oryza sativa var. *indica* (IR20, IR22, IR64)	*Xa4*	11	Highly resistant to Philippine races 1, 4, 5, 7, 8, and 10 (effective under low temperature)	Yoshimura et al. (1995), Chattopadhyay et al. (2017)
Oryza sativa ssp. *indica* (DV85, DV86, DV78)	*Xa5*	5S	Resistant to Philippine races 1 and 4; but susceptible to race 6 (recessive in nature)	Blair et al. (2003), Iyer and McCouch (2004), Chattopadhyay et al. (2017)
Oryza sativa ssp. *indica* (DZ78)	*Xa7*	6	Dominant but not race specific and effective under high temperature	Porter et al. (2003), Chattopadhyay et al. (2017)
PI231129 (American cultivar)	*Xa8*	7	Recessive provide race-specific resistance to Philippine and North Indian *Xanthomonas oryzae* pv. *oryzae* races at seedling and adult plant phase	Vikal et al. (2014), Chattopadhyay et al. (2017)
Cas 209	*Xa10*	11L	Dominant at all developmental stages; race-specific resistance to Philippine races like PXO86 (R2), PXO112 (R5), and PXO145 (R7)	Yoshimura et al. (1983), Gu et al. (2008), Chattopadhyay et al. (2017)
IR8	*Xa11*	3L	Dominant and provide race-specific resistance to different Japanese races like IB, II, IIIA, and V	Goto et al. (2009), Chattopadhyay et al. (2017)
Oryza sativa sp. *japonica* (cv. Kogyoku)	*Xa12*	4	Dominant and provide race-specific resistance to Philippine race 5 and Japanese race V	Taura et al. (1992b), Chattopadhyay et al. (2017)
Oryza sativa sp. *indica Aus-Boro* line (cv. BJ1)	*Xa13*	8L	Provide Philippine race 6-specific resistance	Sanchez et al. (1999), Chu et al. (2006), Chattopadhyay et al. (2017)

(continued)

Table 2 (continued)

Source material	Gene	Ch No.	Nature of resistance	References
Oryza sativa sp. *indica* (cv. TN 1)	*Xa14*	4L	Highly resistant to Philippine race 5	Bao et al. (2010), Yuan et al. (2010), Chattopadhyay et al. (2017)
Oryza sativa sp. *japonica* (cv. M41)	*Xa15*	NII	Provide maximum resistance to Japanese races	Gnanamanickam et al. (1999), Chattopadhyay et al. (2017)
Oryza sativa sp. *indica* (cv. Tetep)	*Xa16*	NI	Dominant and give resistance to Japanese isolates like J8581 and H8584	Noda and Ohuchi (1989), Oryzabase (2011), Chattopadhyay et al. (2017)
Oryza sativa sp. *japonica* (cv. Asominori)	*Xa17*	NII	Dominant and give resistance to Japanese isolates like J8513	Ogawa et al. (1989), Oryzabase (2011), Chattopadhyay et al. (2017)
Oryza sativa sp. *japonica* (cv. Toyonishiki)	*Xa18*	NI	Not effective against Asian strains but successful against African and Burmese strains	Noda et al. (1996), Gonzalez et al. (2007), Oryzabase (2011), Chattopadhyay et al. (2017)
Oryza sativa sp. *indica* cv. XM5	*Xa19*	NI	Resistant to utmost Philippine races	Taura et al. (1991), Chattopadhyay et al. (2017)
Oryza sativa sp. *indica* cv. XM6	*Xa20*	NII	Resistant to entire Philippine races	Taura et al. (1992a), Chattopadhyay et al. (2017)
Wild rice (*O. longistaminata*)	*Xa21*	11L	Provide widespread resistance at post-seedling stages to Indian and Philippine races	Song et al. (1995), Chattopadhyay et al. (2017)
Oryza sativa sp. *japonica* (cv. Zhachanglong)	*Xa22* (t)	11	Provide maximum resistance to 16 different strains from Japan, China, and the Philippines	Lin et al. (1996), Wang et al. (2003), Chattopadhyay et al. (2017)
Oryza rufipogon (wild rice)	*Xa23*	11L	Provide resistance to several Chinese, Philippine, and Japanese races	Wang et al. (2014), Chattopadhyay et al. (2017)
Oryza sativa sp. *indica Aus-boro line* (cv. DV86)	*Xa24*	2L	Dominant and provide resistance to several Chinese, Philippine, and Japanese races	Mir and Khush (1990), Wu et al. (2008), Khush and Angeles (1999), Chattopadhyay et al. (2017)
Oryza sativa sp. *indica* (cv. HX-3)	*Xa25a* (t)	4L	Provide resistance to several Chinese, Philippine, and Japanese races	Gao et al. (2001, 2005), Chattopadhyay et al. (2017)

(continued)

Table 2 (continued)

Source material	Gene	Ch No.	Nature of resistance	References
Oryza sativa sp. *indica* (cv. Minghui 63)	*Xa25*b (t)	12	Give race-specific resistance to Philippine races	Chen et al. (2002), Liu et al. (2011), Chattopadhyay et al. (2017)
Oryza sativa sp. *indica* (cv. Minghui 63)	*Xa26*	11L	Give broad-spectrum resistance to Philippine and Chinese races	Yang et al. (2003), Sun et al. (2004), Chattopadhyay et al. (2017)
Oryza minuta (wild rice)	*Xa27* (t)	6L	Give broad-spectrum resistance to strain no. 27	Gu et al. (2004), Wang et al. (1996), Chattopadhyay et al. (2017)
Oryza sativa sp. *indica* (cv. Lota Sail)	*Xa28*	NI	Recessive gene	Lee et al. (2003), Chattopadhyay et al. (2017)
Oryza officinalis	*Xa29* (t)	1	Dominant resistance to various races	Tan et al. (2004), Chattopadhyay et al. (2017)
Oryza rufipogon germplasm (Y238)	*Xa30* (t)	11L	Not clear	Jin et al. (2007), Chattopadhyay et al. (2017)
Zhachanglong	*Xa31* (t)	4L	Give resistance against the strain OS105 but susceptible to Px061	Wang et al. (2009), Chattopadhyay et al. (2017)
Oryza australiensis	*Xa32*	11L	Resistant to strains P1 (PXO61), P4 (PXO71), P5 (PXO112), etc. but susceptible to P2 (PXO86) and P3 (PXO79)	Zheng et al. (2009), Chattopadhyay et al. (2017)
Wild rice (*Oryza nivara*); (Acc. No. 105710)	*Xa33*	7	Provide broad-spectrum resistance	Kumar et al. (2012), Chattopadhyay et al. (2017)
Oryza sativa sp. *indica* (cv. BG1222)	*Xa34* (t)	1	Highly resistant to the Chinese race V	Chen et al. (2011), Chattopadhyay et al. (2017)
Oryza minuta (Acc. No. 101133)	*Xa35* (t)	11L	Dominant and give resistance to PXO61, PXO112, and PXO339	Guo et al. (2010), Chattopadhyay et al. (2017)
C4059	*Xa36* (t)	11L	Not known	Miao et al. (2010), Chattopadhyay et al. (2017)
Oryza nivara (acc. IRGC 81825)	*Xa38* (t)	4L	Resistant to all the races ubiquitous to northern states of India	Vikal et al. (2007), Cheema et al. (2008), Bhasin et al. (2012), Chattopadhyay et al. (2017)

(continued)

Table 2 (continued)

Source material	Gene	Ch No.	Nature of resistance	References
FF329	*Xa39* (t)	11	Provide broad-spectrum resistance to bacterial blight	Zhang et al. (2015), Chattopadhyay et al. (2017)
Oryza sativa sp. indica line IR65482-7-216-1-2	*Xa40* (t)	11	High levels of resistance to entire Korean races	Kim et al. (2015), Chattopadhyay et al. (2017)

Ch, chromosome number; NI, not identified

8 Genes and Techniques Employed to Rice Research

Various techniques have been utilized to produce stable transgenic rice plants in the market till date. However, transformation through *Agrobacterium tumefaciens* has been accepted as a routine technique in most of the laboratories (Toki et al. 2006; Delteil et al. 2010). Through this technique, efficiency of different rice varieties like japonica, indica, etc. has been improved sufficiently (Delteil et al. 2010). Later on, marker-assisted selection techniques were familiarized to the breeders for crop improvement (Ballini et al. 2009; Delteil et al. 2010). White and Yang (2009) describe the specific roles of major *Xa* resistance genes which confer the resistance against *Xanthomonas*. According to Peng et al. (2015), *Xa21* was the most prime gene in bacterial blight resistance which is also connected to signaling pathways. Other genes such as OsBRR1 and OsWAK1 were shown to be helpful in coding for receptor-like proteins and provide basal resistance to rice plant (Delteil et al. 2010). Moreover, genes which are utilized for the making of transgenic rice are basically related to defense signaling and transcription factors including XB15, OsPLDB1, OsDR8, SPL18, SPL11, PACK1, OsGAP1, and OsRac1 (Delteil et al. 2010). Moreover, few PR genes out of 14 found in rice have been overexpressed (Van Loon et al. 2006; Delteil et al. 2010).

In a recent study on RNA-Seq showed that rice cultivar IRBB61 containing *Xa7* when infected with *Xanthomonas oryzae* at high temperature stress, gives protection against the pathogen and was not dependent on salicylic acid pathway but related to abscisic acid (Cohen et al. 2017).

9 Future Goal and Conclusion

To find out the major constraints in rice production, it has been observed that bacterial blight has huge effect on yield loss. Though various approaches are available to control this disease, nowadays, the cultivation of resistant varieties is considered as the most economical tool. Many researchers till date working with the disease to understand the detailed molecular mechanism of pathogenesis. To protect rice from this devastating pathogen, it is an urgent requirement to identify and characterize a large number of defense genes. Marker-assisted breeding and various transgenic approaches can be taken as potential tools to protect rice against this disease. Identification, characterization, and functional analysis of resistant genes can open the downstream signaling pathway associated with this disease. That may be altered at desired steps to check the efficacy of the pathogen. If we think in other way, application of various biotic and abiotic elicitors can also be taken as a tool to induce innate immunity against this disease. Application of newer genome editing tool as CRISPR against the disease can also be accepted as future area of research. Many transcriptomic, proteomic, and metabolomic approaches can be taken as tools to draw the defense signaling network.

To sum up at this point, our major goal is to protect rice plant from this pathogen. To achieve this goal and to secure our food, further research works are required for better understanding of pathogenesis and identifying probable easy tool to combat against this disease.

References

Adhikari TB, Mew TW (1991) Effect of bacterial blight on growth and yield of rice. J Inst Agric Anim Sci 12:29–40

Akhtar MA, Zakria M, Abbassi FM, Masod MA (2003) Incidence of bacterial blight of rice in Pakistan during 2002. Pak J Bot 35:993–997

Ballini E, Vergne E, Tharreau D, Nottéghem JL, Morel JB (2009) ARCHIPELAGO: towards bridging the gap between molecular and genetic information in rice blast disease resistance. In: Wang GL, Valent B (eds) Advances in genetics, genomics and control of rice blast disease. Springer, Berlin, pp 417–425

Banito A, Kadai EA, Sere Y (2012) Screening of rice varieties for resistance to bacterial leaf blight. J Appl Biosci 53:3742–3748

Bao SY, Tan MP, Lin XH (2010) Genetic mapping of a bacterial blight resistance gene *Xa14* in rice. Acta Agron Sin 36:422–427

Basso A, Onasanya A, Issaka S, Sido AY, Haougui A, Adam T, Sere Y, Saadou M (2011) Bacterial leaf blight of rice in Niger: pathological diversity of isolates collected on irrigated lands. J Appl Biosci 38:2551–2563

Bhasin H, Bhatia D, Raghuvanshi S, Lore JS, Sahi GK, Kaur B, Vikal Y, Singh K (2012) New PCR-based sequence-tagged site marker for bacterial blight resistance gene *Xa38* of rice. Mol Breed 30:607–611

Blair MW, Garris AJ, Iyer AS, Chapman B, Kresovich S, McCouch SR (2003) High resolution genetic mapping and candidate gene identification at the *xa5* locus for bacterial blight resistance in rice (*Oryza sativa* L.). Theor Appl Genet 107:62–73

Boch J, Bonas U, Lahaye T (2014) TAL effectors-pathogen strategies and plant resistance engineering. New Phytol 204:823–832

Buddenhagen IW, Vuong HH, Ba DD (1979) Bacterial blight found in Africa. Int Rice Res Newsl 4:11

Chattopadhyay A, Nagaich D, Lima JM, Verma A, Tiwari KK (2017) Molecular aspects of bacterial blight resistance in rice: recent advancement. In: Shamim M, Singh KN (eds) Biotic stress management in rice molecular approaches. Apple Academic Press Inc., Waretown, pp 17–45

Cheema KK, Grewal NK, Vikal Y, Sharma R, Lore JS, Das A, Bhatia D, Mahajan R, Gupta V, Bharaj TS, Singh K (2008) A novel bacterial blight resistance gene from *Oryza nivara* mapped to 38 kb region on chromosome 4L and transferred to *Oryza sativa* L. Gen Res (Camb) 90:397–407

Chen H, Wang S, Zhang Q (2002) New gene for bacterial blight resistance in rice located on chromosome 12 identified from Minghui 63, an elite restorer line. Phytopathology 92:750–754

Chen S, Lin XH, Xu CG, Zhang Q (2000) Improvement of bacterial blight resistance of Minghui 63, an elite restorer line of hybrid rice, by molecular marker-assisted selection. Crop Sci 40:239–244

Chen S, Liu X, Zeng L, Ouyang D, Yang J, Zhu X (2011) Genetic analysis and molecular mapping of a novel recessive gene *xa34*(t) for resistance against *Xanthomonas oryzae* pv. *oryzae*. Theor Appl Genet 7:1331–1338

Chu Z, Yuan M, Yao J, Ge X, Yuan B, Xu C, Li X, Fu B, Li Z, Bennetzen JL, Zhang Q, Wang S (2006) Promoter mutations of an essential gene for pollen development result in disease resistance in rice. Genes Dev 20:1250–1255

Cohen SP, Liu H, Argueso CT, Pereira A, Vera Cruz C, Verdier V et al (2017) RNA-Seq analysis reveals insight into enhanced rice *Xa7*-mediated bacterial blight resistance at high temperature. PLoS One 12(11):e0187625. https://doi.org/10.1371/journal.pone.0187625

Corral R, Leach JE, Verdier V, Vera Cruz CM (2013) Recovery plan for *Xanthomonas oryzae* causing bacterial blight and bacterial leaf streak of rice. Bulletin, NPDRS, 22

Delteil A, Zhang J, Lessard P, Morel J-B (2010) Potential candidate genes for improving rice disease resistance. Rice 3:56–71. https://doi.org/10.1007/s12284-009-9035-x

Devadath S (1992) Bacterial blight of paddy. In: Singh US, Mukhopadhaya AN, Kumar J, Chaube HS (eds) Plant diseases of international importance: diseases of cereals and pulses. Prentice Hall, Englewood Clifffs, pp 158–185

Djedatin G, Ndjiondjop MN, Mathieu T, Vera Cruz CM, Sanni A, Ghesquière A, Verdier V (2011) Evaluation of African cultivated rice *Oryza glaberrima* for resistance to bacterial blight. Plant Dis 95:441–447

Dossa GS, Sparks A, Cruz CV, Oliva R (2015) Decision tools for bacterial blight resistance gene deployment in rice-based agricultural ecosystems. Front Plant Sci 6:305. https://doi.org/10.3389/fpls.2015.00305

Ezuka A, Kaku H (2000) A historical review of bacterial blight of rice. Bulletin of the National Institute of Agrobiological Resources (Japan), No. 15 (March), 207 pp

Gao DY, Liu AM, Zhou YH, Cheng YJ, Xiang YH, Sun LH, Zhai WX (2005) Molecular mapping of a bacterial blight resistance gene *Xa-25* in rice. Acta Genet Sin 32:183–188

Gao DY, Xu ZG, Chen ZY, Sun LH, Sun QM, Lu F, Hu BS, Liu YF, Tang LH (2001) Identification of a new gene for resistance to bacterial blight in a somaclonal mutant HX-3 (indica). Rice Genet Newslett 18:66

Gnanamanickam SS, Brindha PV, Narayanan NN, Vasudevan P (1999) *Kavitha, S.* An overview of bacterial blight disease of rice and strategies for its management. Curr Sci 77:1435–1443

Gonzalez C, Szurek B, Manceau C, Mathieu T, Sere Y, Verdier V (2007) Molecular and pathotypic characterization of new *Xanthomonas oryzae* strains from West Africa. Mol Plant Microbe Interact 20:534–546

Goto T, Matsumoto T, Furuya N, Tsuchiya K, Yoshimura A (2009) Mapping of bacterial blight resistance gene *Xa11* on rice chromosome 3. Jpn Agric Res Q 43:221–225

Gu K, Sangha JS, Li Y, Yin Z (2008) High-resolution genetic mapping of bacterial blight resistance gene *Xa10*. Theor Appl Genet 116:155–163

Gu K, Tian D, Yang F, Wu L, Sreekala C, Wang D, Wang GL, Yin Z (2004) High-resolution genetic mapping of *Xa27*(t), a new bacterial blight resistance gene in rice, *Oryza sativa* L. Theor Appl Genet 108:800–807

Guo S, Zhang D, Lin X (2010) Identification and mapping of a novel bacterial blight resistance gene *Xa35*(t) originated from *Oryza minuta*. Sci Agric Sin 43:2611–2618

Guvvala LD, Koradi P, Shenoy V, Marella LS (2013) Making an Indian traditional rice variety Mahsuri, bacterial blight resistant using marker-assisted selection. J Crop Sci Biotechnol 6:111–121

He Q, Li D, Zhu Y, Tan M, Zhang D, Lin X (2006) Fine mapping of *Xa2*, a bacterial blight resistance gene in rice. Mol Breed 17:1–6

Hur YJ, Jeung JU, Kim YS, Park HS, Cho JH, Lee JY, Sohn YB, Song YC, Park DS, Lee CW, Sohn JG, Nam MH, Le JH (2013) Functional markers for bacterial blight resistance gene *Xa3* in rice. Mol Breed 31:981–985

Ishiyama S (1922) Studies on bacterial blight of rice. Rep Agric Exp Stat Tokyo 45:233–261

Iyer AS, McCouch SR (2004) The rice bacterial blight resistance gene *xa5* encodes a novel form of disease resistance. Mol Plant Microbe Interact 17:1348–1354

Jin X, Wang C, Yang Q, Jiang Q, Fan Y, Liu G, Zhao K (2007) Breeding of near-isogenic line CBB30 and molecular mapping of *Xa30(t)*, a new resistance gene to bacterial blight in rice. Sci Agric Sin 40:1094–1100

Jones RK, Barnes LW, Gonzalez CF, Leach JE, Alvarez AM, Benedict AA (1989) Identification of low virulence strains of *Xanthomonas campestris* pv. *oryzae* from rice in the United States. Phytopathology 79:984–990

Khan MAI, Bhuiyan MR, Hossain MS, Sen PP, Ara A, Siddique MA, Ali MA (2014) Neck blast disease influences grain yield and quality traits of aromatic rice. C R Biol 337:635–641

Khan TZ, Gill MA, Khan MG (2000) Screening of rice varieties/lines for resistance to bacterial leaf blight. Pak J Phytopathol 12:71–72

Khush GS (2005) What it will take to feed 5.0 billion rice consumers in 2030. Plant Mol Biol 59:1–6

Khush GS, Angeles ER (1999) A new gene for resistance to race 6 of bacterial blight in rice *Oryza sativa*. Rice Genet Newslett 16:92–93

Khush GS, Bacalangco E, Ogawa T (1990) A new gene for resistance to bacterial blight from *O. longistaminata*. Rice Genet Newslett 7:121–122

Khush GS, Mackill DJ, Sidhu GS (1989) Breeding rice for resistance to bacterial leaf blight. In: IRRI (ed) Bacterial blight of rice. IRRI, Manila, pp 207–217

Kim SM, Suh JP, Qin Y, Noh TH, Reinke RF, Jena KK (2015) Identification and fine-mapping of a new resistance gene, *Xa40*, conferring resistance to bacterial blight races in rice (*Oryza sativa* L.). Theor Appl Genet 128:1933–1943

Kumar PN, Sujatha K, Laha GS, Rao KS, Mishra B, Viraktamath BC, Hari Y, Reddy CS, Balachandran SM, Ram T, Madhav MS, Rani NS, Neeraja CN, Reddy GA, Shaik H, Sundaram RM (2012) Identification and fine-mapping of *Xa33*, a novel gene for resistance to *Xanthomonas oryzae* pv. *oryzae*. Phytopathology 102:222–228

Laha GS, Reddy CS, Krishnaveni D, Sundaram RM, Srinivas Prasad M, Ram T, Muralidharan K, Viraktamath BC (2009) Bacterial blight of rice and its management. Technical Bulletin No. 41, Directorate of Rice Research (ICAR), Rajendranagar, Hyderabad, 37 pp

Laha GS, Singh R, Ladhalakshmi D, Sunder S, Prasad MS, Dagar CS, Babu VR (2017) Importance and management of rice diseases: a global perspective. In: Chauhan BS et al (eds) Rice production worldwide. Springer, pp 303–360. https://doi.org/10.1007/978-3-319-47516-5_13

Lee KS, Rasabandith S, Angeles ER, Khush GS (2003) Inheritance of resistance to bacterial blight in 21 cultivars of rice. Phytopathology 93:147–152

Lin XH, Zhang DP, Xie YF, Gao HP, Zhang Q (1996) Identifying and mapping a new gene for bacterial blight resistance in rice based on RFLP markers. Phytopathology 86:1156–1159

Liu Q, Yuan M, Zhou Y, Li X, Xiao J, Wang S (2011) A paralog of the MtN3/saliva family recessively confers race-specific resistance to *Xanthomonas oryzae* in rice. Plant Cell Environ 34:1958–1969

Lozano JC (1977) Identification of bacterial leaf blight in rice caused by *Xanthomonas oryzae* in America. Plant Dis Rep 61:644–648

Mew TW, Alvarez AM, Leach JE, Swings J (1993) Focus on bacterial blight of rice. Plant Dis 77:5–12

Miao L, Wang C, Zheng C, Che J, Gao Y, Wen Y, Li G, Zhao K (2010) Molecular mapping of a new gene for resistance to rice bacterial blight. China Agric Sci 43:3051–3058

Mir GN, Khush GS (1990) Genetics of resistance to bacterial blight in rice cultivar DV86. Crop Res 3:194–198

Noda T, Ohuchi A (1989) A new pathogenic race of *Xanthomonas campestris* pv. *oryzae* and its inheritance of differential rice variety Tetep to it. Ann Phytopathol Soc Japan 55:201–207

Noda T, Yamamoto T, Kaku H, Horino O (1996) Geographical distribution of pathogenic races of *Xanthomonas oryzae* pv. *oryzae* in Japan in 1991 and 1993. Annu Phytopathol Soc Japan 62:549–553

Ogawa T, Kaku H, Yamamoto T (1989) Resistance gene of rice cultivar, *Asaminori* to bacterial blight of rice. Jpn J Breed 39:196–197

Oryzabase (2011) Integrated rice science database. Available at: http://www.shigen.nig.ac.jp/rice/oryzabase

Ou SH (1985) Rice diseases, 2nd edn. Commonwealth Mycological Institute, Kew, Surrey, 380 pp

Peng H, Chen Z, Fang Z, Zhou J, Xia Z, Gao L, Chen L, Li L, Li T, Zhai W, Zhang W (2015) Rice *Xa21* primed genes and pathways that are critical for combating bacterial blight infection. Sci Rep 5:12165. https://doi.org/10.1038/srep12165

Pinta W, Toojinda T, Thummabenjapone P, Sanitchon J (2013) Pyramiding of blast and bacterial leaf blight resistance genes into rice cultivar RD6 using marker assisted selection. Afr J Biotechnol 12:4432–4438

Porter BW, Chittoor JM, Yano M, Sasaki T, White FF (2003) Development and mapping of markers linked to the rice bacterial blight resistance gene *Xa7*. Crop Sci 43:1484–1492

Qi Z (2009) Genetics and improvement of bacterial blight resistance of hybrid rice in China. Rice Sci 16(2):83–92

Rajpurohit D, Kumar R, Kumar M, Paul P, Awasthi A, Basha OP, Puri A, Jhang T, Singh K, Dhaliwal HS (2011) Pyramiding of two bacterial blight resistance and a semi-dwarfing gene in type 3 basmati using marker-assisted selection. Euphytica 178:111–126

Rao Y, Li Y, Qian Q (2014) Recent progress on molecular breeding of rice in China. Plant Cell Rep 33:551–564

Sanchez AC, Ilag LL, Yang D, Brar DS, Ausubel F, Khush GS, Yano M, Sasaki T, Li Z, Huang N (1999) Genetic and physical mapping of *xa13*, a recessive bacterial blight resistance gene in rice. Theor Appl Genet 98:1022–1028

Sere Y, Fargette D, Abo ME, Wydra K, Bimerew M, Onasanya A, Akator SK (2013) Managing the major diseases of rice in Africa. In: Wopereis MCS, Johnson DE, Ahmadi N, Tollens E, Jalloh A (eds) Realizing Africa's rice promise. Commonwealth Agricultural Bureau International, pp 213–228

Singh A, Singh VK, Singh SP, Pandian RTP, Ellur RK, Singh D, Bhowmick PK, Gopala Krishnan S, Nagarajan M, Vinod KK, Singh UD, Prabhu KV, Sharma TR, Mohapatra T, Singh AK (2012a) Molecular breeding for the development of multiple disease resistance in basmati rice. AoB Plants:pls029. https://doi.org/10.1093/aobpla/pls029

Singh R, Sunder S, Dodan DS (2012b) Sources of resistance, effectiveness of Xa/xa genes and evaluation of botanicals and non-conventional chemicals against bacterial blight of rice. Plant Dis Res 27:200–208

Singh R, Sunder S, Dodan DS (2013) Estimation of losses in grain yield due to bacterial blight and neck blast of rice in Haryana. Indian Phytopathol 66:249–251

Singh RA, Das B, Ahmed KM, Pal V (1980) Chemical control of bacterial leaf blight of rice. Trop Pest Manag 26:21–25

Singh S, Sidhu JS, Huang N, Vikal Y, Li Z, Brar DS, Dhaliwal HS, Khush GS (2001) Pyramiding three bacterial blight resistance genes (*xa5*, *xa13* and *Xa21*) using marker-assisted selection into indica rice cultivar PR106. Theor Appl Genet 102:1011–1015

Song WY, Wang GL, Chen LL, Kim HS, Pi LY, Holsten T, Gardner J, Wang B, Zhai WX, Zhu LH, Fauquet C, Ronald P (1995) A receptor kinase-like protein encoded by the rice disease resistance gene, *Xa21*. Science 270:1804–1806

Srinivasan MC, Thirumalachar MJ, Patel MK (1959) Bacterial blight disease of rice. Curr Sci 28:469–470

Srivastava DN (1972) Bacterial blight of rice. Indian Phytopathol 26:1–16

Sun X, Cao Y, Yang Z, Xu C, Li X, Wang S, Zhang Q (2004) *Xa26*, a gene conferring resistance to *Xanthomonas oryzae* pv. *oryzae* in rice, encodes an LRR receptor kinase-like protein. Plant J 37:517–527

Sundaram RM, Chatterjee S, Oliva R, Laha GS, Cruz LJE, Sonti RV (2014) Update on bacterial blight of rice: fourth international conference on bacterial blight. Rice 7:12

Tagami Y, Mizukami T (2008) Historical review of the researches on bacterial leaf blight of rice caused by Xanthomonas. Special report on plant disease and insect pest forecasting service, vol 10. Ministry of Agriculture, Japan, pp 1–112

Tan GX, Ren X, Weng QM, Shi ZY, Zhu LL, He GC (2004) Mapping of a new resistance gene to bacterial blight in rice line introgressed from *Oryza officinalis*. Yi Chuan Xue Bao 31:724–729

Taura S, Ogawa T, Yoshimura A, Ikeda R, Iwata N (1992a) Identification of a recessive resistance gene to rice bacterial blight of mutant line XM6, *Oryza sativa* L. Jpn J Breed 42:7–13

Taura S, Ogawa T, Yoshimura A, Ikeda R, Omura T (1991) Identification of a recessive resistance gene in induced mutant line XM5 of rice to rice bacterial blight. Jpn J Breed 41:427–432

Taura S, Tabien RE, Khush GS, Yoshimura A, Omura T (1992b) Resistance gene of rice cultivar Taichung native 1 to Philippine races of bacterial blight pathogens. Jpn J Breed 42:195–201

Toki S, Hara N, Ono K, Onodera H, Tagiri A, Oka S et al (2006) Earl infection of scutellum tissue with *Agrobacterium* allows high speed transformation of rice. Plant J 47(6):969–976

van Loon LC, Rep M, Pieterse CMJ (2006) Significance of inducible defense-related proteins in infected plants. Annu Rev Phytopathol 44(1):135–162

Verdier V, Vera Cruz C, Leach JE (2012) Controlling rice bacterial blight in Africa: needs and prospects. J Biotechnol 159:320–328

Vikal Y, Chawla H, Rajiv S, Lore JS, Singh K (2014) Mapping of bacterial blight resistance gene *xa8* in rice (*Oryza sativa* L.). Indian J Genet Plant Breed 74:589–595

Vikal Y, Das A, Patra B, Goel RK, Sidhu JS, Singh K (2007) Identification of new sources of bacterial blight (*Xanthomonas oryzae* pv. *oryzae*) resistance in wild *Oryza* species and *O. glaberrima*. Plant Genet Res 5:108–112

Wang C, Fan Y, Zheng C, Qin T, Zhang X, Zhao K (2014) High-resolution genetic mapping of rice bacterial blight resistance gene *Xa23*. Mol Gen Genomics 289:745–753

Wang C, Tan M, Xu X, Wen G, Zhang D, Lin X (2003) Localizing the bacterial blight resistance gene, *Xa22*(t), to a 100-kilobase bacterial artificial chromosome. Phytopathology 93:1258–1262

Wang C, Wen G, Lin X, Liu X, Zhang D (2009) Identification and fine mapping of the new bacterial blight resistance gene, *Xa31*(t), in rice. Eur J Plant Pathol 123:235–240

Wang GL, Song WY, Wu RL, Sideris S, Ronald PC (1996) The cloned gene, *Xa27*, confers resistance to multiple *Xanthomonas oryzae* pv. *oryzae* isolates in transgenic plants. Mol Plant Microbe Interact 9:850–855

White FF, Yang B (2009) Host and pathogen factors controlling the rice—Xanthomonas oryzae interaction. Plant Physiol 150(4):1677–1686

Win KM, Korinsak S, Sirithunya P, Lanceras-Siangliw J, Jamboonsri W, Da T, Patarapuwadol S, Toojinda T (2013) Marker assisted introgression of multiple genes for bacterial blight resistance into aromatic Myanmar rice MK-75. Field Crop Res 154:164–171

Wu X, Li X, Zu C, Wang S (2008) Fine genetic mapping of *xa24*, a recessive gene for resistance against *Xanthomonas oryzae* pv. *oryzae* in rice. Theor Appl Genet 118:185–191

Xiang Y, Cao Y, Xu C, Li X, Wang S (2006) *Xa3*, conferring resistance for rice bacterial blight and encoding a receptor kinase-like protein, is the same as *Xa26*. Theor Appl Genet 113:1347–1355

Yang Z, Sun X, Wang S, Zhang Q (2003) Genetic and physical mapping of a new gene for bacterial blight resistance in rice. Theor Appl Genet 106:1467–1472

Yoshimura A, Mew T, Khush G, Omura T (1983) Inheritance of resistance to bacterial blight in rice cultivar Cas 209. Phytopathology 73:1409–1412

Yoshimura S, Yamanouchi U, Katayose Y, Toki S, Wang ZX, Kono I, Kurata N, Yano M, Iwata N, Sasaki T (1998) Expression of *Xa1*, a bacterial blight-resistance gene in rice, is induced by bacterial inoculation. Proc Natl Acad Sci U S A 95:1663–1668

Yoshimura S, Yoshimura A, Iwata N, McCouch SR, Abenes ML, Baraoidan MR, Mew TW, Neson RJ (1995) Tagging and combining bacterial blight resistance genes in rice using RAPD and RFLP markers. Mol Breed 1:375–378

Yuan BS, Pu TM, Hua LX (2010) Genetic mapping of a bacterial blight resistance gene *Xa14* in rice. Acta Agron Sin 36:422–427

Yugander A, Sundaram RM, Ladhalakshmi D, Shaik H, Sheshu Madhav M, Srinivas Prasad M, Viraktamath BC, Laha GS (2014) Pathogenic and genetic profile of *Xanthomonas oryzae pv. oryzae* isolates from Andhra Pradesh. Indian J Plant Prot 42:149–155

Zhang F, Zhuo DL, Zhang F, Huang LY, Wang WS, Xu JL et al (2014) Xa39, a novel dominant gene conferring broad-spectrum resistance to *Xanthomonas oryzae* pv. *oryzae* in rice. Plant Pathol. https://doi.org/10.1111/ppa.12283

Zhang F, Zhuo DL, Zhang F, Huang LY, Wang WS, Xu JL, Cruz CV, Li ZK, Zhou YL (2015) *Xa39*, a novel dominant gene conferring broad-spectrum resistance to *Xanthomonas oryzae* pv. *oryzae* in rice. Plant Pathol 64:568–575

Zhang J, Li X, Jiang G, Xuz Y, He Y (2006) Pyramiding of Xa7 and Xa21 for the improvement of disease resistance to bacterial blight in hybrid rice. Plant Breed 125:600–605

Zheng CK, Wang CL, Yu YJ, Zhao KJ (2009) Identification and molecular mapping of *Xa32*(*t*), a novel resistance gene for bacterial blight (*Xanthomonas oryzae* pv. *oryzae*) in rice. Acta Agron Sin 35:1173–1180