Biotic Stress Management in Rice (Oryza sativa L.) Through Conventional and Molecular Approaches

Chapter · March 2020

DOI: 10.1007/978-981-15-1322-0_30

8 authors, including:

Prakash Singh
Bihar Agriculture University
71 PUBLICATIONS **156** CITATIONS
SEE PROFILE

Ramlakhan Verma
Central Rice Research Institute
33 PUBLICATIONS **85** CITATIONS
SEE PROFILE

Ravi S Singh
Bihar Agriculture University
64 PUBLICATIONS **274** CITATIONS
SEE PROFILE

Ravi P. Singh
Banaras Hindu University
115 PUBLICATIONS **415** CITATIONS
SEE PROFILE

Biotic Stress Management in Rice (*Oryza sativa* L.) Through Conventional and Molecular Approaches

30

Prakash Singh, Ram Lakhan Verma, Ravi S. Singh, Ravi P. Singh, H. B. Singh, Pandurang Arsode, Manish Kumar, and Pawan Kumar Singh

Abstract

The rice (*Oryza sativa* L.) productivity is often adversely disturbed by several abiotic and biotic stresses such as drought, submergence, fungal, bacterial, and nematode oriented biotic diseases and pest like brown plant hopper (BPH) and stem borer (SB). The major biotic stresses such as bacterial leaf blight (BLB), sheath blight (ShB), blast, brown spot (BS), false smut (FS), brown plant hopper (BPH), yellow stem borer (YSB), and gall midge (GM) play crucial roles in decreasing the productivity and quality of rice grains. Among the several breeding procedures and various control measures available for mitigating the biotic stresses/factors, the host plant resistance is most effective, economic and eco-friendly which is basically developed by traditional breeding approaches. The related species of rice and wild sources are important for identification of many

P. Singh (✉)
Department of Plant Breeding and Genetics, Veer Kunwar Singh College of Agriculture, Dumraon (Bihar Agricultural University, Sabour), Buxar, Bihar, India

R. L. Verma
Crop Improvement Division, ICAR-National Rice Research Institute (ICAR-NRRI), Cuttack, Odisha, India

R. S. Singh
Department of Plant Breeding and Genetics, Bihar Agriculture College, Sabour (Bihar Agricultural University, Sabour), Bhagalpur, Bihar, India

R. P. Singh · P. Arsode · M. Kumar · P. K. Singh
Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India

H. B. Singh
Department of Mycology and Plant Pathology, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India

A. Rakshit et al. (eds.), *New Frontiers in Stress Management for Durable Agriculture*, https://doi.org/10.1007/978-981-15-1322-0_30

resistance genes/QTLs, which are successfully introgressed or deployed or pyramided in numerous breeding lines through resistance breeding program and various molecular approaches. In this chapter, an inclusive valuation of the conventional and molecular approaches for mitigating the biotic stresses in rice by imparting major resistance sources has been presented.

Keywords
Biotic stress · Bacterial leaf blight · Conventional method · Sheath blight · Blast · False smut · Brown plant hopper · Yellow stem borer · Rice

30.1 Introduction

Rice is a staple and most important security food crop as it supports 60% of global food consumption (Sharma et al. 2012) and it is grown in many countries, in about 167 million ha area in the world, producing 510.6 million tonnes of milled rice (769.9 million tonnes of paddy) with an average productivity of 3.06 t/ha (FAO RMM 2019). Asia occupies an area of 137 m ha of rice cultivation wherein India has a lion's share of 44.6 m ha (23.3% of gross cropped area of the country) with an annual production of 115.6 million tonnes (next to China, 141.6 m tonnes) and contributes 25.7% to agricultural GDP (IIRR 2018) with an average productivity of 25.92 q/ha (FAO RMM 2019). The rice consumers are increasing due to rich source of carbohydrates and energy and demand for rice is also moving up due to better living standards. It also provides employment for 30% of the 700 million people in absolute poverty (with income of less than US$ 1 per day) live in rain-fed rice growing areas in South Asia (IRRI, Philippines, 2010), who either work directly in rice production or in related supported activities (Dat 2004). Various studies have shown that to meet the increasing demand for rice, production has to be increased more than 40% by 2030 (Khush 2005). However, rice production and security are threatened by several biotic and abiotic stresses that seriously affect its production (Khush 2005; Sharma et al. 2012). This challenge has to be overcome by the development of high yielding rice varieties with tolerance to abiotic and biotic stresses (Selvaraj et al. 2011). Though the yield potentiality of rice is 10 tonnes/ha whereas at the / farmers on an average harvesting about 5 tonnes/ha (Khush and Jena 2009). This yield difference is due to yield reducing factors i.e., diseases, pests, weeds, and vagaries of natural calamities. Among the diseases, sporadic but potentially devastating diseases like blast, bacterial blight, and diseases negatively associated with higher attainable yields like sheath blight, false smut, and brown spot are known to reduce yields up to 10–15% in different seasons and years. In severe epidemics, it has been reported that the yield losses due to bacterial leaf blight (BLB) ranging from 20 to 40% (Sonti 1998; Agarwal et al. 2005) and 50% or more in case of blast (Khush and Jena 2009). However, in case of sheath blight, it has been reported to cause 20–30% yield loss depending on the severity of infection (Savary and Mew 1996). So that realizing the economic losses caused by the several biotic diseases,

efforts have been directed to understand the genetic basis of resistance and susceptibility and to bred new varieties which are resistant to these diseases/stresses.

30.2 The Major Constraints of Rice

Rice is one of the most widely cultivated food crops and placed on second position in cereal cultivation around the globe, unfortunately, its production is affected by a wide range of pathogens, insects, nematodes, and other pests attack the rice plant in different parts of the world (Fig. 30.1). Among them, diseases (more than 70) are the major factors for low yields of rice in the world including Asia (Ou 1985). The diseases may appear at any stage of the growth and the development of plant, attacking the seed sown, root system, foliage, stalk, leaf sheath, inflorescence, and even the developing grain. The fungi, bacteria, nematode, and viruses cause different infectious diseases.

Among the biotic diseases, bacterial leaf blight (BLB) caused by bacteria *Xanthomonas oryzae* pv. *oryzae*, blast caused by the fungal pathogen *Magnaporthe oryzae,* sheath blight (ShB) caused by *Rhizoctonia solani* Kuhn., brown spot with causal organism *Helminthosporium oryzae* (sexual stage: *Cochilobolus miyabeanus*), and false smut caused by *Ustilaginoidea virens* not only cause severe yield losses but also impair the quality of the rice grains (Singh et al. 2011, 2014). Apart from the diseases, insects i.e., gall midge, brown plant hopper and stem borer and nematodes are also the major biotic stresses of rice which let the yield penalty to rice production. In Asia, rice gall-midge (GM), *Orseolia oryzae* (wood-mason), is a serious pest of rice in India, China, Sri Lanka, and other neighbor countries (Katiyar et al. 2000). However, the brown plant hopper (BPH), *Nilaparvata lugens,* has been one of the most devastating pests to rice crops in Vietnam and India.

30.2.1 Major Biotic Diseases of Rice and Their Impact in Rice Production

In rice, more than 70 diseases caused by fungi, bacteria, viruses, and nematodes have been reported (Ou 1985). Bacterial leaf blight (BLB), rice blast, sheath blight (ShB), brown spot, false smut, tungro virus, etc. are the major biotic diseases of rice which play an important role in rice production. The diseases may appear at any stage of the growth and the development of plant, attacking the seed sown, root system, foliage, stalk, leaf sheath, inflorescence, and even the developing grain. In India, systematic research efforts to impart host plant resistance in rice is undergoing from more than 65 years. The biotic stress breeding program at the several institute have evolved over time depending on the dynamic pest profile of the crop and advances in the technologies available. The occurrence of Bengal famine caused due to *Helminthosporium* leaf spot in 1946 in the backdrop of the development. Hence during the first two decades, the emphasis was mainly given to developing brown spot resistant genotypes. Eventually, breeding for tolerance against blast and

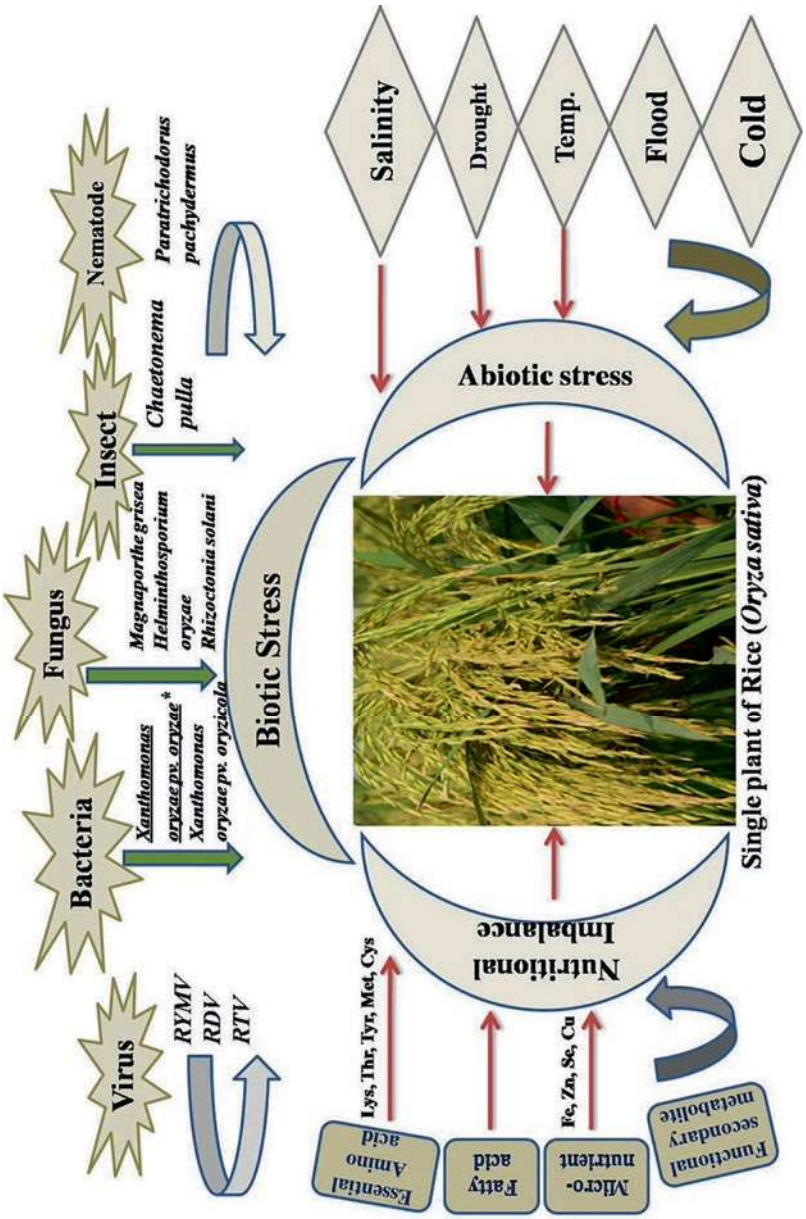

Fig. 30.1 Major constraints of rice production across the world

yellow stem borer (YSB) was also taken up. With the introduction of high yielding semi-dwarf varieties like TN-1 during early 1960s and IR-8 during 1970s, BLB became a severe threat to rice production. The 1970s and 1980s saw the major focus being directed toward breeding for BLB tolerance. With the outbreak of brown plant hopper in the late 1970s, breeding for BPH tolerance has also taken a center stage. Sheath blight, though very severe even during 1960s in countries like the Philippines, was not a stress capable of causing economic damage to the rice industry in India until recently. But the severe incidence of sheath blight is being reported of late especially in the most productive parts of the country like Punjab and even in many regions of Odisha and Bihar where intensive farming is practiced to raise the crop. Thus far, however, single-gene-mediated BSR is only associated with blast, BLB, bacterial streak, sheath blight, rice stripe, bacterial seedling rot, bacterial grain rot, and brown spot diseases based on our knowledge. This restriction mainly reflects the fact that rice resistance to other pathogen species has not been well studied.

30.3 Approaches to Mitigate the Major Biotic Stresses of Rice

The global and national efforts toward understanding the mechanism of resistance and developing cultivars for biotic stress resistance or tolerance against the major rice insect, pest, and diseases through conventional and molecular approaches have been reviewed in this chapter, with major emphasis being given to the major work carried out in premier institution.

30.3.1 Conventional Breeding Approach to Combat the Biotic Stresses of Rice

Conventional approaches are important for producing novel genetic variants, conserving wild germplasm and sexual hybridization between contrasting parental lines. In conventional breeding program, various methods including pedigree method, backcrossing, recurrent selection, and mutation breeding are used. The pedigree method is the most widely used in rice improvement (Allard 1999). The pedigree method is highly suitable to develop rice with resistance to insects and diseases if the resistance is governed by major genes. It is possible to combine genes for resistance to six or seven major diseases and insects within a short period (Khush 1978). The major lacuna of pedigree breeding is that requires more time to evaluate lines periodically throughout the growing season and to maintain records on which selection is based at maturity. Out of all breeding methods, the pedigree method requires the greatest familiarity with the material and with the relative effects of genotype and environment on character expression. For polygenic traits, this breeding technique is not the most effective approach. For example, resistance to sheath blight appears to be under polygenic control. For this trait, diallel selective mating system is suitable (Jensen 1970; Khush 1978). Backcrossing is a most commonly used technique in rice breeding for introgression or substitution of a target gene

from donor parent to recipient. It provides a precise way to improve varieties that excel in a large number of attributes (Allard 1960, 1999). The main purpose of backcrossing is to decline the donor genome content into the progenies (Xi et al. 2008). Backcross breeding has been adopted in the South and Southeast Asia (Joseph et al. 2004; Toojinda et al. 2005) as breeding strategy to improve elite varieties such as KDML105 and Basmati for their resistances to blast and bacterial leaf blight (Sreewongchai et al. 2010).

Heterosis/hybrid vigor is manifested as an improved performance for F_1 hybrids generated by crossing two inbred parents. Occurrence of heterosis in rice was first reported by Jones (1926) and this concept has been continuously evolving. In spite of complexity of this biological phenomenon, breeders in many crops and across countries have successfully exploited it to enhance the level of productivity, production for food security. The next era will be the era of hybrids. Population progression demands the commercial exploitation of the heterosis in several crops especially in rice, which has received the top priority to enhance the productivity (Alam et al. 2004).

Recurrent selection is another traditional breeding method used in rice for male sterility (Fujimaki 1979). It allows defined and shorter breeding cycles, more precise follow-up of genetic gains, and provides opportunity to develop wide range genetic diversity breeding lines (Rangel et al. 2005). Using this method, upland cultivar CG-91 was developed with resistance to rice blast (Courtois et al. 1997). In almost all self-pollinated crops including rice, breeders chose to use pedigree selection which is alternative to recurrent selection.

Mutation breeding in rice is used to complement conventional breeding, since this technique is very effective for improving major traits, such as agronomic traits, resistance to pests and diseases and grain physical parameters and eating quality (Ahloowalia et al. 2004; Singh et al. 2015a). In classical mutation breeding, induced mutations are used for developing a new variety, whereby it is difficult to trace the mutated genes in subsequent breeding (Ahloowalia et al. 2004; Singh et al. 2015a). It is now possible to tag mutated genes, pyramid them into a single elite breeding line, and follow up them in subsequent breeding programs (Azlan et al. 2004; Shu 2009). The advantage of mutation breeding is to create combination of new alleles that do not exist in germplasm pools and the induction of new gene alleles into the new varieties that can be used directly as a commercial variety (Gangadharan and Mathur 1976; Hadzim et al. 1988; Shu et al. 1997; Mohamad et al. 2006). The disadvantage of mutation breeding is limited scope in generating the dominant alleles that might be desired; it is less effective as compared to crossbreeding for a trait combination of multiple alleles. Many attempts have been made to improve disease resistance in rice through mutation breeding (Kaur et al. 1975; Khambanonda 1978; Ahloowalia et al. 2004; Singh et al. 2015a).

Through conventional breeding programs, major genes of blast and BLB resistance i.e., *Pib*, *Pita*, *Pia*, *Pi1*, *Pikh*, *Pi2, Pi4* and *Xa21* have been introduced into rice varieties for blast and BLB disease (Kiyosawa 1982; Khush, 1989; Koizumi 2007). Identifying key genomic regions associated with blast resistance against a broad spectrum of isolates in backcross introgression lines have been developed through

conventional breeding program (Korinsaka et al. 2011). Some components of breeding strategies suggest prolonged durability of resistance which generally can be adopted for stabilization and control of blast disease in rice are discussed in status of biotic stress resistance sub-heading (30.4.1). However, backcrossing for concentration of slow-blasting components, breakdown of varietal resistance to rice blast disease attributed to the failure of varieties to capture the entire complement of genetic factors for disease resistance from the respective parent sources in their parentage (Nottegham 1993). The combination of major genes (vertical resistance) with slow-blasting components (minor genes) is believed to provide increased stability of the resistance mechanism to blast, because the genes for vertical and horizontal resistance in combination increase the effectiveness of each other. This strategy is easier to introduce but need to ensure their agronomical uniformity.

30.3.2 Multiple Lines Breeding Approach

This strategy involves the use of varieties which have distinct type of disease resistance mechanism. The durability resistance of multiline varieties depends upon the rate of blast races develop, the number of lines component in a mixture, and the extent of planted area (Ise 1990; Nakajima 1994; Nakajima et al. 1996; Zhu et al. 2005). Development of multiline varieties using blast resistant isogenic lines had been attempted for "Nipponbare" (Higashi et al. 1981; Horisue et al. 1984) and "Sasanishiki BL" (Matsunaga 1996; Tsuji et al. 1999). Based on rice cultivation practices, seasonal and regional preferences for different location specific varieties are used. As a result, distinct varieties could be developed using diverse sources of blast resistance, BLB resistance (Ise 1990; Koizumi et al. 1996). This situation will slow down the development of new virulent races, and improve the durability of blast resistance in present varieties.

Among many strategies, distinct gene deployment in different maturity groups may help to improve the durability of blast, bacterial leaf blight resistance in newly developing rice varieties. Nevertheless, the conventional resistance breeding has apparent weakness, such as long breeding cycle, selection efficiency and difficulty in distant crossing, leading to the lag between the developments of new resistant variety.

30.3.3 Molecular Approaches for Biotic Stress Resistance

Breakdown of biotic stresses resistance especially blast and bacterial leaf blight (BLB) are the major cause of yield instability in several rice growing areas. There is a need to develop strategies providing long-lasting disease resistance against a broad spectrum of pathogens, giving protection for a long time over a broad geographic area, promising for sustainable rice production in the future. So far, molecular breeding approaches involving DNA markers, such as QTL mapping, marker-aided selection, gene pyramiding, allele mining, genetic transformation, and novel approaches of gene editing have been used to develop new resistant rice

cultivars. Such techniques now are used as a low cost, high-throughput alternative to conventional methods allowing rapid introgression of disease resistance genes into susceptible varieties as well as the incorporation of multiple genes into individual lines for more durable blast resistance. New information and knowledge gained from previous research on the recent strategy and challenges toward improvement of blast, BLB, sheath blight disease such as pyramiding disease resistance gene for creating new rice varieties with high resistance against multiple diseases will undoubtedly provide new insights into the rice disease control (Singh 2016). Breeding work utilizing both phenotypic and genotypic markers are more reliable and fast. DNA marker technology refers to the application of DNA-based markers in breeding programs to improve the selection efficiency (Singh et al. 2001; Sundaram et al. 2008, 2009). Selection for segregants carrying desired traits has always been the hallmark of plant breeding activities since the beginning of crop improvement. Plant breeders generally use phenotype as the basis along with morphological markers and statistical methods to select superior segregants. But selection criteria based on morphological markers has many limitations like influence of the environment on the expression of the trait phenotype, less abundance of morphological markers and stage and environment specific expression of traits. As compared to morphological markers, analysis of polymorphism at DNA level can lead to better inferences. DNA markers which are located near a gene controlling a trait co-segregate with the trait phenotype across generations and because of this property, DNA markers are highly useful (Charcosset and Moreau 2004). Breeders can use these markers to complement classical breeding techniques and can select segregating plants based on the DNA marker genotype rather than waiting to observe the phenotype.

Moreover, marker assisted selection (MAS) offer better selection strategies in rice breeding with a shorter period of time. MAS are more efficient, effective, and reliable than phenotypic selection. Furthermore, MAS can shorten the development time of varieties significantly, so in some cases it will be more cost effective than selection based on phenotypes. MAS also allow the breeding of complex traits which is not feasible through conventional methods. Recently, many rice varieties with complete resistance to blast (*Magnaporthe grisea*), bacterial leaf blight (*Xanthomonas oryzae* pv. *oryzae*) and sheath blight (*Rhizoctonia solani* Kuhn.) have been developed (Variar and Singh 2018). Transferring blast resistance genes to different genetic backgrounds is difficult to identify using conventional breeding approaches instead of MAS to facilitate at early stage selection with greater accuracy. Therefore, future breeding strategies should focus at broadening the genetic and cytoplasmic background of new varieties that are being developed not only for these devastating diseases and pest as well.

30.3.4 Marker Assisted Backcrossing

Marker assisted backcrossing (MABC) is the process of using markers to select for target loci, minimize the length of the donor segment containing a target locus, and/or accelerate the recovery of the recurrent parent genome during backcrossing

(Hospital 2005). These three levels of selection have been referred to as foreground, recombinant, and background selection, respectively. Terms were described after Hospital and Charcosset (1997), who referred to foreground selection as the selection of a target locus and background selection as the selection of the recurrent parent genome using markers on noncarrier chromosomes and also on the carrier chromosome. MABC is superior to conventional backcrossing in precision and efficiency. Background selection can greatly accelerate the backcross breeding program as compared to conventional backcrossing. Furthermore, recombinant selection can minimize the size of the donor chromosome segment, thus reducing "linkage drag"—a "universal enemy" of the plant breeder. This approach has been widely used and, due to the prevalence of several rice "mega varieties", it is likely to continue being a successful approach (Singh 2016).

MAS led to the development and release of a number of improved rice varieties against blast and bacterial leaf blight in the recent past. Marker-assisted backcross breeding (MABB) was used for incorporating bacterial leaf blight resistance genes (*xa13* and *Xa21*) into the genetic background of Pusa Basmati1, which resulted into development of Improved Pusa Basmati 1 (Pusa1460) as one of the first basmati improved products of molecular breeding (Singh et al. 2011). Improved PR 106 and Improved Samba Mahsuri (RP Bio 226) was developed by MABB with three bacterial blight resistance genes, *xa5*, *xa13,* and *Xa21* (Singh et al. 2001; Sundaram et al. 2008). And later on, so many products have been developed through gene deployment in India like Improved Lalat and Improved Tapaswini with *xa5*, *xa13,* and *Xa21* genes (Dokku et al. 2013a, b). RP BIO 226 was released in 2008 as a replacement of Samba Mahsuri (BPT 5204) in the southern states of India. A survey conducted on the adoption of RP Bio 226 in Andhra Pradesh, revealed that the trait value, which represents the value that farmers have obtained by cultivating RP Bio 226 instead of Samba Mahsuri, was Rs. 245 Crores (Reddy 2017).

30.3.5 Gene Pyramiding Approach

Resistant cultivars with one or two major resistant genes are unsustainable in the field and the only way to delay such a breakdown of BLB resistance is to pyramid many resistance genes using MAS (Singh et al. 2001; Rafique et al. 2010). Resistant germplasm carrying both major and minor R genes are the important genetic resource for rice breeders by which blast resistance will be improved in elite rice varieties. In resistant varieties, most of the R genes were conserved with the point mutations and InDels. Hence, the identification of these R genes/alleles with the help of genomic tools will be helpful in modern plant breeding by the utilization of genetic and genomic resources (Kumari et al. 2013).

Pyramiding R genes, instead of quantitative resistance genes which are difficult to accumulate, has been the breeding strategy in case of bacterial blight and blast. However, with the evolution of new races/biotypes it has become necessary to develop broad-spectrum, race nonspecific resistance to combat the evolution of new virulence. Breeders therefore need a wide array of genetic options in order to

diversify the arsenal of resistance traits deployed in crops, thereby reducing this selection pressure (Van der Plank 1975; Vincelli 2016).

Development of host plant resistance is the most effective means of disease management. As many as genes conferring resistance (bacterial blight) and some genes for resistance to blast have been identified to various races of the pathogen and utilized in rice breeding programs. However, large-scale and long-term cultivation of varieties carrying a single gene for resistance resulted in a significant shift in pathogen race frequency with consequent breakdown of resistance in this cultivar (Van der Plank 1975). To combat the problem of resistance breakdown, pyramiding of resistance genes into different cultivars is being carried out.

Improved Lalat and Improved Tapaswini with *xa5*, *xa13,* and *Xa21* genes were developed at the National Rice Research Institute (Dokku et al. 2013a, b). Lalat was further improved with resistance to blast (*Pi2, Pi9*), gall midge (*Gm1, Gm4*), submergence (*Sub1*) and salinity (*Saltol*) genes (Das and Rao 2015). Marker-assisted transfer of genes conferring resistance to three different diseases in rice was also accomplished (Singh et al. 2012a, b; Singh and Gopalakrishnan 2016) wherein genes *xa13* and *Xa21* for BLB resistance, *Pi54* for blast resistance, and a major QTL *qSBR11*-1 against sheath blight were combined through marker-assisted

Table 30.1 Biotic stress resistant varieties developed by MABB and released in India

Improved variety	Parent variety	Disease targeted	Genes used	References
Improved Samba Mahsuri/RP Bio-226	Samba Mahsuri	BLB	*Xa21, xa13,* and *xa5*	Sundaram et al. (2008)
Improved Pusa 1121	–Pusa 1121	BLB	*Xa21* and *Xa38*	Ellur et al. (2016)
Improved Pusa Basmati 1/PB 1460	Pusa Basmati 1	BLB	*xa13, Xa21*	Singh et al. (2011)
Pusa 1608	Improved Pusa Basmati 1	Blast, BLB, and sheath blight	*Pi-54, qSBR11-1*	Singh et al. (2012a, b)
Punjab Basmati-3	Basmati 386	BLB	*xa13, Xa21*	Singh et al. (2014)
Pusa 1609 and Pusa 1612	Pusa Sugandh 5	Blast	*Piz5, Pi54*	DARE-ICAR Ann. Rep., 2016–17
Improved Lalat	Lalat	BLB	*xa5, xa13, Xa21*	Dokku et al. (2013a)
Improved Tapaswini BB	Tapaswini	BLB	*xa5, xa13, Xa21*	Dokku et al. (2013b)
Improved Lalat-2	Improved Lalat	Blast, gall midge	*Pi2, Pi9, Gm1, Gm4, Sub1, Saltol*	Das and Rao (2015)
CR Dhan 800	Swarna	BLB	*xa5, xa13, Xa21*	DARE-ICAR Ann. Rep., 2017–18

backcross breeding or gene pyramiding to improve basmati type varieties. The strategy was to add stable resistance to popular varieties that are renowned for their wide adaptation and production stability across environments (Table 30.1). Although breeding and deployment of resistance cultivars using R genes have been an effective approach to managing rice resistance against bacterial blight and blast diseases, this resistance can be rapidly overcome due to the strong selection pressure against and the rapid evolution of the pathogens.

30.3.6 Allele and Data Mining

Wild relatives and local landraces of rice constitute a large store house of valuable genes that can be used to develop varieties with improved tolerance to stresses and other agronomic traits. Several resistance genes have been identified in germplasm collections using differential physiological races of pathogens. Advancement in molecular techniques such as fine mapping and cloning of many blast and bacterial blight resistance genes and development of PCR-based markers have enabled faster screening and identification of such genes using allele mining approaches (Lin et al. 1995; Bhasin et al. 2012; Kumari et al. 2013; Kim et al. 2015; Kim et al. 2019) . Allele mining has been used to identify novel alleles or allelic variants of a gene/or candidate genes of interest, based on the available information about the genes, from a wide range of germplasm (Imam et al. 2014a, b; Singh et al. 2015b).

30.3.7 Multi-parent Populations

Potential use of landraces can be identified but its use in breeding is usually hindered by unfavorable linkages. So that efficient breeding designs are needed to transfer useful diversity in plant breeding. Multi-parent advanced generation intercross (MAGIC) is a breeding design to produce highly recombined populations. It involves several cycles of inter-mating among multiple parental lines (Cavanagh et al. 2008). MAGIC populations will have greater genotypic diversity, a higher level of recombination, and reduced linkage drag. Because of these advantages, the MAGIC approach has been applied to many crop and plant species for genetic research and breeding (Bandillo et al. 2013; Huang et al. 2015).

30.3.8 Genome/Gene Editing Technologies

Genome editing is a relatively new technology that is gaining importance as a tool for crop improvement because of its advantages over routinely used methods of genetic engineering. (Arora and Narula 2017) Gene editing uses site directed mutagenesis (as opposed to random mutagenesis) to delete, insert, or replace a DNA sequence (Variar and Singh 2018). Development of engineered site specific nucleases (SSNs) has paved the way for single nucleotide excision mechanism for crop improvement (Table 30.2).

Table 30.2 Gene edited using SSNs to improve disease resistance (Source: Variar and Singh 2018)

Disease	Pathogen	Gene	Targeted method	Reference
Blast	*Magnaporthe oryzae*	OsSWEET14	TALEN	Li et al. 2012
Bacterial blight	*Xanthomonas oryzae*	OsSWEET11, OsSWEET14	CRISPR/CAS 9	Jiang et al. (2013)
Blast	*Magnaporthe oryzae*	OsERF922 ethylene responsive mediated transformation factor	CRISPR/CAS9 SSN	Wang et al. (2016)

30.4 Status of Biotic Stress Resistance Through Conventional and Molecular Approaches

The global and national efforts toward understanding the mechanism of resistance and developing cultivars with biotic stress tolerance against the six major rice pests, viz., blast, bacterial blight, sheath blight, false smut, brown plant hopper, and yellow stem borer have been reviewed in this chapter, with major emphasis being given to the work carried out in India at premier institution.

30.4.1 Rice Blast Disease: *Magnaporthe grisea* (Hebert) Barr.

Rice blast disease is caused by the hemi bio-trophic, filamentous heterothallic ascomycetous fungus, *Pyricularia grisea*, which is known as *Magnaporthe grisea* (Hebert) Barr. in its sexual state (Divya et al. 2014). It is the most devastating fungal disease of rice, causing huge losses to rice yield and there by posing a great threat to world food security (Miah et al. 2013). The annual loss of rice production caused by blast could fulfil the annual rice consumption of 60 million people (Parker et al. 2008). *Magnaporthe oryzae* can infect all parts of the rice plant, including the roots (Duan et al. 2014). Blast disease was first reported in India in 1913 and the first devastating epidemic due to rice blast was reported in 1919 in Tanjore delta. Since then several works were carried out in various parts of the country.

Use of blast resistant cultivars is the most effective, economical, and environmentally sustainable way of managing this pathogen (Ishizaki et al. 2005; Singh et al. 2013a). Till today more than 100 blast resistance genes and over 350 quantitative trait loci (QTLs) have been identified to date, of which 21 have been cloned and characterized in detail (Kou and Wang 2012; Sharma et al. 2012). Of these, 45% are from *japonica* cultivars, 51% from *indica* cultivars, and the rest 4% are from wild species of rice (Chen et al. 2008). Blast resistance genes and their genetic location in different rice cultivars have been reviewed by Sharma et al. (2012). However, Hittalmani et al. (2000) used closely linked RFLPs and polymerase chain reaction (PCR)-based markers to put three blast resistance genes *Pi1*, *Piz-5,* and *Pita* into a susceptible cultivar CO39. It was reported that plants carrying two or three gene combinations showed enhanced resistance as compared to *Piz-5* alone. An important gene for blast resistance, *Pi-kh* was identified from *indica* variety Tetep at

ICAR-National Research Centre for Plant Biotechnology, New Delhi. They further characterized, fine mapped, cloned, and functionally validated the resistance gene. The corresponding virulent gene, *AvrPi54* in the pathogen was also successfully cloned by the team, which contributed significantly in the detailed understanding of host–pathogen interaction (Ray et al. 2016). Recently, Liang et al. (2016) reported that *pi 66(t)* is one of the three recessive genes controlling rice blast, and is the first major gene for resistance to be mapped on chromosome 3. Li et al. (2017) identified a new gene from a rice variety Digu which is effective against broad spectrum of *M. oryzae* races. An exhaustive list of the reported blast resistance genes with their corresponding sources and their chromosomal locations have been mentioned in Table 30.3. Singh et al. (2013b) improved the parental lines of rice hybrid P RH 10 by introgressing the blast resistant gene *Piz5* and *Pi 54* into them. This group has also developed and released a blast-resistant basmati variety, Pusa Basmati 1637 through transfer of *Pi9* using marker-assisted selection. Introgression of blast resistance genes *Pi1*, *Pi2,* and *Pi33* into rice variety ADT43 was carried out at Tamil Nadu Agricultural University, Coimbatore. At ICAR-NRRI, Yadav et al. (2017) attempted to find out the status of 12 major blast resistance genes and their diversity among 80 released rice varieties of the institute (ICAR-National Rice Research Institute, Cuttack). Linked molecular markers for genes *Pi54*, *Pib*, *Piz*, *Piz-t*, *Pik*, *Pi-kh*, *Pik-p*, *PikmPik-h*, *Pita/Pita*-2, *Pi2*, *Pi9*, *Pi1,* and *Pi5* were used in the study. Among the 80 varieties used, 19 were resistant, 21 were moderately resistant, and 40 were susceptible to the disease. The blast resistance genes in the different varieties varied from 4 to 12 and the frequencies of the resistance genes ranged from 0 to100%.

Marker assisted backcross breeding strategy was applied for pyramiding blast resistance genes (*Pi2* and *Pi9*), into Vandana and Kalinga III through the crosses (Kalinga III/C101A51 (*Pi-2(t)*)//O. *minute* der. WHD IS 75-127(*Pi-9(t)*) and Vandana/C101A51//O. *minute* der. WHD IS 75-127). Many lines in the background of Vandana and Kalinga III were developed. Among the promising lines, CR 2619-2, CR 2619-5, CR 2619-7 and CR 2619-9 are in the background of Vandana while CR 2620-1, CR 2620-2, CR 2620-3 and CR 2620-4 are in Kalinga III background. The promising lines were tested in Disease Screening Nursery (DSN) under AICRIP for multi-location trials in all over India.

30.4.2 Bacterial Leaf Blight (BLB): *Xanthomonas oryzae* pv. *oryzae*

BLB is caused by gram negative bacterium *Xanthomonas oryzae* pv. *oryzae (Xoo)* is a devastating disease in the rice-growing countries and it had been observed first by farmers in the Fukuoka area of Japan during 1884 and its bacterial nature was established in 1922 (Ishiyama 1922; Mizukami and Wakimoto 1969). Subsequently, the disease was reported from most of the rice growing countries including Australia, China, India, Bangladesh, Cambodia, Indonesia, Korea, Malaysia, Srilanka, Thailand, Philippines, the USA, West Africa, Vietnam, and many other rice growing countries (Choi et al. 1998; Ezuka and Kaku 2000; Niño-Liu et al. 2006; CABI 2011). The disease was first reported in India in 1951, but it was not noticed until

Table 30.3 Blast resistance genes reported in rice

SI no.	Gene name	Location/ Chr. no.	Sources of resistance	SI no.	Gene name	Location/ Chr. no.	Sources of resistance
1	*Mpiz*	11	Zenith	52	*Pi9*	6	*O. minuta*
2	*Pb1*	11	Modan	53	*Pia*	11	*Aichi Asahi*
3	*PBR*	11	St-No 1	54	*Pib*	2	*Tohoku IL9*
4	*Pi(t)*	4	P167	55	*Pib2*	11	*Lemont*
5	*Pi1*	11	LAC23	56	*PiCO39(t)*	11	*CO39*
6	*Pi10*	5	Tongil	57	*Pid(t)1*	2	*Digu*
7	*Pi11*	8	Zhai-Ya-Quing8	58	*Pid2*	6	*Digu*
8	*Pi12*	12	K80-R-Hang, Jiao-Zhan, Moroberekan	59	*Pif*	11	*Chugoku 31-1*
9	*Pi13(t)*	6	*O. minuta*(W), Kasalath (I), Maowangu	60	*Pig(t)*	2	*Guangchangzhan*
10	*Pi14(t)*	2	Maowangu	61	*PiGD1*	8	*Sanhuangzhan 2*
11	*Pi15*	9	GA25	62	*PiGD-2*	10	*Sanhuangzhan 2*
12	*Pi15(t)*	12	Moroberekan	63	*PiGD3*	12	*Sanhuangzhan 2*
13	*Pi16(t)*	2	Aus373	64	*Pigm(t)*	6	*Gumei4*
14	*Pi17*	7	DJ123	65	*Pii*	9	*Ishikari Shiroke, Fujisaa5*
15	*Pi18(t)*	11	Suweon365	66	*Pii1*	6	*Fujisaka 5*
16	*Pi19(t)*	12	Aichi Asahi	67	*Pii2*	9	*Ishikari Shiroke*
17	*Pi20*	12	IR24	68	*Piis1*	11	*ImochiShirazu*
18	*pi21*	4	Owarihatamochi	69	*Piis2*	–	*ImochiShirazu*
19	*Pi22(t)*	6	Suweon365	70	*Piis3*	–	*ImochiShirazu*
20	*Pi23*	5	Suweon365	71	*Pik*	11	*Kusabue*
21	*Pi24(t)*	1	Azucena	72	*Pikg*	11	*GA20*
22	*Pi25*	6	Gumei 2	73	*Pikh (Pi54)*	11	*Tetep*
23	*Pi25(t)*	2	IR6	74	*Pikm*	11	*Tsuyuake*
24	*Pi26*	6	Gumei 2	75	*Pikp*	11	*HR22*
25	*Pi26(t)*	5	Azucena	76	*Piks*	11	*Shin 2*
26	*Pi27*	1	Q14	77	*Pikur1*	4	*Kuroka*
27	*Pi27(t)*	6	IR64	78	*Pikur2*	11	*Kuroka*
28	*Pi28(t)*	10	IR64	79	*Pilm2*	11	*Lemont*
29	*Pi29(t)*	8	IR64	80	*Pir2-3(t)*	2	*IR64*
30	*Pi3(t)*	6	Pai-kan-tao	81	*Pirf2-1(t)*	2	*O. rufipogon*
31	*Pi30(t)*	11	IR64	82	*Pise*	11	*Sensho*
32	*Pi31(t)*	12	IR64	83	*Pise2*	–	*Sensho*
33	*Pi32(t)*	12	IR64	84	*Pise3*	–	*Sensho*
34	*Pi33*	8	IR64	85	*Pish*	1	*Shin 2*
35	*Pi34*	11	Chubu32	86	*Pish*	11	*Nipponbare*
36	*Pi35(t)*	1	Hokkai 188	87	*Pit*	1	*Tjahaja*
37	*Pi36*	8	Q61	88	*Pita*	12	*Tadukan*

(continued)

Table 30.3 (continued)

SI no.	Gene name	Location/ Chr. no.	Sources of resistance	SI no.	Gene name	Location/ Chr. no.	Sources of resistance
38	*Pi37*	1	St-No 1	89	*Pita2*	12	*Shimokita*
39	*Pi38*	11	Tadukan	90	*Pitp(t)*	1	*Tetep*
40	*Pi39(t)*	4, 12	Chubu 111, Q15	91	*Pitq1*	6	*Teqing*
41	*Pi40(t)*	6	*O. australiensis*	92	*Pitq2*	2	*Teqing*
42	*Pi41*	12	93-11	93	*Pitq3*	3	*Teqing*
43	*Pi42(t)*	12	DHR9	94	*Pitq4*	4	*Teqing*
44	*Pi44*	11	Moroberekan	95	*Pi-tq5*	2	*Teqing*
45	*Pi47*	11	Xiangzi 3150	96	*Pitq6*	12	*Teqing*
46	*Pi48*	12	Xiangzi 3150	97	*Piy1(t)*	2	*Yanxian No 1*
47	*Pi5(t)*	9	Moroberekan	98	*Piy2(t)*	2	*Yanxian No 1*
48	*Pi6(t)*	12	Apura	99	*Piz*	6	*Zenith (J), Fukunishiki, Toride 1, Tadukan*
49	*Pi62(t)*	12	Yashiro-mochi	100	*Pizh*	8	*Zhai-Ya-Quing8*
50	*Pi67*		Tsuyuake	101	*Pi157*	12	*Moroberekan*
51	*Pi8*	6	Kasalath	102	*Pi-jnw1*	11	*Jiangnanwan*

Source: Updated from Sharma et al. (2012)

1963 that an epiphytotic occurred. In the states of Punjab, major epidemics occur in 1979 and 1980 and total crop failure was reported by Mew (1987) and the disease has been occurring every year as an epidemic form. Infection at maximum tillering stage results in blighting of leaves, which eventually causes significant yield losses in severely infected fields ranging from 20 to 50% (Singh 2016), but this, can reach as high as 80% (Singh et al. 1997) and even 100% under very severe conditions (Agarwal et al. 2005). Development of cultivars carrying major resistance (R) genes have been the most effective and economic strategy to control BLB disease (Agrios 2005). To date, at least 44 BLB resistance genes, designated from *Xa1* to *xa44* conferring host resistance against various strains of *Xoo* have been identified (Table 30.4) from cultivated and wild species of rice (Lin et al. 1995; Bhasin et al. 2012; Kim et al. 2015; Vikal and Bhatia 2017; Busungu et al. 2018; Kim 2018; Chukwu et al. 2019; Kim et al. 2019). Among these R genes, 14 are recessive; 9 R genes have been cloned and characterized encoding different types of proteins. All of these genes follow a Mendelian pattern of inheritance and express resistance to a diverse group of *Xoo* pathogens (Lin et al. 1995; Singh et al. 2014, 2018; Kumar et al. 2019). Several of these genes have already been incorporated into rice cultivars, which are now widely cultivated in many countries. BLB resistance gene *Xa21* is one of the most widely exploited resistance genes and it confers durable resistance in many commercial rice cultivars (Khush, 1989). Two genes *Xa 33(t)* and *Xa 38* were identified from *Oryza nivara* (Bhasin et al. 2012). A new mutant named "XM14" was obtained from IR24, which was resistant to all Japanese *Xoo* races. The gene identified in XM14 was designated as *xa42* (Busungu et al. 2018).

In IRRI, IR24 NILs (IRBB lines) containing *Xa4*, *xa5*, *Xa7*, *xa13,* and *Xa21* genes and their combinations were developed and extensively used in the breeding

Table 30.4 List of BLB resistance genes reported in rice

SI. no.	R-gene	Location on Chr.	Nature of gene	Resistance to Xoo race	Donor cultivar
01	*Xa1*	4L	D	Japanese race-I	Kogyoku, IRBB 1
02	*Xa2*	4L	D	Japanese race-II	IRBB2
03	*Xa3/ Xa26*	11	D	Chinese, Philippine, and Japanese races	Wase Aikoku 3, Minghui 63, IRBB3
04	*Xa4*	11	D	Philippine race-I	TKM6, IRBB4
05	*xa5*	5S	R	Philippine races-I, II, III	IRBB5
06	*Xa6/xa3*	11	D	Philippine race-I	Zenith
07	*Xa7*	6	D	Philippine races	DZ78
08	*xa8*	7	R	Philippine races	P1231128
09	*Xa9*	11	D	Philippine races	Khao Lay Nhay and Sateng
10	*Xa10*	11L	D	Philippine and Japanese races	Cas 209
11	*Xa11*	3L	D	Japanese races IB, II, IIIA, V	IRS
12	*Xa12*	4	D	Indonesian race-V	Kogyoku, Java14
13	*xa13*	8L	R	Philippine race 6	BJ1, IRBB13
14	*Xa14*	4L	D	Philippine race 5	TN1
15	*xa15*	ND	R	Japanese races	M41 Mutant
16	*Xa16*	ND	D	Japanese races	Tetep
17	*Xa17*	ND	D	Japanese races	Asominori
18	*Xa18*	ND	D	Burmese races	IR24, Miayang 23, Toyonishiki
19	*xa19*	ND	R	Japanese races	XM5 (Mutant of IR24)
20	*xa20*	ND	R	Japanese races	XM6 (Mutant of IR24)
21	*Xa21*	11L	D	Philippine and Japanese races	*O. longistaminata*, IRBB21
22	*Xa22(t)*	11	D	Chinese races	Zhachanglong
23	*Xa23*	11L	D	Indonesian races	*O. rufipogon* (CBB23)
24	*xa24*	2L	R	Philippine and Chinese races	DV86
25	*xa25(t)*	12	R	Chinese and Philippine races	Minghui 63, HX-3 (Somoclonal mutant of Minghui 63)
26	*Xa26*	11L	D	Philippine races	Nep Bha Bong
27	*Xa27*	6L	D	Chinese strains and Philippine race 2–6	*O. minuta*, IRGC 101141, IRBB27
28	*xa28 (t)*	ND	R	Philippine race 2	Lota sail
29	*Xa29(t)*	1	D	Chinese races	*O. officinalis* (B5)
30	*Xa30 (t)*	11L	D	Indonesian races	*O. rufipogon* (Y235)
31	*Xa31(t)*	4L	D	Chinese races	Zhachanglong
32	*Xa32(t)*	11L	D	Philippine races	*O. australiensis* (introgression line C4064)
33	*Xa33*	7	D	Philippine races	*Oryza* wild species

(continued)

Table 30.4 (continued)

SI. no.	R-gene	Location on Chr.	Nature of gene	Resistance to Xoo race	Donor cultivar
34	*xa33(t)*	6	R	Thai races	Ba7 *O. nivara*
35	*xa34 (t)*	1	R	Thai races, Srilanka	BG1222
36	*Xa35(t)*	11L	D	Philippine races	*O. minuta* (Acc.No.101133)
37	*Xa36(t)*	11L	D	Philippine races	C4059
38	*Xa38*	4L	D	Indian Punjab races	*O. nivara* IRGC81825
39	*Xa39*	11	D	Chinese and Philippine races	FF329
40	*Xa40(t)*	11	D	Korean BB races	IR65482-7-216-1-2
41	*xa41(t)*	11	R	Various Xoo strains	Rice germplasm
42	*xa42*	3	R	Japanese Xoo races	XM14, a mutant of IR24
43	*Xa43*	11	D	Korean BB races	P8 and Ilpum
44	*xa44*	11	R	Philippine race	IR73571-3B-11-3-K3 and Ilpum

Source: Updated from Singh (2016) and Chukwu et al. (2019)

programs of many countries including India. Indian scientists from the Agricultural Research and Education system used these IRBB lines for transfer of BLB resistance genes in many popular high yielding varieties (Singh et al. 2001; Sundaram et al. 2008; Singh et al. 2012a, b; Pandey et al. 2013; Pradhan et al. 2015; Dash et al. 2016). The gene combinations chosen by breeders, however, remained confined to *xa13* and *Xa21* or *xa5, xa13* and *Xa21 or Xa4, xa5, xa13, and Xa21*. However, Ellur et al. (2016) incorporated *Xa38* in the basmati background of PB1121 and found that it provides resistance to an additional race of the pathogen when compared with its NIL pyramided with *xa13* + *Xa21*. The *Xa21* gene was identified at ICAR-NRRI in the wild species *Oryza longistaminata*, which was highly effective against BLB races in South and South-eastern Asia (Khush 1989). The gene was later mapped and cloned at ICAR-IRRI and is being extensively utilized by breeders across the globe. Varietal improvement program was initiated to improve the BLB resistance in popular high yielding varieties as recurrent parents and BLB resistance genotypes viz., Ajaya (*xa5*), IRBB 8 (*xa8*), IRBB 21 (*XXa21*), PR 106 (*xa5*, *xa13* and *Xa21*), IRBB 60 (*Xa4*, *xa5, xa13 and Xa21*), PR 114 (*Xa38*) and IRBB66 (*Xa4*, *xa5*, *Xa7*, *xa13* and *Xa21*) as donors through pedigree breeding coupled with artificial screening.

Resistance genes (*Xa4*, *xa5*, *xa13,* and *Xa21;* either singly or in different combinations) pyramided lines were developed through marker-assisted backcross breeding in the genetic background of Swarna and IR64 under the Asian Rice Biotechnology Network (Reddy et al. 1997 and Singh et al. 2001) . The promising pyramided lines identified through DSN of AICRIP in different locations across the country were recommended for registration for their use as potential donors in future breeding programs (DRR Annual Progress Report, 2003, 2005). Two lines CRMAS 2231-37 and CRMAS 2231-48 in the background of IR 64 were found promising for BLB endemic areas of Uttarakhand, Andhra Pradesh and Haryana,

respectively, while one line CRMAS 2232-85 (IET 20672) in the background of Swarna was recommended for the endemic areas of Gujarat and Maharashtra. Pradhan et al. (2015) introgressed three BLB resistance genes (*xa5, xa13* and *Xa21*) by marker-assisted backcrossing, in the background of the popular, but highly BLB susceptible deep water variety, Jalmagna and showed a high level of BLB resistance with significant yield advantage over Jalmagna under conditions of BLB infection. Lines carrying two BLB gene combinations (*Xa21* + *xa13* and *Xa21* + *xa5*) were also developed in the background of Jalmagna (Pradhan et al. 2016) and showed increased resistance to BLB isolates prevalent in the region. The parental line improvement for BLB resistance has been successfully undertaken in case of popular rice hybrid of ICAR-NRRI, Rajalaxmi, by introgressing four resistance genes (*Xa4*, *xa5, xa13* and *Xa21*) through MAB breeding (Dash et al. 2016). However, the varietal improvement program in India for BLB resistance resulted in the release of Improved PR 106, Improved Lalat: CRMAS 2621-7-1 (IET 21066), Improved PR 114, Improved Tapaswini: CRMAS 2622-7-6 (IET 21070), CR Dhan 800, RP BIO 226 in the genetic background of popular rice varieties PR 106, Lalat, PR 114, Tapaswini, Swarna and BPT 5204, respectively. Improved Lalat and Improved Tapaswini carry four genes (*Xa4, xa5, xa13,* and *Xa21*) while CR Dhan 800 has three resistance genes *Xa21, xa13,* and *xa5*. All have been effective for growing in the "bacterial leaf blight" endemic areas of India.

30.4.3 Sheath Blight (ShB) Disease: *Rhizoctonia solani* Kuhn.

ShB is a disease of rice caused by the fungus, *Rhizoctonia solani* Kuhn, is becoming a major threat to rice production worldwide (Sinha and Prasad 2008). Though first reported as early as in 1910 from Japan by Miyaki. But in India, Paracer and Chahal reported this disease from Gurdaspur (Punjab) only in 1963 as a prominent disease only after the introduction of high yielding semi-dwarf varieties with intensive practices (Laha and Venkataraman 2001; Agrios 2005). The intensive cropping involving cultivation of a single variety over a large area and the high use of nitrogenous fertilizer led to a dramatic increase in the incidence of sheath blight in major rice-growing countries of the world as well as India (Singh and Srivastava 2015). Almost all the prominent varieties grown in the country are highly susceptible to the ShB disease and it reduces trivial yield ranging from 5.2 to 69% depending on the extent of severity and crop stages at which the disease appears and the environmental condition in rice-growing areas around the globe (Naidu 1992; Yellareddygari et al. 2014; Yadav et al. 2015).

Development of genotypes tolerant to the disease is considered as the most sustainable, ecofriendly, and economical way to combat the disease. However, the breeding for ShB tolerance in rice poses many unique challenges as compared to other pests and diseases. Being caused by a necrotrophic fungus, ShB tolerance or resistance is a complex, quantitative trait controlled by polygenes or polygenic QTLs as reported in genetic studies (Pinson et al. 2005). Lack of a well-standardized screening protocol compounded with the influence of environment and various

plant morphological features on trait expression make identification of truly resistant lines a daunting task (Singh and Srivastava 2015). Genotypes with moderate disease resistance have been reported in the past, but a strong ShB resistant source is not yet identified from both the cultivated and wild gene pool of rice.

From the moderate resistance sources identified, more than 45 QTLs (Table 30.5) have been reported for ShB tolerance in rice on all the 12 rice chromosomes, but most of them have minor effects and are correlated with various plant morphological features, especially plant height and heading date (Zuo et al. 2010; Wang et al. 2012; Dey et al. 2019). Even for the major ShB QTLs having plant morphology-independent effect, the expression is highly affected by the genetic background, limiting the usefulness of the QTLs in practical plant breeding. The breeding potential of few ShB QTLs viz., *qSB9-2*^{TQ}, *qSB-11*^{LE}and *qSB-9*^{TQ} have been tested in different genetic backgrounds and their effect on sheath blight tolerance was validated. Two of these QTLs *qSB-11*^{LE}and *qSB-9*^{TQ} were fine mapped.

There are only limited reports of utilization of identified ShB QTLs in practical plant breeding, with only limited resistance genotypes viz., Teqing, Tetep, Lemont and Jasmine 85 being regularly used as donors of ShB tolerance. Pinson et al. (2008) have improved the ShB tolerance of the popular American rice genotype Lemont by introgressing ShB tolerance QTLs from Teqing. Three Teqing-into-Lemont backcross introgression lines (TILs) containing eight ShB QTLs and having significantly less sheath blight susceptibility compared to the recurrent parent were released in the USA in 2007. Wang et al. (2012) have developed Teqing-into-Lemont backcross introgression lines (TILs) of QTLs *qSB9-2* and *qSB12-1* and found that resistant alleles of the QTLs from Teqing significantly improved ShB tolerance of the TILs. Chen et al. (2014) have transferred the QTLs *qSB-7* and *qSB-9* from Teqing into the genetic background of commercial japonica varieties by MAS. The two QTLs were also pyramided in the background of the *japonica* variety WLJ1. There was a significant reduction in SB incidence and yield loss in the introgressed lines and pyramiding of two QTLs were found to be more effective rather than using single QTL. Zuo et al. (2014) have shown that pyramiding of QTLs for ShB tolerance and tiller angle, *qSB-9*^{TQ} and *TAC1*^{TQ}, had significantly increased disease tolerance in the near-isogenic lines (NILs) carrying them. Both the QTLs have improved the ShB tolerance of the NILs but *qSB*-9^{TQ} was more effective than *TAC1*^{TQ}. The NILs having both the QTLs had more tolerance to sheath blight compared to the NILs having any one of them.

In India, ShB tolerance breeding relies mainly on the genotype Tetep, which is a multiple biotic stress tolerant *indica* genotype from Vietnam (Channamallikarjuna et al. 2010) . In studies conducted at Indian Agricultural Research Institute (IARI), one major ShB QTL *qSBR11-1*^{TE} from Tetep was functionally characterized and the candidate gene, a novel chitinase gene (LOC_Os11g47510), for sheath blight tolerance was identified in the QTL region. The QTL *qSBR11-1*^{TE} was introgressed into the background of 'Improved Pusa Basmati 1/Pusa1460' by marker-assisted backcrossing (MABB). In another study, the sheath blight tolerance of the line Pusa 6B, the Basmati quality maintainer line of the popular superfine aromatic rice hybrid Pusa RH10, was enhanced by introgressing three ShB resistance QTLs (*qSBR11-1*^{TE}, *qSBR11-2*^{TE} and *qSBR7-1*^{TE}) from Tetep by MAB.

Table 30.5 List of reported QTLs for sheath blight tolerance

SI no.	QTL	Chr. no.	Resistant parent	Susceptible parent	Mapping population
1	*qSBR1-1*	1	Tetep	HP2216	RIL
2	*qSB-1*	1	Lemont	Teqing	RIL
3	*QRh1*	1	Jasmine 85	Lemont	RIL
4	*qSB1-1^{HJX74}*	1	Amol 3 (Sona)	Huan Jing Xian 74	Chr. Seg. Sub. Lines
5	*qSB-2*	2	Jasmine 85	Lemont	F2
6	*qSBR2a*	2	Teqing	Lemont	RIL
7	qSBR-2	2	Jingxi 17	Zhaiyeqing 8	DH
8	*qSB-3*	3	Jasmine 85	Lemont	F2
9	*qSBR-3*	3	Jingxi 17	Zhaiyeqing 8	DH
10	*qSBR-3a*	3	Teqing	Lemont	F4 Bulk
11	*qSBR-3-1*	3	Tetep	HP2216	RIL
12	*qSB-3*	3	WSS2	Hinohikari	BC1F1
13	*qSB-3-1*	3	Teqing	Lemont	RILs
14	*qSB-3-2*	3	Teqing	Lemont	RILs
15	*qSB-4-1*	4	Teqing	Lemont	RILs
16	*qSB*-4-2	4	Teqing	Lemont	RILs
17	*qSB-5*	5	Minghui 63	Zhenshan 97B	RILs
18	*qShb5.1*	5	RP 2068-18-3-5	TN1	RILs
19	*Rsb1*	5	4011	XZX19	F2's
20	*qSB-5*	5	Teqing	Lemont	RILs
21	*qSB-6-1*	6	Teqing	Lemont	RILs
22	*sSB-6-2*	6	Teqing	Lemont	RILs
23	*qSBR-7*	7	Jingxi 17	Zhaiyeqing 8	DH
24	*qSB-7*	7	Jasmine 85	Lemont	F2's
25	*qSB-7*	7	Teqing	Lemont	RILs
26	*qShB7.3*	7	ARC10531	BPT-5204	BC_1F_2
27	*qSBR7-1*	7	Tetep	HP2216	RILs
28	*qSBR8-1*	8	Tetep	HP2216	RILs
29	*qSh8a*	8	Teqing	Lemont	RILs
30	*qSh8b*	8	Teqing	Lemont	RILs
31	*qSB*-9	9	Minghui 63	Zhenshan 97B	RILs
32	*qSB*-9	9	Teqing	Lemont	RILs
33	*qShb9.2*	9	ARC10531	BPT-5204	BC_1F_2
34	*qShB9-1*	9	Jasmine 85	Lemont	RIL
35	*qSBR-9*	9	Jarjan	Koshihikari	BC_2F_3 (BIL)
36	*qSB-9-1*	9	Tetep	HP2216	RIL
37	*qSB-9-2*	9	Jasmine 85	Lemont	RIL
38	*qSBR9a*	9	Teqing	Lemont	F4 Bulk
39	*qSB-9^{Tq}*	9	Lemont	Teqing	BC1F1s
40	*qSB-10*	10	Teqing	Lemont	RILs
41	*qSB-11*	11	Jasmine 85	Lemont	F2
42	*qSBR-11*	11	Jingxi 17	Zhaiyeqing 8	DH
43	*qSBR11-1*	11	Tetep	HP2216	RIL
44	*qSBR11-2*	11	Tetep	HP2216	RIL

(continued)

Table 30.5 (continued)

SI no.	QTL	Chr. no.	Resistant parent	Susceptible parent	Mapping population
45	*qSBR11-3*	11	Tetep	HP2216	RIL
46	*qSB-11^{HJX}*	11	Lemont	Yangdao	NIL
47	qSB-12	12	Teqing	Lemont	RILs
48	*RSB-2(t)*	–	A Mutant	Shuhui 881	–
49	–	–	Pecos	Rosemont	F_2

Source: Updated from Srinivasachary et al. (2011) and Dey et al. (2019)

The resistance reaction of a genotype may vary depending on the strain of the pathogen used. Screening experiments conducted at the ICAR-National Rice Research Institute (NRRI) using the local strains of the pathogen has shown that international check genotypes for ShB tolerance like Jasmine 85 and Teqing are susceptible to the local strains. Only two genotypes, Tetep and CR 1014, a variety released from ICAR-NRRI, showed consistent moderate resistant phenotype for sheath blight. Conventional breeding has been less effective for the development of ShB tolerant genotypes because of the polygenic nature of the trait. In the segregating generations of the crosses made at ICAR-NRRI, using CR1014 as the donor for ShB tolerance, selection of superior recombinants has been difficult since ShB tolerance has tight linkage with plant height. A novel ShB QTL on chromosome 1 was identified from an $F_{2:3}$ population derived from the cross Swarna Sub1 × CR 1014, which need to be fine mapped and its effects in different genetic backgrounds need to be validated.

30.4.4 False Smut (FS): *Ustilaginoidea virens*

False smut (green smut), caused by *Ustilaginoidea virens*(Cooke) Tak, was a minor fungal disease with occasional outbreaks in rice growing Asian countries particularly in India and China in the 1950s (Deng 1989; Sugha et al. 1993). In recent years, false smut is one of the most severe diseases of rice emerged of increasing importance in more than 40 countries especially in the rice planting countries in Asia, such as China, India, and Burma areas since the widespread adoption of high-yielding semi-dwarf rice cultivars and heavy application of N fertilizer since the 1990s (Yaegashi et al. 1989; Sugha et al. 1993; Andargie et al. 2018). The disease can cause 2.8–81% yield losses in different rice-producing areas depending on the rice variety and disease intensity (Biswas 2001a, b; Yang et al. 2012). *U. virens* infects young rice panicles at the booting stage (Biswas 2001a, b) and inhibits floral organs from fertilizing and developing. False smut is a soilborne fungus, where the spores released in late summer from one crop persist in the soil over winter, and infect the rice planted in subsequent years. There are no known visual symptoms of the disease until the grain begin to fill. At that time, spore balls emerge from between the hulls of infected kernels, covered at first by a silvery or off-white membrane that ruptures to reveal a coating of orange or yellow spores (Webster and Gunnell 1992). Resistance to false smut disease is a complex, quantitative trait controlled by

polygenes. Although there is no rice variety that has yet been identified to have complete or high level of resistance to false smut, cultivars do exhibit significant differences in quantitative resistance to *U. virens* (Biswas 2001a, b). Resistance of genes against *U. virens* has not been identified yet, but numerous efforts have been undertaken to study the inheritance of the resistance. Xu et al. (2002) evaluated the 266 near-isogenic introgression lines derived from susceptible cultivar Teqing and resistant Lemont under natural infection in field and identified two QTLs contributing resistance which are *QFsr10* and *QFsr12*, located on chromosome 10 and 12, respectively. Later on, Zhou et al. (2014) identified the 10 QTLs for false smut resistance. Li et al. (2008) developed a population of 157 recombinant inbred lines (RILs) from crossing a susceptible landrace Daguandao (*O. sativa* subsp. *japonica*) and a resistant cultivar IR28 (*Oryza sativa* subsp. *indica*). Subsequently, different RILs and parents were evaluated following effective artificial inoculation under field conditions and reported that the resistance was controlled by two major genes with equal effect of 11.41 and polygenes with minor effects (Wang et al. 2019). Further work identified seven QTLs for false smut resistance on chromosomes 1, 2, 4, 8, 10, 11, and 12, and the phenotypic variance ranged from 9.8 to 22.5% (Li et al. 2011). More than 52 false smut resistance quantitative trait loci have been reported with moderately to highly resistant reaction on all the 12 rice chromosomes (Li et al. 2011; Zhou et al., 2014; Andargie et al. 2018; Wang et al. 2019) by using the resistant parents Lemout, IR 28 and others. However, QTL for false smut resistance in rice has not yet been isolated and resistance mechanisms are largely unknown.

30.4.5 Brown Plant Hopper (BPH): *Nilaparvata lugens* Stål

BPH (*Nilaparvata lugens* Stål) is one of the most destructive insect-pests of rice in all over the Asia. Besides affecting the rice crop directly, it also serves as a vector that transmits rice grassy stunt virus and ragged stunt virus. The host resistance of rice against BPH was first reported in the variety Mudgo and the first BPH resistance gene (*BPH* 1) was identified from the same in 1967. After that 31 more genes have been discovered (Table 30.6) besides several QTLs from the gene pool of cultivated and wild rice (Deen et al. 2017). They are mapped to five of the 12 chromosomes (3, 4, 6, 11, and 12) of rice (Cheng et al. 2013). Among those, only 17 genes (*BPH1, BPH2, BPH6, BPH9, BPH12, BPH14, BPH15, BPH17, BPH18, BPH19, BPH25, BPH26, BPH27, BPH28, BPH29, BPH30,* and *BPH32*) have been fine-mapped and seven of them (*BPH14, BPH17, BPH18, BPH26, BPH29, BPH9,* and *BPH32*) have been cloned and characterized (Jena et al. 2017). Among the cloned genes *BPH 9* and *BPH 26* turned out to be the same gene (LOC_Os12g37280), and the locus IDs for *BPH 17* and *BPH 18* have not been yet assigned. However, almost all the identified resistance genes are biotype/population specific and do not provide strong resistance to other BPH biotypes/populations. Hence search for broad-spectrum resistance should continue besides taking efforts for pyramiding multiple combinations of genes and understanding the detailed molecular mechanisms involved therein.

Table 30.6 BPH resistance genes and their source germplasm

SI no.	Resistance gene	Source
1	*Bph1*	Mudgo, CO22 (IT 000588), TKM6, Milyang30, Milyang34 (IT 006216), Nampungbyeo, Chilseongbyeo, Andabyeo, Kanto PL4 (IT173362), Cheongcheongbyeo, Changsongbyeo, Baekunchalbyeo, IR26 (IT001886), IR28 (IT001892), IR29 (IT001893), IR30 (IT001899), Hangangchalbyeo, Yeongpungbyeo, Namyeongbyeo, Gayabyeo, Samgangbyeo, Namcheonbyeo, MTU15, IR26, IR28, IR29, IR30, IR34, IR44, IR45, IR46, IR64 and MGL2
2	*bph2*	ASD7, ASD9, IR 1154-243, Norin-PL4, Hwacheongbyeo, PTB18, PTB33, H105, Palasithari 601, H5, IR32, IR36, IR38, IR40, IR42, IR48, IR50, IR52, IR54, IR65
3	*Bph3*	RathuHeenati, PTB19, Gangala, HoranaMawee, Muthumanikam, Kuruhondarawala, Mudu, Kiriyal, PTB33, IR56, IR58, IR60, IR62, IR68, IR70, IR72, IR74
4	*bph4*	Babawee, Gambada Samba, Hotel Samba, Kahata Samba, Thirissa, Sulai, VellaiIllankali, Heenhoranamawee, KuluKuruwee, Lekam Samba, Senawee and IR66
5	*bph5*	ARC10550
6	*Bph6*	Swarnalata, *O. officinalis* (acc.00896)
7	*Bph7*	T12
8	*bph8*	Chin Saba, Col. 5 Thailand and Col. 11 Thailand
9	*Bph9*	Pokkali, Balamee and Kaharamana
10	*Bph10*	*O. australiensis* and IR65482-4-136-2-2
11	*bph11*	*O. officinalis*, DV85 and IR 54751-2-44-15-24-3
12	*Bph12*	*O. officinalis, O. latifolia,* B14 and IR54751-2-34-10-6-2
13	*Bph13*	*O. eichingeri, O. officinalis* (acc.00896), acc105159 and IR54745-2-21-12-17-6
14	*Bph14*	*O. officinalis*, RI35 and B5
15	*Bph15*	*O. officinalis* and B5
16	*Bph17*	Rathu Heenati
17	*Bph18*	*O. australiensis* and IR65482-7-216-1-2
18	*bph19*	AS20-1
19	*Bph20*	*O. minuta* (acc. 101,141), IR71033-121-15 and ADR 52
20	*bph21*	ADR52, *O. minuta* (acc. 101,141) and IR71033-121-15
21	*Bph22*	IR 75870-5-8-5-B-2-B and IR 75870-5-8-5-B-1-B
22	*Bph23*	IR 71033-121-15
23	*bph24*	IR 73678-6-9-B
24	*Bph25(t)*	ADR52
25	*Bph26(t)*	ADR52
26	*Bph27*	GX2183
27	*Bph28(t)*	DV85
28	*Bph29*	RBPH54 (introgression from *O rufipogon*)
29	*Bph31*	CR2711-76
30	*Bph32*	PTB33

Updated from Ali and Chowdhury (2014)

A series of BPH tolerant varieties (e.g., IR26, IR36, IR50, and IR72) have been developed and released from the IRRI since the 1970s, by transferring BPH resistance genes in the background of elite susceptible cultivars. However, the improved cultivars carrying single resistance gene lose effectiveness due to the evolution of new biotypes and this has become a serious threat to its management in Asia. Pyramiding of BPH resistance genes/QTLs may provide a sustainable means for developing durable resistance against frequently evolving new biotypes. Several studies have been reported for pyramiding of insect resistance genes. The most elaborate work was carried out by Jena et al. (2017) in which the resistance levels of *bph* genes were studied by introgressing them into the genetic background of the variety IR 24. Near-isogenic lines carrying only one *bph* gene (25) and NILs with combinations of two (11) and three (5) gene combinations were developed. The insect resistance of the NILs, in terms of the level of antibiosis was assessed. It was found that NILs pyramided with multiple *bph* genes were having more level of antibiosis compared to NILs with single *bph* gene. The study throws significant inroads into the concept of R gene deployment in which different *bph* gene/gene combinations can be used in different geographical areas depending on the biotype prevalent in the region. Deen et al. (2017) reported the occurrence of multiple loci instead of a single recessive gene (reported earlier) conferring resistance to the insect in case of *bph5.* They identified five QTLs *qBphDs6, qBphNp1, qBphNp12, qBphDw3,* and *qBphDw8* associated with BPH (biotype 4) resistance in ARC10550. The two major QTLs *qBphDs6* for damage score and *qBphDw8* for days to wilt were important for further investigation and use in the breeding program. Pyramiding of BPH resistance genes, *Bph1* and *Bph2,* has been successfully achieved by marker-assisted breeding (Sharma et al. 2004).

However, at ICAR-NRRI, several landraces showing a very high degree of resistance were used for breeding varieties resistant to BPH. The breeding lines CR 3005-77-2 (Samba Mahsuri/Salkathi), CR 3006-8-2 (Pusa 44/Salkathi), CR 3005-230-5 (SambaMahsuri/Salkathi), CR 2711-76 (Tapaswini/Dhobanumberi) were found to be promising in plant hopper screening trials of AICRIP, 2011 and 2012. Molecular mapping of resistance genes/QTLs from these two landraces—Salkathi and Dhobanumberi is underway. Two QTLs designated as *qBph4.3* and *qBph4.4* were identified from Salkathi landrace among which *QBph4.3* is novel (Mohanty et al. 2017). Transfer of these two QTLs into two popular susceptible varieties Naveen and Pooja are in progress. Recently, Prahalada et al. (2017) at IRRI identified a single dominant gene, *BPH31* on the long arm of chromosome 3 in CR2711-76.

30.4.6 Yellow Stem Borer (YSB) of Rice: *Scirpophaga incertulas*

YSB is a major threat to rice production in tropical and subtropical rice-growing areas. Lack of availability of an effective source of resistance to this insect in primary gene pool poses a challenge in the study and improvement of this trait. The complex inheritance pattern and screening methodologies for resistance create further complications. In absence of any significant report of studies related to YSB resistance in

literature, the works carried out at ICAR-NRRI and other institutes of India are discussed. Unlike the four other biotic stresses mentioned above, comprehensive molecular studies for identification of genes and QTLs conferring resistance to YSB are not available. Most of the studies are confined to classical genetic studies.

Efforts to introgress YSB tolerance in the elite genetic background started immediately after the establishment of the institute. Screening studies conducted during 1950s at NRRI resulted in the identification of YSB tolerant genotypes viz., TKM6, Slo-12, CB-1, MTU 15, Tepa-1, ADT-14, and JBS 1638. Among these, TKM6 was extensively used in the resistance breeding program at the institute. Three YSB tolerant varieties were released from NRRI using TKM6 as the donor. The varieties are, Ratna (TKM6 × IR 8) which is highly tolerant to YSB especially at the vegetative stage, Saket 4 (sister selection of Ratna) and CR138-928 (Jaya × TKM6). Other popular YSB tolerant varieties released from NRRI include Vijaya (T90 × IR8), Supriya (IR8//GEB24/T(N)1), Dharitri (Pankaj × Jagannath), and Panidhan (CR151-79 × CR1014). Mutation breeding was also attempted to develop YSB tolerant lines; a mutant line of Tainan3 was released in 1980 as the variety Indira (CR MUT 587-4) which possess a fair degree of YSB tolerance in addition to tolerance to blast and BLB. Besides NRRI, two more varieties, Sasyasree and Vikas with a moderate level of resistance to YSB were released in India using TKM6 as the donor source. YSB resistance was mapped by RAPD markers from a cross of Co43 × W1263. Though the high yielding rice varieties enlisted above are moderately resistant to YSB, no rice variety truly resistant to YSB has yet been developed.

Since gene(s) for resistance to YSB has not been found in the primary gene pool of rice efforts were made to incorporate alien genes from wild species belonging to the secondary gene pool, which are reservoirs of such traits. Wild rice germplasm has been screened against YSB. *O. brachyantha, O. officinalis, O. ridleyi,* and *Porteresia coarctata* were found to be resistant/tolerant against the pest. Subsequently, backcross population of *O. sativa* cv. Savitri/*O. brachyantha* was developed to transfer YSB resistance to the cultivated rice (Behura et al. 2011). The cytogenetic analysis of the chromosomal variants leads to the development of monosomic alien addition lines (MAALs). Of the 8 MAALs screened, MAAL 11 was found to be moderately resistant to YSB.

30.5 Status of Related Gene Pool for Biotic Stress Tolerance/Resistance

The genus *Oryza* comprises of several wild species besides the two cultivated species *Oryza sativa* (Asian rice) and *Oryza glaberrima* (African rice). These wild relatives of cultivated rice are found to be grown naturally in different ecologies around the world. The term species complex is used "for a group of species where distinct taxonomic keys are lacking and the categorization to species or subspecies level is rather arbitrary" (Vaughan et al. 2005). Four major species complexes of *Oryza* were identified which were designated as *O. sativa* complex (contains AA genome), *O. officinalis* complex (comprises diploid and allotetraploid species of BB, CC, DD or EE genomes), *O. granulata* complex (GG genome), and *O. ridleyi* complex

(allotetraploids of HH and JJ or KK genome). There is also a prominent outgroup consisting of a lone species *O. brachyantha* (FF genome). These wild relatives are considered as virtually untapped reservoir of agronomically important genes especially for genes conferring resistance to biotic and abiotic stresses (Table 30.7).

Table 30.7 Different species of genus *Oryza* and their useful traits for biotic stress tolerance

Oryza species	Chr. no.	Genome	Origin	Useful traits
O. sativa complex				
O. rufipogon	24	AA	Tropical Asia	Resistance to BLB and tolerance to tungro
O. nivara	24	AA	Tropical Asia	Resistance to grassy stunt virus and BLB
O. longistaminata	24	AA	Africa	Resistance to BLB
O. barthii	24	AA	Africa	–
O. meridionalis	24	AA	Tropical Australia	–
O. glumaepatula	24	AA	South and Central America	–
O. officinalis complex				
O. punctata	24, 48	BB, BBCC	Africa	Resistance to BPH
O. minuta	48	BBCC	Philippines and Papua New Guinea	Resistance to sheath blight, blast, BLB, BPH
O. malampuzhaensis	48	BBCC	Southern India	Resistance to BLB
O. officinalis	24	CC	Tropical Asia	Resistance to BPH, WBPH and GLH
O. rhizomatis	24	CC	Sri Lanka	–
O. eichingeri	24	CC	South Asia and East Africa	Resistance to BPH, WBPH and GLH
O. latifolia	48	CCDD	South America	Resistance to BPH
O. alta	48	CCDD	South America	Resistance to stem borer
O. grandiglumis	48	CCDD	South America	–
O. australiensis	24	EE	Tropical Australia	Resistance to BPH and blast
O. granulata complex				
O. granulata	24	GG	Southeast Asia	–
O. meyeriana	24	GG	Southeast Asia	–
O. ridleyi complex				
O. longiglumis	48	HHJJ	Indonesia	Resistance to blast and BLB
O. ridleyi	48	HHJJ	South Asia	Resistance to blast, BLB and stemborer
O. schlechteri	24	HHKK	Papua New Guinea	–
O. coarctata	48	HHKK	India	–
Outgroup				
O. brachyantha	24	FF	Africa	Resistance to yellow stem borer

30.6 Mapping of Genes/QTLs from Related Species of Rice and Their Utilization

The rice breeders have mostly preferred hybridization among the members of cultivated gene pool like *indica-indica*, *japonica-japonica*, *indica-japonica*, *indica*-tropical *japonica* in their regular breeding programs. Utilization of wild species remained limited although in several cases, genetic variability for target agronomic traits were lacking in the primary gene pool. The wild species of rice have been utilized as a valuable source of genes for tolerance to various biotic and abiotic stresses. Several major genes for resistance to brown plant hopper (BPH), white backed plant hopper (WBPH), gall midge, bacterial leaf blight (BLB), sheath rot and leaf/neck blast have been identified from them. Several alien introgressed lines developed using wild *Oryza* as the donor has been released in different countries (Brar and Singh 2011).

The transfer of wild genes in cultivated rice depends on multiple factors like the inheritance pattern of the trait (quantitative/qualitative or monogenic/oligogenic/polygenic), phylogenetic relationship of cultivated and wild species and the presence of reproductive incompatibility barriers. Several pre- and post-fertilization barriers create difficulty in hybridization of wild and cultivated rice. The transfer of desired genes or QTLs from wild rice is difficult as the wild species are associated with several weedy traits like grain shattering, low grain yield/quality, and unwanted plant types. Along with advancements IN plant tissue culture techniques especially embryo rescue and protoplast fusion, wild species are increasingly being used. Cytogenetic techniques along with the availability of cross-transferrable markers derived from genome sequencing projects have created further opportunities for precise transfer of genomic regions from wild species.

Among several species of *O. sativa* complex, wild introgression lines for biotic stress tolerance have been developed mostly for resistance to bacterial blight. Three important genes for BLB resistance have been mapped from the members of this species complex namely *Xa30 (t)* from *O. nivara*, *Xa23* from *O. rufipogon,* and *Xa21* from *O. longistaminata*. These genes have further been utilized worldwide for rice breeding.

Ten distinct species are found in *O. officinalis* complex which are either diploid or allotetraploid. The basic genomic groups are BB, CC, DD, or EE. Two C-genome species have mostly been used, namely *O. officinalis* and *O. eichingeri*. Many of the introgression lines derived from *O. officinalis* complex confers resistance to BPH besides genes for resistance to WBPH, BLB, and sheath rot. In Vietnam, four *O. officinalis* derived BPH resistance lines have been released as varieties (Brar and Singh 2011). *O. eichingeri* have also been used for transfer of BPH resistance genes to cultivated rice. Although interspecific hybrids were derived between *O. sativa* and tetraploid wild species *O. minuta*, *O. punctata,* and *O. malampuzhaensis;* development of advanced introgression lines was only possible with *O. minuta* for transferring resistance to BPH, BLB, and blast. Among the three species with CCDD genome *O. latifolia*, *O. grandiglumis,* and *O. alta*, the third one is yet to be utilized in rice breeding. However, introgression lines were derived from the rest

two species. BPH, WBPH, and BLB resistant lines have been developed by transfer of genes from *O. latifolia*. From backcross progeny lines of *O. sativa* × *O. grandiglumis*, although no genes for stress tolerance were transferred, QTLs for yield contributing traits have been mapped successfully. *O. australiensis* (EE) derived introgression with resistance to BPH and leaf blast have been developed. Several important genes like *Bph10, Bph18,* and *Pi40 (t)* have been tagged from these lines (Sanchez et al. 2014).

Introgression line development from *O. ridleyi* and *O. granulata* complex, as well as *O. brachyantha* for biotic stress tolerance especially for the stresses considered in this book chapter, is still lacking. However, MAAL lines with tolerance to many of these stresses have been successfully developed by several researchers.

30.7 Future Perspectives

Till date, the substantial progress has been made in understanding of resistance to pathogens. Yet in ever-changing environmental condition, technological advancement and socioeconomic scenario, there is ample scope of developing more efficient strategies for deployment of resistance to control the various biotic diseases and insect-pest of rice. Moreover, the focus should be on following points:

- The most important improvement in understanding molecular mechanisms of disease resistance has been the cloning of R genes against bacterial blight, blast, and other diseases.
- As a model crop with an entirely sequenced genome, rice delivers good opportunities to look insight into the molecular mechanisms governing disease resistance, and engineer the development of rice varieties with diversified resource of resistance with broad-spectrum efficacy against numerous diseases.
- An important consideration for successful development, diffusion and impact for new rice varieties is the need to constantly improve yield, grain quality, multiple stress tolerance and hence fitness in the targeted ecosystem.
- The effective QTLs or genes identified though biparental mapping approaches should be supplemented with genome wide association mapping for resistance genes to identify genes/QTLs which will work across populations.
- Multi-parent populations are considered an advance over bi-parental populations and association mapping as the former focuses only on difference in the genomic regions of two individuals and the latter, even though it captures far greater diversity, requires very large samples to detect genomic regions of interest. MAGIC is an attractive alternative from both theoretical and practical standpoints.
- With advancements in genome sequencing, the scope for utilization of genome sequences of both pest and host for understanding mechanism of resistance as well as breakdown of resistance have increased. For identification of functional markers, identification of superior functional haplotypes of resistance genes from both wild and cultivated species is highly required.
- Induction of specific mutations by means of site specific-nucleases (gene editing) would allow direct modification of effector targets leading to resistant mutants.

- More focus should be given to vertical expansion of disease resistant varieties in identified epidemic areas rather than horizontal expansion into areas that are not, seriously affected.
- Reducing selection pressure toward overcoming resistance traits by integrated disease management will help to extend the life of resistance genes in a particular cultivar/region.
- There is urgent need for inclusion of more numbers of wild species in breeding programs of rice through pre-breeding and marker assisted selection for their judicious utilization in resistance breeding of rice.
- Strategic gene deployment integrated with crop and nutrient management can contribute to improvement in farmer livelihood and income through reduced fungicide use and reduced production costs in a sustainable manner.

References

Agarwal PK, Sidu GS, Gosal SS (2005) Induction of bacterial blight resistance in elite Indian rice (*Oryza Sativa L.*) cultivars using gamma irradiation and ethyl methane sulfonate. Mutat Breed Newsl Rev 1:17–18

Agrios GN (2005) Plant pathology, 5th edn. Elsevier Academic Press, Amsterdam

Ahloowalia BS, Maluszynski M, Nichterlein K (2004) Global impact of mutation-derived varieties. Euphytica 135(2):187–204

Alam MF, Khan MR, Nuruzzaman M, Parvez S, Swaraz AM, Alam I, Ashan N (2004) Genetic basis of heterosis and inbreeding depression in rice (*Oryza sativa* L.). J Zhejiang Univ Sci 5(4):406–411

Ali MP, Chowdhury TR (2014) Tagging and mapping of genes and QTLs of *Nilaparvata lugens* resistance in rice. Euphytica 195(1):1–30

Allard RW (1960) Principles of plant breeding, 1st edn. Wiley, New York

Allard RW (1999) Principles of plant breeding, 2nd edn. Wiley, New York

Andargie M, Lia L, Aiqing F, Xiaoyuan Z, Lia J (2018) Mapping of the quantitative trait locus (QTL) conferring resistance to rice false smut disease. Curr Plant Biol 15:38–43

Arora L, Narula A (2017) Gene editing and crop improvement using CRISPR-Cas9 system. Front Plant Sci 8:1932

Azlan S, Alias I, Saad A, Habibuddin H (2004) Performance of potential mutant lines of MR 180. In: Sivaprasagam et al (ed) Modern rice farming, Proceedings of the international rice conference Serdang, Malaysia: MARDI, 2003, pp 293–296

Bandillo N, Raghavan C, Muyco PA, Sevilla MA, Lobina IT, Dilla-Ermita CJ, Tung CW, McCouch S, Thomson M, Mauleon R, Singh RK, Gregorio G, Redona E, Leung H (2013) Multi-parent advanced generation inter-cross (MAGIC) populations in rice: progress and potential for genetics research and breeding. Rice (N.Y) 6:11

Basavaraj SH, Singh VK, Singh A, Singh A, Singh A, Anand D, Yadav S, Ellur RK, Singh D, Gopalakrishnan S, Nagarajan M, Mohapatra T, Prabhu KV, Singh AK (2010) Marker-assisted improvement of bacterial blight resistance in parental lines of Pusa RH10, a superfine grain aromatic rice hybrid. Mol Breed 26:293–305

Behura N, Sen P, Kar MA (2011) Introgression of yellow stem borer (*Scirpophaga incertulus*) resistance genes into cultivated rice (*Oryza* sp.) from wild species. Indian J Agric Sci 81(4):359–362

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* in rice. Mol Breed 30:607–611

Biswas A (2001a) False smut disease of rice: a review. Environ Ecol 19(1):67–83
Biswas A (2001b) Field reaction of hybrid rice varieties to false smut and kernel smut disease in West Bengal, India. Environ Ecol 19:299–230
Brar DS, Singh K (2011) Oryza. In: Kole C (ed) Wild crop relatives: genomic and breeding resources, cereals. Springer, Berlin, pp 321–365. https://doi.org/10.1007/978-3-642-14228-4_7
Busungu C, Taura S, Sakagami JI, Anai T, Ichitani K (2018) High-resolution mapping and characterization of *xa42*, a resistance gene against multiple *Xanthomonas oryzae* pv. *oryzae* races in rice (*Oryza sativa* L.). Breed Sci 68(2):188–199. https://doi.org/10.1270/jsbbs.17094
CABI (2011) Crop protection compendium. http://www.cabi.org/cpc
Cavanagh C, Morell M, Mackay I, Powell W (2008) From mutations to MAGIC: resources for gene discovery, validation and delivery in crop plants. Curr Opin Plant Biol 11:215–221
Charcosset A, Moreau L (2004) Use of molecular markers for the development of new cultivars and the evaluation of genetic diversity. Euphytica 137:81–94
Channamallikarjuna V, Sonah H, Prasad M, Rao GJN, Chand S, Upreti HC, Singh NK, Sharma TR (2010) Identification of major quantitative trait loci *qSBR11-1* for sheath blight resistance in rice. Mol Breed 25(1):155–166. https://doi.org/10.1007/s11032-009-9316-5
Chen HQ, Chen ZX, Ni S, Zuo SM, Pan XB, Zhu XD (2008) Pyramiding three genes with resistance to blast by marker assisted selection to improve rice blast resistance of Jin 23B, application, Zhongguo Shuidao Kexue. Chin J Rice Sci 22(1):23–27
Chen ZX, Zhang YF, Feng F, Feng MH, Jiang W, Ma YY, Pan CH, Hua HL, Li GS, Pan XB, Zuo SM (2014) Improvement of japonica rice resistance to sheath blight by pyramiding qSB-9TQ and qSB-7TQ. Field Crop Res 161:118–127
Cheng X, Zhu L, G H (2013) Towards understanding of molecular interactions between rice and the brown planthopper. Mol Plant 6(3):621–634
Choi SH, Vera Cruz CM, Leach J (1998) Distribution of *Xanthomonas oryzae* pv. *oryzae* DNA modification systems in Asia. Appl Environ Microbiol 64(5):1163–1668
Chukwu SC, Rafii MY, Ramlee SI, Ismail SI, Hasan MM, Oladosu YA, Magaji UG, Ibrahim A, Olalekan KK (2019) Bacterial leaf blight resistance in rice: a review of conventional breeding to molecular approach. Mol Biol Rep 46(1):1519–1532. https://doi.org/10.1007/s11033-019-04584-2
Courtois B, Nelson R, Roumen E (1997) Creation of a gene pool to improve *Pyricularia* on resistance partial secanano rice through recurrent selection. In: Guimaraes EP (ed) Recurrent selection in rice. International Center for Tropical Agriculture, Cali, pp 189–202
Das G, Rao GJN (2015) Molecular marker assisted gene stacking for biotic and abiotic stress resistance genes in an elite rice cultivar. Front Plant Sci 6:698
Dash AK, Rao RN, Rao GJ, Verma RL, Katara JL, Mukherjee AK, Singh ON, Bagchi TB (2016) Phenotypic and marker-assisted genetic enhancement of parental lines of Rajalaxmi, an elite rice hybrid. Front Plant Sci 7:1005
Dat VT (2004) Rice agriculture: prospects and strategies in Asia. Paper presented at the workshop on sustainable use of agricultural resources and environment management with focus on the role of rice farming, Tokyo, Japan
Deen R, Ramesh K, Padmavathi G, Viraktamath BC, Ram T (2017) Mapping of brown planthopper [*Nilaparvata lugens* (Stål)] resistance gene (bph5) in rice (*Oryza sativa* L.). Euphytica 213(2):35
Deng GS (1989) Present status of research on false smut in China. Plant Prot 15:39–40
Dey S, Badri J, Ram K, Chhabra AK, Janghel DK (2019) Current status of rice breeding for sheath blight resistance. Int J Curr Microbiol Appl Sci 8(2):163–175. https://doi.org/10.20546/ijcmas.2019.802.020
Divya B, Robin S, Rabindran R, Senthil S, Raveendran M, Joel AJ (2014) Marker assisted backcross breeding approach to improve blast resistance in Indian rice (*Oryza sativa*) variety ADT43. Euphytica 200(1):61–77
Dokku P, Das KM, Rao GJN (2013a) Pyramiding of four resistance genes of bacterial blight in Tapaswini, an elite rice cultivar, through marker assisted selection. Euphytica 192:87–96

Dokku P, Das KM, Rao GJN (2013b) Genetic enhancement of host plant resistance of the Lalat cultivar of rice against bacterial blight employing marker assisted selection. Biotechnol Lett 35:1339–1348

Duan L, Liu H, Li X, Xiao J, Wang S (2014) Multiple phytohormones and phytoalexins are involved in disease resistance to *Magnaporthe oryzae* invaded from roots in rice. Physiol Plant 152:486–500

Ellur RK, Khanna A, Bhowmick PK, Vinod KK, Nagarajan M, Mondal KK, Singh NK, Singh K, Prabhu KV, Singh AK (2016) Marker-aided incorporation of *Xa38*, a novel bacterial blight resistance gene, in PB1121 and comparison of its resistance spectrum with *xa13*+ *Xa21*. Sci Rep 6:29188

Ezuka A, Kaku H (2000) A historical review of bacterial blight of rice. Department of Genetic Resources II and I. Bull Natl Inst Agrobiol Res 15:1–207

FAO, RMM (2019) Food and Agriculture Organization of the United Nation. Rice Marker Monitor. http://faostat.fao.org/site/339/default.aspx

Fujimaki H (1979) Recurrent selection by using male sterility for rice improvement. Jpn Agric Res Q 13(3):153–156

Gangadharan C, Mathur SC (1976) Di-ethyl sulphate induced blast resistant mutants in rice variety MTU 17. Sci Cult 42(4):226–228

Hadzim K, Ajimilah NH, Othman O, Arasu NT, Latifah A, Saad A (1988) Mutant Mahsuri: Baka untuk beras bermutu. Teknologi Padi 4:7–13

Higashi T, Sato H, Horisue N, Fujimaki H (1981) Breeding of isogenic lines for blast resistance in rice and comparison of characters between B4F2 lines and their recurrent, 'Nipponbare'. Breed Sci 31(Suppl 1):46

Hittalmani S, Parco A, Mew TV, Zeigler RS, Huang N (2000) Fine mapping and DNA marker-assisted pyramiding of the three major genes for blast resistance in rice. Theor Appl Genet 100(7):1121–1128

Horisue N, Higashi T, Sato H, Koizumi S (1984) Breeding of isogenic lines for blast resistance in rice, agronomical characteristics of kanto-IL1-14. Breed Sci 34(Suppl 1):316

Hospital F (2005) Selection in backcross programs. Philos Trans R Soc B 360:1503–1511

Hospital F, Charcosset A (1997) Marker-assisted introgression of quantitative trait loci. Genetics 147:14691485

Huang BE, Verbyla KL, Verbyla AP, Raghavan C, Singh VK, Gaur P, Leung H, Varshney RK, Cavanagh CR (2015) MAGIC populations in crops: current status and future prospects. Theor Appl Genet 128(6):999–1017

IIRR (2018) ICAR-Indian Institute of Rice Research, Progress report, 2018, vol 1, Varietal Improvement-AICRIP, Rajendranagar Hyderabad, India

Imam J, Mahto D, Mandal NP, Maiti D, Shukla P, Variar M (2014a) Molecular analyses of Indian rice germplasm accessions with resistance to blast pathogen. J Crop Improv 28(6):729–739

Imam J, Alam S, Mandal NP, Variar M, Shukla P (2014b) Molecular screening for identification of blast resistance genes in North East and East Indian rice germplasm (*Oryza sativa* L.) with PCR based markers. Euphytica 196(2):199–211

IRRI (2010) Global rice science partnership (GRisP) proposal for a CGIAR research program on rice based production systems. Los Banos, Philippines, p 84

Ise K (1990) Effect of mixing planting of near isogenic lines of 'Nippobare' rice to reduce blast disease. Breed Sci 40(Suppl 1):288

Ishiyama S (1922) Studies on the white leaf disease on rice plants. Rep Agric Exp Stat Tokyo 45:233–261

Ishizaki K, Hoshi T, Abe S, Sasaki Y, Kobayashi K, Kasaneyama H, Matsui T, Azuma S (2005) Breeding of blast resistant isogenic lines in rice variety 'Koshihikara' and evaluation of their characters. Breed Sci 55(3):371–377

Jena KK, Hechanova SL, Verdeprado H, Prahalada GD, Kim SR (2017) Development of 25 near-isogenic lines (NILs) with ten BPH resistance genes in rice (*Oryza sativa* L.): production, resistance spectrum, and molecular analysis. Theor Appl Genet 130(11):2345–2360

Jiang W, Zhou H, Bi H, Fromm M, Yang B, Weeks DP (2013) Demonstration of CRISPR/Cas9/sgRNA-mediated targeted gene modification in Arabidopsis, tobacco, sorghum and rice. Nucleic Acids Res 41(20):e188–e188. https://doi.org/10.1093/nar/gkt780.

Jensen NF (1970) A diallel selective mating system for cereal breeding. Crop Sci 10(6):629–635

Jones JW (1926) Hybrid vigor in rice. J Am Soc Agron 18:424–428

Joseph M, Gopalakrishnan S, Sharma RK, Singh VP, Singh AK, Singh NK, Mohapatra T (2004) Combining bacterial blight resistance and basmati quality characteristics by phenotypic and molecular marker-assisted selection in rice. Mol Breed 13(4):377–387

Katiyar SK, Chandel G, Tan Y, Zhang Y, Huang B, Nugaliyadde L, Fernando K, Bentur JS, Inthavong S, Constantino S, Bennet J (2000) Biodiversity of Asian rice gall midge (*Orseolia oryzae* Wood Mason) from five countries examined by AFLP analysis. Genome 43(2):322–332. https://doi.org/10.1139/g99-119

Kaur S, Padmanabhan SY, Rao M (1975) Induction of resistance to blast disease (Pyricularia oryzae) in the high yielding variety, Ratna (IRE 9 TKM 6). In: Proceedings of the IAEA research coordination, Geoling, Ames, Iowa, pp 141–145

Khambanonda P (1978) Mutation breeding in rice for high yield and better blast resistance. Thai J Agric Sci 11(4):263–271

Khush GS (1978) Breeding methods and procedures employed at IRRI for developing rice germplasm with multiple resistance to diseases and insects. In: Symposium on methods of crop breeding. Tropical agricultural research series, vol 11, pp 69–76

Khush GS (1989) Multiple disease and insect resistance for increased yield stability in rice. In: Progress in irrigated rice research, International Rice Research Institute, Manila, Philippines, pp 79–92

Khush GS (2005) What it will take to feed 5.0 billion rice consumers in 2030. Plant Mol Biol 59:16

Khush GS, Jena KK (2009) Current status and future prospects for research on blast resistance in rice (*Oryza sativa* L.). In: Wang GL, Valent B (eds) Advances in genetics, genomics and control of rice blast disease. Springer, Dordrecht, pp 1–10. https://doi.org/10.1007/978-1-4020-9500-9_1

Kim S-M (2018) Identification of novel recessive gene xa44(t) conferring resistance to bacterial blight races in rice by QTL linkage analysis using an SNP chip. Theor Appl Genet 131(12):2733–2743. https://doi.org/10.1007/s00122-018-3187-2

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(10):1933–1943

Kim SM, Reinke RF, Sundaram RM (2019) A novel resistance gene for bacterial blight in rice, Xa43(t) identified by GWAS, confirmed by QTL mapping using a bi-parental population. PLoS One 14(2):e0211775. https://doi.org/10.1371/journal.pone.0211775

Kiyosawa S (1982) Gene analysis for blast resistance. Oryza 18:196–203

Koizumi S (2007) Durability of resistance to rice blast disease. JIRCAS Work Rep 53:1–10

Koizumi S, Tani T, Fuji S (1996) Control of rice blast by multilines. J Agric Sci 51:89–93

Korinsaka S, Sirithunyab P, Meakwatanakarnd P, Sarkarunge S, Vanavichitc A, Toojindaa T (2011) Changing allele frequencies. Mol Biol Rep 40:2369–2388

Kou Y, Wang S (2012) Toward an understanding of the molecular basis of quantitative disease resistance in rice. J Biotechnol 159:283–290

Kumar M, Singh RP, Singh ON, Singh P, Arsode P, Namrata CM, Jena D, Singh V, Rout D, Mukherjee AK, Samantaray S, Verma RL (2019) Genetic analysis for bacterial blight resistance in indica rice (*Oryza sativa* L.) cultivars. Oryza 56(3):247–255. https://doi.org/10.35709/ory.2019.56.3.1

Kumari A, Das A, Devanna BN, Thakur S, Singh PK, Singh NK, Sharma TR (2013) Mining of rice blast resistance gene *Pi54* shows effect of single nucleotide polymorphisms on phenotypic expression of the alleles. Eur J Plant Pathol 137:55–65

Laha GS, Venkataraman S (2001) Sheath blight management in rice with biocontrol agents. Indian Phytopathol 54:461–464

Li YS, Zhu Z, Zhang YD, Zhao L, Wang CL (2008) Genetic analysis of rice false smut resistance using mixed major genes and polygenes inheritance model. Acta Agron Sin 34:1728–1733. https://doi.org/10.1016/S1875-2780(09)60007-9

Li YS, Huang SD, Yang J, Wang CL (2011) Analysis of quantitative trait loci for resistance to rice false smut. Acta Agron Sin 37:778–783. https://doi.org/10.3724/SP.J.1006.2011.00788
Li T, Liu B, Spalding MH, Weeks DP, Yang B (2012) High-efficiency TALEN-based gene editing produces disease-resistant rice. Nat Biotechnol 30(5):390–392
Li W, Zhu Z, Chern M, Yin J, Yang C, Ran L, Cheng M, He M, Wang K, Wang J, Zhou X (2017) A natural allele of a transcription factor in rice confers broad-spectrum blast resistance. Cell 170(1):114–126
Liang Z, Wang L, Pan Q (2016) A new recessive gene conferring resistance against rice blast. Rice 9(1):47
Lin XH, Zhang DP, Xie YF, Gao HP, Zhang QF (1995) Identifying and mapping a new gene for bacterial blight resistance in rice based on RFLP markers. Phytopathology 86:1156–1159
Matsunaga K (1996) Breeding of a multiline rice cultivar 'Sasanishiki BL' and its use for control of blast disease in Miyagi prefecture. J Agric Sci 51:173–176
Mew TW (1987) Current status of future prospects of research on bacterial blight of rice. Annu Rev Phytopathol 25:359–382
Miah GMY, Rafii MY, Ismail MR, Puteh AB, Rahim HA, Asfaliza R, Latif MA (2013) Blast resistance in rice: a review of conventional breeding to molecular approaches. Mol Biol Rep 40:2369–2388
Mizukami T, Wakimoto S (1969) Epidemiology and control of bacterial blight of rice. Annu Rev Phytopathol 7:51–72
Mohamad O, Nazir BM, Alias I, Azlan S, Abdul Rahim H, Abdullah MZ, Othman O, Hadzim K, Saad A, Habibuddin H, Golam F (2006) Development of improved rice varieties through the use of induced mutations in Malaysia. Plant Mutat Rep 1(1):27–33
Mohanty SK, Panda RS, Mohapatra SL, Nanda A, Behera L, Jena M, Sahu RK, Sahu SC, Mohapatra T (2017) Identification of novel quantitative trait loci associated with brown planthopper resistance in the rice landrace Salkathi. Euphytica 213(2):38
Naidu VD (1992) Influence of sheath blight of rice on grain and straw yield in some popular local varieties. J Res Publ 10:78–80
Nakajima T (1994) Mechanism of rice blast disease control by multilines. J Agric Sci 49:390–395
Nakajima T, Sonoda R, Yaegashi H (1996) Effect of a multiline of rice cultivar Sasanishiki and its isogenic lines on suppressing rice blast disease. Ann Phytopathol Soc Jpn 62(3):227–233
Niño-Liu DO, Darnielle L, Bogdanove AJ (2006) *Xanthomonas oryzae* pathovars: model pathogens of a model crop. Mol Plant Pathol 7(5):303–324
Nottegham JL (1993) Durable resistance to blast disease. In: Jacobs TH, Parlievliet JE (eds) Durability of disease resistance. Kluwer, London, pp 125–134
Ou SH (1985) Rice diseases, 2nd edn. Commonwealth Mycological Institute, Kew
Pandey MK, Rani NS, Sundaram RM, Laha GS, Madhav MS, Rao KS, Sudharshan I, Hari Y, Varaprasad GS, Rao LVS, Suneetha K, Sivaranjani AKP, Viraktamath BC (2013) Improvement of two traditional basmati rice varieties form bacterial blight resistance and plant stature through morphological and marker-assisted selection. Mol Breed 31:239–246
Parker D, Beckmann M, Enot P, Overy DP, Rios ZC, Gilbert M, Draper J (2008) Rice blast infection of Brachypodium distachyon as a model system to study dynamic host/pathogen interactions. Nat Protoc 3:435–445
Pinson SRM, Capdevielle F, Mand Oard JH (2005) Confirming QTLs and finding additional loci conditioning sheath blight resistance in rice using recombinant inbred lines. Crop Sci 45:503–510
Pinson SR, Oard JH, Groth D, Miller R, Marchetti MA, Shank AR, Jia MH, Jia Y, Fjellstrom RG, Li Z (2008) Registration of TIL: 455, TIL: 514, and TIL: 642, three rice germplasm lines containing introgressed sheath blight resistance alleles. J Plant Registrat 2(3):251–254
Pradhan SK, Nayak DK, Mohanty S, Behera L, Barik SR, Pandit E, Lenka S, Anandan A (2015) Pyramiding of three bacterial blight resistance genes for broad-spectrum resistance in deepwater rice variety, Jalmagna. Rice 8(1):19
Pradhan SK, Nayak DK, Pandit E, Behera L, Anandan A, Mukherjee AK, Lenka S, Barik DP (2016) Incorporation of bacterial blight resistance genes into lowland rice cultivar through marker-assisted backcross breeding. Phytopathology 106(7):710–718

Prahalada GD, Shivakumar N, Lohithaswa HC, Sidde Gowda DK, Ramkumar G, Kim SR, Ramachandra C, Hittalmani S, Mohapatra T, Jena KK (2017) Identification and fine mapping of a new gene, BPH31 conferring resistance to brown planthopper biotype 4 of India to improve rice, *Oryza sativa* L. Rice 10:41

Rafique ZM, Zia M, Rashid HF, Chaudhary M, Chaudhry Z (2010) Comparison of transgenic plant production for bacterial blight resistance in Pakistani local rice (*Oryza sativa* L.) cultivars. Afr J Biotechnol 9(13):1892–1904. https://doi.org/10.5897/AJB09.868

Rangel PHN, Cordeiro ACC, Lopes SIG, de Morais OP, Brondani C, Brondani RPV, Yokoyama S, Schiocchet M, Bacha R, Ishy T (2005) Advances in population improvement of irrigated rice in Brazil. In: Guimarães EP (ed) Population improvement, a way of exploiting rice genetic resources in Latin America. FAO, Rome, pp 145–186

Ray S, Singh PK, Gupta DK, Mahato AK, Sarkar C, Rathour R, Singh NK, Sharma TR (2016) Analysis of *Magnaporthe oryzae* genome reveals a fungal effector, which is able to induce resistance response in transgenic rice line containing resistance gene, *Pi54*. Front Plant Sci 7:1140

Reddy A (2017) The case of improved Samba Mahsuri. Econ Polit Wkly 52(39):17–19

Reddy JN, Baraoidan MR, Bernardo MA, George ML, Sridhar R (1997) Application of marker-assisted selection in rice for bacterial blight resistance gene, Xa21. Curr Sci 73(10):873–875

Sanchez PL, Wing RA, Brar DS (2014) The wild relative of rice: genomes and genomics. In: Zhang Q, Wing RA (eds) Genetics and genomics of rice, plant gentics and genomics: crop and model 5. Springer Science+Business Media, New York. https://doi.org/10.1007/978-1-4614-7903-1_2

Savary S, Mew TW (1996) Analyzing crop losses due to *Rhizoctonia solani*: rice sheath blight, a case study. In: Sneh B, Jabajihare S, Neate S, Dijst G (eds) Rhizoctonia species: taxonomy, molecular biology, mecology, pathology and disease control. Kluwer Academic Publisher, Dordrecht, pp 237–245

Selvaraj CI, Nagarajan P, Thiyagarajan K, Bharathi M, Rabindran R (2011) Studies on heterosis and combining ability of well known blast resistant rice genotypes with high yielding varieties of rice (*Oryza sativa* L.). Int J Plant Breed Genet 5(2):111–129

Sharma PN, Torii A, Takumi S, Mori N, Nakamura C (2004) Marker-assisted pyramiding of brown planthopper (*Nilaparvata lugens* Stål) resistance genes Bph1 and Bph2 on rice chromosome 12. Hereditas 140(1):61–69

Sharma TR, Rai AK, Gupta SK, Vijayan J, Devanna BN, Ray S (2012) Rice blast management through host plant resistance: retrospect and prospects. Agric Res 1(1):37–52

Shu QY (2009) Induced plant mutations in the genomics era. Food and Agriculture Organization of the United Nations, Rome, pp 425–427

Shu Q, Wu D, Xia Y (1997) The most widely cultivated rice variety 'Zhefu 802' in China and its geneology. Mutat Breed Newsl 43:3–5

Singh P (2016) Marker assisted selection for improvement of aromatic rice (*Oryza sativa L.*) against bacterial leaf blight (*Xanthomonas oryzae* pv. Oryzae). PhD thesis, Banaras Hindu University, India, pp 1–223

Singh AK, Gopalakrishnan S (2016) Genetic improvement of basmati rice-the journey from conventional to molecular breeding. In: Rajpal V, Rao S, Raina S (eds) Molecular breeding for sustainable crop improvement. Sustainable development and biodiversity, vol 11. Springer, Cham

Singh AK, Srivastava JN (2015) Sheath blight disease of paddy and their management. In: Awasthi LP (ed) Recent advances in the diagnosis and management of plant diseases. Springer, Berlin. https://doi.org/10.1007/978-81-322-2571-3_9

Singh GP, Srivastava MK, Singh RB, Singh RM (1997) Variation and quantitative losses caused by bacterial blight in different rice varieties. Indian Phytopathol 30:180–185

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 PR-106. Theor Appl Genet 102:1011–1015

Singh AK, Gopalakrishnan S, Singh VP, Prabhu KV, Mohapatra T, Singh NK, Sharma TR, Nagarajan M, Vinod KK, Singh D, Singh UD, Chander S, Atwal SS, Seth R, Singh VK, Ellur RK, Singh A, Anand D, Khanna A, Yadav S, Goel N, Singh A, Shikari AB, Singh A, Marathi B

(2011) Marker assisted selection: a paradigm shift in Basmati breeding. Indian J Genet 71((2) Special issue):120–128

Singh A, Singh VK, Singh SP, Pandian RTP, Ellur RK, Singh D, Bhowmick PK, Gopalakrishnan 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 29:1–13

Singh VK, Singh A, Singh SP, Ellur RK, Choudhary V, Sarkel S, Singh D, Gopalakrishnan S, Nagarajan M, Vinod KK, Singh UD, Rathore R, Prashanthi SK, Agarwal PK, Bhatt JC, Mohapatra T, Prabhu KV, Singh AK (2012b) Incorporation of blast resistance into "PRR78", an elite basmati rice restorer line, through marker assisted backcross breeding. Field Crop Res 128:8–16

Singh MK, Singh P, Singh RP, Mohapatra C (2013a) Association analysis for yield and quality attributes in indica rice and screening of hybrids against Blast disease (*Magnaporthe grisea* Barr.). Journal of Plant Sciences 8 (2):45-56. DOI: 10.3923/jps.2013.45.56

Singh VK, Singh A, Singh SP, Ellur RK, Singh D, Gopalakrishnan S, Bhowmick PK, Nagarajan M, Vinod KK, Singh UD, Mohapatra T, Prabhu KV, Singh AK (2013b) Marker-assisted simultaneous but stepwise backcross breeding for pyramiding blast resistance genes *Piz5* and *Pi54* into an elite basmati rice restorer line 'PRR78'. Plant Breed 132(5):486–495

Singh P, Singh RP, Singh HB, Singh ON, Samantray S, Singh MK, Jaiswal HK (2014) Inheritance of resistance in *indica* rice cultivar HUR 4-3 against bacterial leaf blight (*Xanthomonas oryzae* pv. *oryzae*). Int J Agric Environ Biotechnol 7:777–785

Singh S, Sharma RK, Singh P, Chakravarti SK (2015a) Gamma ray and EMS induced effectiveness and efficiency of chlorophyll mutations in aromatic rice (*Oryza sativa* L.). Ecoscan 9(3–4):975–979

Singh AK, Singh PK, Arya M, Singh NK, Singh US (2015b) Molecular screening of blast resistance genes in rice using SSR markers. Plant Pathol J 31(1):12–24

Singh P, Singh RP, Verma RL, Singh HB, Singh PK, Singh S, Samantaray S, Singh ON (2018) Inheritance of resistance studies for bacterial leaf blight (*Xanthomonas oryzae* pv. *Oryzae*) disease in indica rice (*Oryza sativa* L.) basmati cv. HUBR 10-9. Int J Agric Environ Biotechnol:917–924

Sinha AP, Prasad G (2008) Integrated management of sheath blight disease of rice. In: Proceeding of the 19th training on "Plant Disease Management on Small Farms" at G.B. Pant University of Agriculture and Technology, Pantnagar, pp 177–182

Sonti RV (1998) Bacterial leaf blight of rice: new insights from molecular genetics. Curr Sci 74:206–212

Sreewongchai T, Toojinda T, Thanintorn N, Kosawang C, Vanavichit A, Tharreau D, Sirithunya P (2010) Development of elite Indica rice lines with wide spectrum of resistance to Thai blast isolates by pyramiding multiple resistance QTLs. Plant Breed 129:176–180

Srinivasachary C, Willocquet L, Savary S (2011) Resistance to rice sheath blight (*Rhizoctonia solani* Kuhn) [teleomorph: *Thanatephorus cucumeris* (AB Frank) Donk.] disease: current status and perspectives. Euphytica 178:1–22. DOI: 10.1007/s10681-010-0296-7

Sugha SK, Sharma OP, Kaushik RP (1993) Performance of rice genotypes against false smut pathogen under rainfed conditions. Plant Dis Res 8:76–87

Sundaram RM, Vishnupriya MR, Biradar SK, Laha GS, Reddy AG, Rani NS, Sarma NP, Sonti RV (2008) Marker assisted introgression of bacterial blight resistance in Samba Mahsuri, an elite indicarice variety. Euphytica 160:411–422

Sundaram RM, Vishnupriya MR, Laha GS, Rani NS, Rao PS, Balachandran SM, Reddy GA, Sarma NP, Sonti RV (2009) Introduction of bacterial blight resistance into Triguna, a high yielding, mid-early duration rice variety. Biotechnol J 4:400–407

Toojinda T, Tragoonrung S, Vanavichit A, Siangliw JL, Pa-In N, Jantaboon J, Siangliw M, Fukai S (2005) Molecular breeding for rainfed lowland rice in the Mekong region. Plant Prod Sci 8(3):330–333

Tsuji H, Sasahara M, Kanno H, Ohba A, Kanagawa M (1999) Change of pathogenic races of rice blast fungus on multiline cultivars 'Sasanishiki BL' in recent years. Annu Rep Soc Plant Protect N Jpn 50:16–20

Van der Plank JE (1975) Horizontal resistance: six suggested projects in relation to blast disease in rice. In: Horizontal resistant to blast disease in rice, CIAT series, CE-9, Cali, Colombia, pp 21–26

Variar M, Singh US (2018) Strategies to manage rice diseases in the post genomic era. Oryza 55(Spl issue):71–81

Vaughan DA, Kadowaki KI, Kaga A, Tomooka N (2005) On the phylogeny and biogeography of the genus Oryza. Breed Sci 55(2):113–122

Vikal Y, Bhatia D (2017) Genetics and genomics of bacterial blight resistance in rice. In: Li J (ed) Advances in international rice research. Intech publishers, London, pp 175–213

Vincelli P (2016) Genetic engineering and sustainable crop disease management: opportunities for case-by case decision-making. Sustainability 8:495

Wang Y, Pinson SRM, Fjellstrom RG, Tabien RE (2012) Phenotypic gain from introgression of two QTL, qSB9-2 and qSB12-1, for rice sheath blight resistance. Mol Breed 30(1):293–303

Wang F, Wang C, Liu P, Lei C, Wand H, Gao Y, Zhao K (2016) Enhanced rice blast resistance by CRISPR/Cas9-targeted mutagenesis of the ERF transcription factor gene OsERF922. PLoS One 11(4):e0154027. https://doi.org/10.1371/journal.pone.0154027

Wang MW, Fan J, Jeyakumar JMJ (2019) Rice false smut: an increasing threat to grain yield and quality. In: Protecting rice grains in the post-genomic era. https://doi.org/10.5772/intechopen.84862

Webster RK, Gunnell PS (1992) Compendium of rice diseases. American Phytopathological Society, St. Paul

Xi ZY, He FH, Zeng RZ, Zhang ZM, Ding XH, Li WT, Zhang GQ (2008) Development of a wide population of chromosome single-segment substitution lines in the genetic background of an elite cultivar of rice (*Oryza sativa* L.). Genome 49(5):476–484

Xu J, Xue Q, Luo L, Li Z (2002) Preliminary report on quantitative trait loci mapping of false smut resistance using near-isogenic introgression lines in rice. Acta Agric Zhejiangensis 14:14–19

Yadav S, Anuradha G, Kumar RR, Vemireddy LR, Sudhakar R, Donempudi K, Venkata D, Jabeen P, Narasimhan YK, Marathi B, Siddiq EA (2015) Identification of QTLs and possible candidate genes conferring sheath blight resistance in rice (*Oryza sativa* L.). SpringerPlus 4:175

Yadav MKSA, Ngangkham U, Subudhi HN, Bag MK (2017) Correction: use of molecular markers in identification and characterization of resistance to rice blast in India. PLoS One 12(6):e0179467

Yaegashi H, Fujita Y, Sonoda R (1989) Severe outbreak of false smut of rice in 1988. Plant Prot 43:311–324

Yang LML, Chen J, Xu JC, Liu KJ, Ding (2012) Estimation of yield loss caused by rice false smut. J Anhui Agric Univ 39:474–477

Yellareddygari SKR, Reddy MS, Kloepper JW, Lawrence KS, Fadamiro H (2014) Rice sheath blight: a review of disease and pathogen management approaches. J Plant Pathol Microbiol 5:241

Zhou YL, Xie XW, Zhang F, Wang S, Liu XZ, Zhu L-H, Xu J-L, Gao Y-M, Li Z-K (2014) Detection of quantitative resistance loci associated with resistance to rice false smut (*Ustilaginoidea virens*) using introgression lines. Plant Pathol 63:365–372. https://doi.org/10.1111/ppa.12091

Zhu YY, Fang H, Wang YY, Fan JX, Yang SS, Mew TW, Mundt CC (2005) Panicle blast and canopy moisture in rice cultivar mixtures. Phytopathology 95:433–438

Zuo SM, Zhang YF, Chen ZX, Chen XJ, Pan XB (2010) Current progress on genetics and breeding in resistance to rice sheath blight. Sci Sin Vita 40:1014–1023

Zuo SM, Zhang YF, Chen ZX, Jiang W, Feng MH, Pan XB (2014) Improvement of rice resistance to sheath blight by pyramiding QTLs conditioning disease resistance and tiller angle. Rice Sci 21(6):318–326

System of Assured Rice Production in *Kharif*: A Resource-Conserving and Climate-Resilient Methodology for Higher Productivity and Profitability

31

Sampad R. Patra and Malay K. Bhowmick

Abstract

The System of Assured Rice Production (SARP) in *kharif* (wet) season is a resource-conserving, climate-resilient and farmers' friendly methodology involving scientific principles and simple practices toward producing healthy and robust seedlings, prolonging nursery duration if required, and shortening main field duration of transplanted rice. The basic principles include production of high potential and healthy seedlings using very low seeding density (15–20 g m^{-2}), adequate addition of organic manure (1.0–2.0 kg m^{-2}), and adopting an integrated nutrient management practice (macro and micronutrients both) in nursery; flexibility in seedling age for transplanting in main field, based on prevailing weather situation; reduced requirement of quality seeds; and significant reduction in nursery area. The seedlings, thus, raised can remain fit in SARP (*Kharif*) nursery for transplanting even up to the age of 60 days, displaying no yield penalty in the main field as compared to the conventional transplanting of rice (CTR). At least 15% yield advantages are common when seedlings are transplanted at normal seedling age. Early sowing, delayed transplanting and early harvesting of *kharif* rice would allow enough time for raising a green manuring crop and its incorporation in rice cultivation through SARP (*Kharif*), and timely sowing of succeeding *rabi* pulses and oilseeds, thereby benefiting soil health and ensuring sustainability of rice-based cropping system. SARP (*Kharif*) also suits better in adopting the common crop sequence of jute-rice in jute growing areas of West Bengal. SARP (*Kharif*) is a two-in-one methodology in one way of realizing higher productivity and another way of contingent cropping to combat unfavorable climatic situations. Thus, SARP (*Kharif*) provides huge prospects and opportunities to the

S. R. Patra (✉)
Department of Agriculture (Government of West Bengal), Kolkata, West Bengal, India

M. K. Bhowmick
Directorate of Agriculture (Government of West Bengal), Kolkata, West Bengal, India

A. Rakshit et al. (eds.), *New Frontiers in Stress Management for Durable Agriculture*, https://doi.org/10.1007/978-981-15-1322-0_31