Plant Pathology Journal

ISSN 1812-5387

science alert

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OPEN ACCESS Plant Pathology Journal

ISSN 1812-5387
DOI: 10.3923/ppj.2020.151.165

Review Article
Impact of Marker Assisted Breeding for Bacterial Blight Resistance in Rice: A Review

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Abstract

Bacterial blight caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo) is the major limiting factor in successful rice production. The disease causes around 20-30 % annual loss in rice production and under severe conditions, the yield loss goes upto 50%. The development of resistant genotypes against this disease is the most effective and economic way to control production loss rather than spraying harmful chemicals that affects the environment. In this direction, several varieties with the single resistant gene have been released for cultivation but due to continuous evolution of new pathotypes, there is a continuous breakdown of resistance against the bacterial blight disease. Although durable resistance can be attained by introducing multiple resistant genes in a single desirable genetic background. But with conventional breeding, it is challenging due to dominance and epistatic effects of disease resistance genes against bacterial blight. However, marker-assisted breeding made it possible to identify and introduce multiple genes into a desirable genetic background with rapid, recurrent parent genome recovery and with minimum linkage drag. Molecular markers play a significant role in speeding up the disease resistance breeding programs with different stages like screening, identification, mapping and cloning of disease-resistant genes y. Hereafter, in this review article the application and achievements of marker-assisted breeding in rice against bacterial blight disease was summarized.

Key words: Bacterial blight, disease resistance, marker-assisted breeding, *xanthomonas oryzae* pv., Xa genes

Citation: Hari Kesh and Prashant Kaushik, 2020. Impact of marker assisted breeding for bacterial blight resistance in rice: A review. Plant Pathol. J., 19: 151-165.

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Competing Interest: The authors have declared that no competing interest exists.

Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Rice is a staple food for more than 60% of the world population. Moreover, rice consumption supplies more than 20% calories requirement of the people in South East Asia. Furthermore, the rice plant parts are also used as animal feed. During the past decade, rice demand has increased from 76-763 million t and this trend is expected to continue in the near future[1]. The continuous supply of rice per the demand of the consumer can only be achieved by maintaining a stable rice production[2]. More than 90% of the rice total production is produced in Asia and China and India are the leading producer countries. In India, rice is cultivated over about 44.1 million ha area with the production of 165.3 million t and productivity[3] of 3.78 t ha^{-1}.

Rice is sensitive to many stresses. In this direction, there are two broad areas of stresses, abiotic (salinity, heat, drought, cold, submergence, radiation and heavy metals) and biotic (pathogens and herbivore) factors[4]. Among biotic stresses, three diseases are considered to be the most devastating worldwide namely, bacterial blight caused by *Xanthomonas oryzae* pv. *oryzae*, blast by *Pyricularia grisea* and sheath blight by *Rhizoctonia solani*.[5]. Several preventive measures such as chemical and biological methods are used to control the spread of these disease and insect pests. Unfortunately, these measures are not very useful. The use of pesticides is expensive and are not environmental-friendly. Therefore, host –plant resistance is the most effective breeding strategy to control the biotic stress in contrast to the environmentally inimical use of pesticides[6-8].

Yield potential of rice can be improved with the help of various strategies, conventional hybridization and selection procedures, ideotype breeding, heterosis breeding, wide hybridization and molecular breeding[9]. But all these methods employ a forward breeding approach based on traits of interest. The selection of advanced pedigree lines and recombinant inbred lines requires a long process that can take up to 8-9 years to generate elite lines for varietal release. With the development of gene identification technologies, the marker-assisted selection (MAS) technique is typically used to improve disease and insect resistance.

The scope of MAS breeding for targeted introgression of bacterial blight (BB) resistance genes[10-19], blast resistance genes[20-24], sheath blight[25] and brown planthoppers resistance genes[26-28] and gall midge[29] have been successfully demonstrated[30]. Hence, molecular breeding offers the opportunity to increase the speed and efficiency of plant breeding. It lays the foundation for modern crop improvement in the 21st century[31] and simultaneously helps to identify superior gene combinations, leading to significant disease resilience. The term molecular breeding is used collectively for several breeding strategies, such as MAS, MABC, marker-assisted recurrent selection (MARS) and genomic selection[32].In this review, the application and achievements of marker-assisted breeding in rice against bacterial blight disease was summarized.

Bacterial blight disease of rice: Bacterial blight is a seed-borne disease caused by a gram-negative bacterium *Xanthomonas oryzae* pv. Oryzae is a severe threat to rice production[33-35]. The disease was first observed by the farmers of the Fukuoka area, in Kyushu prefecture[36] of Japan, in 1884. Whereas, in India, the first incidence of bacterial blight disease in rice was reported in Maharashtra by Srinivasan *et al*.[37]. Earlier, the disease in India was considered to be of minor importance until it broke out in an epidemic form in Shahabad district of Bihar[38] in 1963. This disease can affect rice plants at any plant growth stages. BB in Rice generally causes yield loss ranging from 20-30% [39,40]. In case of severe infection, disease cause yield loss up to 50-100%[41-44] besides severely affected the grain quality[13,17]. Due to the severe damage caused by bacterial blight disease, there is an urgent need for strategies to control this epidemic[45]. Breeding for disease resistance is the most effective and economical method for control of BB that has a neutral impact on the environment. Several germ plasm donors carrying assorted genes for control of BB resistance have been used to develop BB resistant varieties[6].

Breeding rice varieties with multiple disease and insect resistance genes will broaden the resistance spectrum and increase durability for the commonly cultivated varieties[8]. Whereas, the large scale and long term cultivation of varieties with single genes may enable the pathogen to overcome BB resistance. However, this can be delayed by pyramiding multiple resistance genes into rice cultivars. The probability of simultaneous pathogen mutation for virulence to 2 or more effective genes is much lower than for a single gene. Gene pyramiding is difficult using conventional breeding methods due to the dominance and epistasis effects of genes governing disease resistance. However, the availability of molecular markers closely linked with each of the resistance genes makes the identification of plants with several disease resistance genes[46]. Historically, long term cultivation of rice varieties carrying resistance gene has resulted in a significant shift in pathogen-race frequency and consequent breakdown of resistance[47].

An example of this is the failure of Xa4, which was incorporated widely in many high yielding varieties via conventional breeding. Widespread cultivation of varieties

carrying Xa4 has led to the predominance of Xoo race that can easily overcome resistance conferred by this gene[6]. One tangible solution to resistance breakdown is pyramiding of multiple resistance genes in the background of modern high yielding varieties[48]. Xa21 gene in rice breeding program was identified from the wild rice *O. longistaminata*[49,50]. But the resistance due to the presence of this gene was recently broken down by new virulent strains in Southern and Yangtze River Valley in China[51,52]. When two or more genes are introgressed, phenotypic evaluation is unable to distinguish the effect of individual gene precisely since each gene confers resistance to and combats multiple races of the pathogen[53].

Moreover, in the presence of a dominant and recessive allele, the effect of the recessive gene is masked[54]. The effectiveness of resistance genes varies over locations due to geographical structuring of the pathogen. Knowledge of the pathogen population structure and virulence characteristics is therefore essential for a successful breeding program aimed at durable resistance[55].

Bacterial blight resistance genes in the rice wild relatives: During domestication process from wild species to cultivated rice, selection of desirable agronomic traits to develop varieties that are high yielding and more suitable to humankind leads to loss of many useful genes and a significant reduction of genetic diversity in rice gene pool[56]. The number of alleles in cultivated rice had been reduced by 50-60% as compared to wild rice[57]. Therefore, it is necessary, to widen the genetic base of rice through identification and introgression of novel resistance genes from wild relatives of rice to develop cultivars with resistance to *Xanthomonas oryzae* pv. *oryzae*. Wild species of rice are reservoirs of many useful genes[58] but a vast majority of these genes remain untapped, because it is often difficult to identify and transfer these genes into cultivated rice. Recently, many genes resistant to diseases, insects, abiotic stress and also for high yield have been transferred from wild species of rice. Many wild species of cultivated rice such as *O. longistaminata*, *O. rufipogon*, *O. minuta*, *O. barthii*, *O. brachyantha*, *O. granulate*, *O. ridleyi* and *O. nivara* have been reported to be resistant to BB[58]. Khush *et al.*[49] transferred Xa21, a dominant BB resistance gene from *O. longistaminata* into IR24. The F_1 showed resistant to 6 races of bacterial blight in the Philippines, indicating that the resistance of *O. longistaminata* was dominant. Xa23, a dominant resistant gene effective at all growth stages was identified from wild rice species of *Oryza rufipogon*[59,60]. The Xa23 gene was found highly resistant to 10 Philippine races (P1-P10), 7 Chinese pathotypes (C1-C7) and 3 Japanese races (TI-T3) at maximum tillering stage[61]. Jin *et al.*[62] identified a BB resistance gene Xa 30 from wild species *O. rufipogon* and transferred this locus to cultivated rice to breed near-isogenic lines. Tan *et al.*[63] detected Xa 29 locus from *O. officinalis* and mapped within a 1.3 cM region flanked by RFLP markers on Chromosome 1. Similarly, Xa32(t) gene from *Oryzae ustraliensis* resistant to Xoo strains P1, P4, P5, P6, P7, P8, P9, KXO85 but susceptible to P2 and P3 was mapped by two SSR markers on the long arm[64] of chromosome 11. Guo *et al.*[65] transferred Xa35(t), a novel source of BB resistance gene from *O. minuta* (Acc. No. 101133) into IR24 cultivar of *O. sativa* L. The bacterial blight resistance genes identified in the rice wild relatives are presented in Table 1.

Genetics of bacterial blight resistance genes: To date, at least 45 genes conferring BB resistance have been reported[71-77] and designated in a series from Xa1 to Xa45 [69,76,77,78]. Out of these, 17 genes viz. Xa5[79] Xa8[80,81], Xa13[82], Xa15[83,84], Xa19[85], Xa20[86], Xa24[87], Xa25[88], Xa26[89], Xa28[89], Xa31[90], Xa32[67], Xa33[91], Xa34[92], Xa41(t)[73], Xa42[93] and Xa44(t)[74] are recessive and remaining are dominant (Table 2)[88,89]. Of the 45 resistance genes Xa1[94], Xa3/26[95,96], Xa5[97,98], Xa10[99], Xa13[100], Xa21[50], Xa23[101], Xa25[88] and Xa27[78] have been cloned successfully[70,78,99-101] and Xa2, Xa4, Xa7, Xa22, Xa30, Xa31 Xa33, Xa34, Xa38, Xa39, Xa40, Xa42 have been fine mapped (Table 2)[68,69,72,74,77,102]. All these resistance genes follow a Mendelian pattern of gene inheritance and express resistance to a diverse group of Xoo pathogens[69,78,89,91,95]. The risk of recombination between the molecular marker and the gene of interest has led to a false selection in MAS, whereas it was overcome by the use of functional markers (FMs)[103]. Functional markers were successfully designed within the coding sequences of different genes for example, *pvr1* gene for potyvirus resistance[104] in *Capsicum* sp. and *Pm3* gene for powdery mildew resistance in bread wheat[105]. Cloning some of the identified BB resistance genes Xa1, Xa5, Xa13, Xa21, Xa26 and Xa27 (Table 2)[50,78,94,95,97,98,100] made it possible to develop and use FMs[106,107]. Recently, an FM for Xa21 was developed[108] based on the coding sequence of both the alleles (Xa21 and Xa21) reported by Song *et al.*[50]. Disease resistance in rice is usually categorized into 2 main groups: qualitative resistance and quantitative resistance. Qualitative resistance is pathogen race-specific and is controlled by a single R gene whose encoded protein can interact directly or indirectly with a corresponding pathogen effector[109]. It is highly efficient in complete pathogen inhibition and has become favourable to plant breeders due to ease of selection in breeding programme[110].

Table 1: Bacterial blight resistance genes identified in wild species of rice

Wild sp.	Gene identified	Mapping on chromosome	References
O. longistaminata	Xa21	11L	Khush *et al.*[49]
O. rufipogon	Xa23	11	Zhang *et al.*[59,60]
O. rufipogon	Xa30	11	Jin *et al.*[62]
O. minuta	Xa27	6	Gu *et al.*[66]
O. officinalis	Xa29	1	Tan *et al.*[63]
O. ustraliensis	Xa32	11L	Zheng *et al.*[64]
O. meyeriana	Xa32	12	Ruan *et al.*[67]
O. minuta	Xa35	11	Guo *et al.*[65]
O. nivara	Xa33	7	Kumar *et al.*[68]
O. nivara	Xa38	4L	Cheema *et al.*[69], Bhasin *et al.*[70]

Table 2: List of bacterial blight resistance genes identified in the rice cultivars

Genes	Sources	Chromosome location	Dominant/ Recessive	References
Xa1	Kogyoku	4	Dominant	Yoshimura *et al.*[94], Sakaguchi [116], Yoshimura *et al.*[117,118]
Xa2	Rantai-Emas 2	4	Dominant	He *et al.*[102], Sakaguchi[116], Yoshimura *et al.*[118]
Xa3/Xa26	WaseAikoku	11L		Xiang *et al.*[96], Ezuka *et al.*[119]
Xa4	IR20, IR22 and IR1529-680-3	11	Dominant	Petpisit *et al.*[79], Yoshimura *et al.*[94], Yoshimura *et al.*[120], Sidhu *et al.* [121]
Xa5	IR1545-284 and RP291-7 DV85, DV86 and DZ78	5S	Recessive	Petpisit *et al.*[79], Sidhu *et al.*[80], Blair and McCouch[122]
Xa6	Zenith, Malagkit Sungsong,		Dominant	Sidhu and Khush[123]
Xa7	DV85, DV86 and DZ78	6	Dominant	Kaji and Ogawa[124], Porter *et al.*[125], Chen *et al.*[126]
Xa8	PI231129	7	Recessive	Sidhu *et al.*[80], Singh *et al.*[81] , Vikal *et al.*[127]
Xa9	Khao Lay Nhay and Sateng		Recessive	Singh *et al.* [128]
Xa10	Cas 209	11	Dominant	Mew *et al.*[129], Yoshimura *et al.*[130], Gu *et al.*[131]
Xa11	IR944-102-2-3,	3S	Dominant	Ogawa and Yamamoto[132], Goto *et al.*[133]
Xa12	Kogyoku and Java 14	4	Dominant	Yamamoto *et al.*[134], Ogawa *et al.*[135]
Xa13	BJ	8L	Recessive	Zhang *et al.*[136], Sanchez *et al.*[137]
Xa14	TN1	4	Dominant	Taura *et al.*[138], Bao*et al.*[139], Tan *et al.*[140]
Xa15	M41		Recessive	Nakai *et al.*[83]
Xa16	Tetep		Dominant	Ogawa *et al.*[141], Noda and Ohuchi[142]
Xa17	Asominori		Dominant	Ogawa *et al.*[141], Ogawa *et al.*[143]
Xa18	Toyonishiki, Milyang 23, IR24		Dominant	Ogawa *et al.*[141]
Xa19	XM5		Recessive	Taura *et al.*[85]
Xa20	XM6		Recessive	Taura *et al.*[86]
Xa21	*Oryza longistaminata*	11L	Dominant	Khush *et al.*[6], Ronald *et al.*[144], Zhai *et al.*[145]
Xa22	Zhachanglong	11	Dominant	Harushima *et al.*[146], Lin *et al.*[147], Wang *et al.*[148]
Xa23 (t)	*O. rufipogon*	11	Dominant	Zhang[149], Wang *et al.*[150]
Xa24 (t)	DV 86	2	Recessive	Mir and Khush[151], Wu *et al.*[152]
Xa25 (t)/Xa25	Minghui 63	12	Recessive	Liu *et al.*[88], Chen *et al.*[153]
Xa25 (t)	HX-3	4	Dominant	Gao *et al.*[154]
Xa26 (t)	Nep Bha Bong To		Recessive	Lee *et al.*[89]
Xa27 (t)	Arai Raj	6	Dominant	Gu *et al.*[66], Lee *et al.*[89]
Xa28 (t)	Lota Sail		Recessive	Lee *et al.*[89]
Xa29 (t)	B5 (*Oryza officinalis*)	1	Dominant	Tan *et al.* [63]
Xa30 (t)	Y238 *O. rufipogon*	11	Dominant	Jin *et al.*[62]
Xa31 (t)	Zhachanglong	4	Recessive	Wang *et al.*[90]
Xa 32 (t)	*Oryza meyeriana*	12	Recessive	Ruan *et al.*[67]
Xa32 (t)	*Oryzae ustraliensis*	11L	Dominant	Zheng *et al.*[64]
Xa33 (t)	Ba7	6	Recessive	Korinsak *et al.*[91]
Xa33 (t)	*O. nivara* IRGC 105710	7	Dominant	Natrajkumar *et al*[68]
Xa34 (t)	BG 122	1	Recessive	Chen *et al.*[92]
Xa35 (t)	*Oryza minuta* (Acc. No. 101133)	11		Guo *et al.*[65]
Xa36 (t)	C4059	11L	Dominant	Miao *et al.*[155]
Xa38	*O. nivara* IRGC 81825	4L	Dominant	Cheema *et al.*[63], Bhasin *et al.*[70]
Xa39	FF329	11	Dominant	Zhang *et al.*[156]
Xa40 (t)	IR65482-7-216-1-2	11	Dominant	Kim *et al.*[72]
Xa41 (t)	African wild and cultivated species of *O. barthii* and *O. glaberrima*		Recessive	Hutin *et al.*[73]
Xa42	XM 14, a mutant of IR 24	3	Recessive	Busungu *et al.*[93]
Xa43 (t)	Colombia XXI (P8)	11	Dominant	Kim and Reinke[75]
Xa44 (t)	IR73571-3B-11-3-K3 (P6)	11	Recessive	Kim[74]
Xa45 (t)	*Oryza glaberrima* Accession IRGC 102600B	8L	Recessive	Kumari *et al.*[76]

However, this type of resistance can be easily broken down due to the rapid evolution of pathogen[109]. This type of resistance has been successfully used for the control of bacterial blight and blast diseases.

Conventional backcross approach: The backcrossing approach was first proposed by Harlan and Pope[111] and was practised between the 1930s and 1960s in several crops[112]. This method is most commonly used to incorporate one or a few traits into an adapted or elite variety[113]. The other parent, called the 'donor parent', possesses one or more genes controlling an important trait which is lacking in the elite variety. In repeated crossings, the hybrids (BC1-n) is backcrossed with the recurrent parent until most of the genes stemming from the donor parent are eliminated except stress resistance[114]. The expected recurrent parent (RP) genome recovery would be 99.2% by 6 backcrosses, which is most similar to improved variety. The proportion of the RP genome is recovered at a rate of 1(1/2) tC1 for each of the generations of backcrossing[115]. However, any specific backcross progeny (BC3 or BC2), they will deviate during crossing over resulting in a great chance to get the expected result that is not possible to detect phenotypically. For example, in BC1 population, theoretically, the average percentage of the RP genome is 75% for the entire population. But some individuals possess more or less of the RP genome than others. Those individuals that contain the highest RP genome are selected. But for transferring of quantitative traits, conventional backcross is not an effective method. The presence of undesirable linkages during the backcrossing may prevent the cultivar being improved from promoting the performance of the original recurrent parent. Recessive traits take more time to transfer. Loss of genetic information of recurrent parent may occur in the backcross method.

Marker-assisted selective breeding: MAS can be defined as selection for a trait-based on genotype using associated markers rather than the phenotype of the trait[157]. This term for the first time was first utilized by Beckmann and Soller[158]. Since then, accelerated development and availability of molecular markers in plants have made MAS into a major molecular breeding strategy. Molecular marker-assisted selection is recognised to be a highly efficient breeding method because it can offer a rapid and precise selection of the target gene[53]. The primary considerations of utilizing the DNA markers for MAS is the availability of the tightly linked marker (<5 centiMorgans (cM)), along with the ease of the procedure, cost-effectiveness and highly polymorphic marker system[159,160]. Marker-assisted backcrossing (MABC) is one of the most anticipated and frequently cited benefits of molecular markers as indirect selection tools in breeding programs[161]. This approach was first reported for rice by Chen *et al.*[11]. They introduced resistance to BB disease into Chinese hybrid parents. It was also described for submergence tolerance using the sub1 gene at International Rice Research Institute (IRRI)[162].

The basis of MABC is to transfer one or more desirable genes/QTL from one genetic source (donor parent) into a superior, adapted, elite breeding line (which serves as a recurrent parent) to improve the targeted trait with the help of markers. Unlike traditional backcrossing, marker-assisted backcrossing is based on the marker alleles linked to gene(s)/QTL of interest instead of on phenotypic performance of target trait[163]. The MABC is accomplished in 3 levels[164]. In the first level, markers are used for screening the target gene or QTL. This is referred to as 'foreground selection[165,166] although referred to as 'positive selection'[167,168]. Marker-assisted foreground selection was proposed by Tanksley[169] and investigated in the context of introgression of resistance genes by Melchinger[170]. The second level of MABC, known as 'recombinant selection', involves the selection of backcross progenies having the target gene with tightly linked markers to minimize linkage drag. In conventional backcross breeding, the chromosome segment from donor remains large even after many backcross generations (>10)[171,172].

However, the donor chromosome segment (linkage drag) size is significantly reduced[173]. Recombinant selection is performed usually by using 2 backcross generations[160,174] because double recombination events on both sides of target locus are usually rare. The third level of MABC approach involves selecting backcross progenies with the maximum of recurrent parent genomic region by utilizing genome-wide dense molecular markers[165,174]. This was also referred to as 'negative selection' by Takeuchi *et al.*[168]. Hence, background selection is very useful in accelerating the recovery of the recurrent parent's genetic complement, which otherwise takes much longer (6 or more backcross generations) via the conventional backcross method[160]. In MABC, recurrent parent genome is recovered in BC2 or BC3, BC4 generation[165,174-176]. The use of background selection during MABC to accelerate the development of an RP with an additional one or more genes has been referred to as 'variety development or enhancement[177] and 'complete line conversion'[178].

Marker-assisted gene pyramiding: The improvement of rice varieties for resistance to the diseases that are prevalent and destructive is necessary for the sustain ability of rice grain yields. Past attempts to achieve varietal resistance to blast and

BLB disease have been disappointing, largely due to high levels of variability in the disease populations in growing areas[179]. For example, a large number of resistance genes for bacterial blight have been identified and tagged from diverse resources by closely linked markers[42,70,71,72,120,131]. A few of these genes like Xa4 have been incorporated widely in many high yielding varieties through conventional breeding[6]. However, long term cultivation of varieties with single resistance gene Xa4 has resulted in a significant shift in pathogen-race frequency and consequent breakdown of resistance[48]. The breeding can provide varieties with blast resistance in rice. In this direction, the pyramiding of multiple disease-resistant genes into a single genetic background can provide durable disease resistance[180]. The probability of simultaneous pathogen mutations for virulence to defeat two or more effective genes is much lower than with a single gene[48].

But, a pyramiding of multiple resistant genes is very difficult through conventional breeding methods due to linkage with some undesirable traits, dominance and epistatic effects of genes governing disease resistance and problems in screening[53,181]. The advent and easy availability of molecular markers closely associated with each of the resistance genes makes identification of plants with multiple gene possible[54]. Using the gene pyramiding approach, improved rice cultivars with broad-spectrum durable bacterial blight[10,13,15,46,54,182-188], blast resistance genes[189], brown plant hopper[26,190] resistance genes have been developed by combining different genes. Assembling of more than 2 desirable genes from 2 or more donors into a single genotype or line for a specific trait is referred to as marker-assisted gene pyramiding[160].

Marker-assisted breeding for bacterial blight resistance: Marker-assisted backcross breeding (MABB) coupled with phenotypic selection for agronomic, grain and cooking quality traits have been used to incorporate BB resistance genes Xa13 and Xa21 into 'Pusa Basmati 1' using IRBB55 (an isogenic line of IR24) as a donor parent. The CAPS marker RG136 linked to Xa13 and STS marker pTA248 linked to Xa21 were used for the foreground selection[13]. Marker-assisted background analysis integrated with foreground selection was used to identify superior BB resistant lines. One of these lines having maximum genome recovery was released as 'Improved Pusa Basmati 1' for commercial cultivation in 2007[191] and this is one of the first products of MAS to be used in India. Dokku *et al.*[192,193] pyramided three BB resistant genes (Xa4, Xa5, Xa13 and Xa21)through markers assisted backcross breeding into parental lines Tapaswini and Lalat from IRBB60. The resulting lines 'Improved Tapaswini and Improved Lalat' were equivalent to its recurrent parent for yields and grain quality features and possess a high level of resistance to BB.

Similarly, Sundaram *et al.*[15,16] introgressed three BB resistance genesxa5, Xa13 and Xa21into the BB susceptible cultivar Samba Mahsuri and Triguna from a donor line SS1113, lead to the development of IET 19046 as improved samba mahsuri and four elite advanced backcross breeding lines, respectively. These lines have a high yield and broad spectrum of BB resistance. Two traditional basmati varieties namely, Taraori Basmati and Basmati 386 were improved for BB resistance by limited marker-assisted backcrossing coupled with phenotypic selection by transferring Xa21 and Xa13 genes from Improved Samba Mehsuri[194].Three BB resistance genes Xa5, Xa13 and Xa21 were introgressed into an *indica* rice cultivar PR 106 using the marker-assisted selection from a donor line IRBB 62. The pyramided lines with two or three gene combinations exhibited a high level of resistance against different isolates of BB[46]. Similar selection strategies were used by Salgotra *et al.*[195] for the transfer of three BB resistance genes (Xa5, Xa13 and Xa21) into IRS5441-2, an aromatic breeding line.

Recombinants, IRS 5441-2-21, IRS 5441-2-79 and IRS-2-85 possessed all the three BB resistance genes and *fgr* (aroma gene) in the homozygous condition and were found to be superior to IRS5441-2 for agronomic performance, grain quality traits and enhanced resistance to BB. Gidamo and Kumaravadivel[196] improved CO43 for BB resistance through the introgression of a resistance gene Xa33. Shanti *et al.*[54] introgressed four BB resistance genes Xa4, Xa5, Xa13 and Xa21 into the parental lines of hybrid rice KMR 3, PRR 78, IR58025B, Pusa 6B and Mahsuri. The introgression lines were observed to show very high level of disease resistance against all the ten isolates of *Xantomonas*. *Oryzae* pv *oryzae*. Perumalsamy *et al.*[108] used marker-assisted backcrossing to pyramid three BB resistance (Xa5+Xa13+Xa21) genes into 2 high yielding BLB susceptible indica rice cultivars, ADT43 and ASD16. Out of the 30 pyramided lines, 12 were found significantly superior for grain yield and resistance against BB. Two BB resistance genes (Xa21 and xa13) and a semi-dwarfing gene (sd1) were successfully pyramided in a traditional Basmati Type-3[186]. To improve BB resistance of 2 varieties Jyothi and IR50, 4 R-genes were introgressed from a donor line based on existing pathogen population[184].

Similarly, an elite deepwater cultivar, Jalmagna was improved against BB by introgressing three BB resistance genes (Xa5, Xa13 and Xa21) from Swarna BB pyramid line. Under BB infection, the three genes pyramided lines exhibit a significant yield advantage and high level of resistance to BB over Jalmagna[188]. Parental lines (Pusa 6B and PRR78) of hybrid PRH 10 was improved by incorporating BB resistance genes Xa13 and Xa21 from Improved Pusa Basmati 1 (Pusa 1460). Improved lines of Pusa 6B (designated as Pusa 1605) and PRR

Table 3: Commercially released MAS cultivars in Asia

Varieties	Gene combinations	Country	References
Angke	Xa4 and Xa5	Indonesia	Bustamam *et al.*[199]
Conde	Xa4 and Xa7	Indonesia	Bustamam *et al.*[199]
Improved Pusa Basmati-1	Xa5, Xa13 and Xa21	India	Gopalakrishnan *et al.*[191]
PR106	Xa5, Xa13 and Xa21	India	Singh *et al.*[46]
Samba Mahsuri	Xa5, Xa13 and Xa21	India	Sundaram *et al.*[15]
Type 3 Basmati	Xa21, Xa13, sd-1	India	Rajpurohit *et al.*[188]
RD6	Xa5/Blast R	Thailand	Pinta *et al.*[205]
Mahsuri	Xa4, Xa5, Xa13, Xa21	India	Guvvala *et al.*[206]
Zhongyou 6	Xa21	China	Cao *et al.*[202]
Zhongyou 1176	Xa21	China	Cao *et al.*[202]

78 (designated as Pusa 1601) showed yield advantages of up to 8.24 and 5.23%, respectively. The hybrid combinations generated using improved parental lines showed performance on par with or superior to original PRH 10[17,197]. Four BB resistance genes (Xa4, Xa5, Xa13 and Xa21) were successfully transferred into 2 parental lines (CRMS 32B and A) of a popular hybrid Rajlaaxmi, in India[198]. Two BB resistant varieties Angke and Conde were released in 2002, by Department of Agriculture, Indonesia by a combination of phenotypic and marker-aided selection. Angke and Conde carry Xa4 +Xa5 and Xa4+Xa7, respectively[199].

Suh *et al.*[187] transferred three BB resistance genes (Xa4+Xa5+Xa21) into an elite japonica rice cultivar Mangeumbyeo using marker-assisted backcrossing (MAB) breeding strategy that led to the development of three elite advanced backcross breeding lines (ABL). The resistant ABL exhibit broad-spectrum resistance against most of the existing B in South Korea without a yield penalty. In China, marker-assisted selection has been successfully employed for the improvement of photosensitive genetic male sterile line 3418[200], restorer lines '6078'[12] Minghui 63[11], 4183[201] R8006 and R1176[202] using the BB resistance gene Xa21 and three popular restorer lines Minghui 63, YR293 and Y1671 using Xa 23[61]. Three restorer lines (XH2431, 9311 AND WH421) with broad-spectrum and enhanced resistance to BB were developed through marker-assisted breeding and pedigree selection[203]. Xu *et al.*[204] introgressed two resistance genes against BB into Yihui 1577, an elite restorer line widely used in hybrid rice production in China. The pyramided lines carrying both resistance genes and their derived hybrids showed resistant against all the seven Xoo isolates. The commercially released cultivars of rice with bacterial blight resistance are presented in Table 3. Furthermore, important consideration should be given to determine the stability of bacterial blight resistance genotypes across the various agroclimatic zones especially in the rice-growing belts so that released genotypes can perform better irrespective of the challenge of Genotype×Environment interaction[207,208]. Similarly, QTL mapping and various other genomic interventions have been successfully implemented in the major cereals like rice and wheat for the improvement of several traits related to biofortification[209-211].

CONCLUSION

Bacterial blight is a severe disease of rice and its control using harmful chemicals is not ecofriendly and costly. In contrast, the use of MAS strategies for the control of BB can be vital. MAS has allowed the breeders to recover the favourable alleles at an early stage rather than longer cycles of breeding, thus improving the process of varietal development and ideal parent selection. Molecular marker-based technology is developing and becoming more precise at a rapid rate. The MAS has been well utilized in cereals like and it is very helpful in developing varieties with disease resistance traits. But, the economical and technical considerations are essential for the successful deployment of MAS in a breeding program. Cost reduction is vital to popularize MAS in the breeding programs. The DNA extraction methods that lead to a good quality of DNA needs to be standardized before hand.

Similarly, the challenge imposed by the bacterial blight in rice can be overcome with the help of advanced genomic interventions. This will require detail understanding and implementing the outcomes as soon as possible to delay the losses.

SIGNIFICANCE STATEMENT

In this review, the important information have been compiled regarding the efficacy of molecular breeding in the development of bacterial blight resistance varieties of rice. Disease resistance breeding is a more economical and eco-friendly approach to control the bacterial blight disease of rice. It was hoped that this review will broaden the understanding of the bacterial leaf blight resistance in rice.

REFERENCES

1. Khush, G.S., 2013. Strategies for increasing the yield potential of cereals: Case of rice as an example. Plant Breed., 132: 433-436.
2. RoyChowdhury, M., Y. Jia, M.H. Jia, R. Fjellstrom and R.D. Cartwright, 2012. Identification of the rice blast resistance gene Pib in the national small grains collection. Phytopathology, 102: 700-706.
3. Anonymous, 2016. Asian development bank technical assistance consultant's report. Project No. 47163-001, June 2016. IRRI., Los Banos. Philippines.
4. Gomez, S.R., 2013. Abiotic and Biotic Stress in Plants. In: Molecular Stress Physiology of Plants, Rout, G.R. and A.B. Das (Eds.)., Springer, New Delhi, pp: 1-20.
5. Jiang, Y., Z. Cai, W. Xie, T. Long, H. Yu and Q. Zhang, 2012. Rice functional genomics research: Progress and implications for crop genetic improvement. Biotechnol. Adv., 30: 1059-1070.
6. Khush, G.S., D.J. Mackill and G.S. Sidhu, 1989. Breeding rice for resistance to bacterial blight. Proceeding of International Workshop on Bacterial Blight of Rice, March 14-18 1988, Manila, Philippines, pp: 207-217.
7. Suh, J.P., Y.C. Cho, Y.J. Won, E.K. Ahn and M.K. Baek *et al*., 2015. Development of resistant gene-pyramided Japonica rice for multiple biotic stresses using molecular marker-assisted selection. Plant Breed. Biotechnol., 3: 333-345.
8. Ji, Z.J., S.D. Yang, Y.X. Zeng, Y. Liang, C.D. Yang and Q. Qian, 2016. Pyramiding blast, bacterial blight and brown planthopper resistance genes in rice restorer lines. J. Integr. Agric., 15: 1432-1440.
9. Khush, G.S., 2005. What it will take to feed 5.0 billion rice consumers in 2030. Plant Mol. Biol., 59: 1-6.
10. Huang, N., E.R. Angeles, J. Domingo, G. Magpantay and S. Singh *et al*., 1997. Pyramiding of bacterial blight resistance genes in rice: Marker-assisted selection using RFLP and PCR. Theor. Applied Genet., 95: 313-320.
11. Chen, S., X.H. Lin, C.G. Xu and Q. Zhang, 2000. Improvement of bacterial blight resistance of 'Minghui 63', an elite restorer line of hybrid rice, by molecular marker-assisted selection. Crop Sci., 40: 239-244.
12. Chen, S., C.G. Xu, X.H. Lin and Q. Zhang, 2001. Improving bacterial blight resistance of '6078, an elite restorer line of hybrid rice, by molecular marker-assisted selection. Plant Breed., 120: 133-137.
13. Joseph, M., S. Gopalakrishnan, R.K. Sharma, V.P. Singh, A.K. Singh, N.K. Singh and T. Mohapatro, 2004. Combining bacterial blight resistance and Basmati quality characteristics by phenotypic and molecular marker-assisted selection in rice. Mol. Breed., 13: 377-387.
14. Zhang, J., X. Li, G. Jiang, Y. Xu and Y. He, 2006. Pyramiding of Xa7 and Xa21 for the improvement of disease resistance to bacterial blight in hybrid rice. Plant Breed., 125: 600-605.
15. Sundaram, R.M., M.R. Vishnupriya, S.K. Biradar, G.S. Laha and G.A. Reddy *et al*., 2008. Marker assisted introgression of bacterial blight resistance in Samba Mahsuri, an elite indica rice variety. Euphytica, 160: 411-422.
16. Sundaram, R.M., M.R. Vishnupriya, G.S. Laha, N.S. Rani and P.S. Rao *et al*., 2009. Introduction of bacterial blight resistance into Triguna, a high yielding, mid-early duration rice variety. Biotechnol. J.: Healthcare Nutr. Technol., 4: 400-407.
17. Basavaraj, S.H., V.K. Singh, A. Singh, A. Singh and A. Singh *et al*., 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.
18. Hari, Y., K. Srinivasarao, B.C. Viraktamath, A.S. Hariprasad and G.S. Laha *et al*., 2011. Marker-assisted improvement of a stable restorer line, KMR-3R and its derived hybrid KRH2 for bacterial blight resistance and grain quality. Plant Breed., 130: 608-616.
19. Bhatia, D., R. Sharma, Y. Vikal, G.S. Mangat and R. Mahajan *et al*., 2011. Marker-assisted development of bacterial blight resistant, dwarf and high yielding versions of two traditional basmati rice cultivars. Crop Sci., 51: 759-770.
20. Amante-Bordeos, A., L.A. Sitch, R. Nelson, R.D. Dalmacio, N.P. Oliva, H. Aswidinnoor and H. Leung, 1992. Transfer of bacterial blight and blast resistance from the tetraploid wild rice *Oryza minuta* to cultivated rice, *Oryza sativa*. Theor. Applied Genet., 84: 345-354.
21. Hittalmani, S., A. Parco, T.V. Mew, R.S. Zeigler and N. Huang, 2000. Fine mapping and DNA marker-assisted pyramiding of the three major genes for blast resistance in rice. Theor. Applied Genet., 100: 1121-1128.
22. Singh, A.K., S. Gopalakrishnan, V.P. Singh, K.V. Prabhu and T. Mohapatra *et al*., 2011. Marker assisted selection: A paradigm shift in Basmati breeding. Indian J. Genet. Plant Breed., 71: 120-128.
23. Singh, V.K., A. Singh, S.P. Singh, R.K. Ellura and V. Choudhary *et al*., 2012. Incorporation of blast resistance into "PRR78", An elite Basmati rice restorer line, through marker assisted backcross breeding. Field Crops Res., 128: 8-16.
24. Yang, D., J. Tang, D. Yang, Y. Chen, J. Ali and T. Mou, 2019. Improving rice blast resistance of Feng39S through molecular marker-assisted backcrossing. Rice, Vol. 12, No. 1. 10.1186/s 12284-019-0329-3.
25. Wang, Y., S.R.M. Pinson, R.G. Fjellstrom and R.E. Tabien, 2012. Phenotypic gain from introgression of two QTL, qSB9-2 and qSB12-1, for rice sheath blight resistance. Mol. Breed., 30: 293-303.
26. Sharma, P.N., A. Torii, S. Takumi, N. Mori and C. Nakamura, 2004. Marker-assisted pyramiding of brown planthopper (*Nilaparvata lugens* Stål) resistance genes Bph1 and Bph2 on rice chromosome 12. Hereditas, 140: 61-69.

27. Jena, K.K., J.U. Jeung, J.H. Lee, H.C. Choi and D.S. Brar, 2006. High-resolution mapping of a new brown planthopper (BPH) resistance gene, Bph18 (t) and marker-assisted selection for BPH resistance in rice (*Oryza sativa* L.). Theor. Applied Genet., 112: 288-297.
28. Suh, J.P., S.J. Yang, J.U. Jeung, A. Pamplona and J.J. Kim *et al*., 2011. Development of elite breeding lines conferring Bph18 gene-derived resistance to brown planthopper (BPH) by marker-assisted selection and genome-wide background analysis in japonica rice (*Oryza sativa* L.). Field Crops Res., 120: 215-222.
29. Katiyar, S.K., Y. Tan, B. Huang, G. Chandel and Y. Xu *et al*., 2001. Molecular mapping of gene Gm-6 (t) which confers resistance against four biotypes of Asian rice gall midge in China. Theor. Applied Genet., 103: 953-961.
30. Jiang, G.H., C.G. Xu, J.M. Tu, X.H. Li, Y.Q. He and Q.F. Zhang, 2004. Pyramiding of insect-and disease-resistance genes into an elite indica, cytoplasm male sterile restorer line of rice, 'Minghui 63 . Plant Breed., 123: 112-116.
31. Moose, S.P. and R.H. Mumm, 2008. Molecular plant breeding as the foundation for 21st century crop improvement. Plant Physiol., 147: 969-977.
32. Ribaut, J.M., M.C. de Vicente and X. Delannay, 2010. Molecular breeding in developing countries: Challenges and perspectives. Curr. Opin. Plant Biol., 13: 213-218.
33. Ishiyama, S., 1922. Studies of bacterial leaf blight of rice. Rep. Imperial Agric. Stn. Konosu., 45: 233-261.
34. Srivastava, D.N. and Y.P. Rao, 1963. Epidemic of bacterial blight disease of rice in North India. Ind. Phytopathol., 16: 393-394.
35. Verdier, V., C.V. Cruz and J.E. Leach, 2012. Controlling rice bacterial blight in Africa: Needs and prospects. J. Biotechnol., 159: 320-328.
36. Tagami, Y. and T. Mizukami, 1962. Historical review of the researches on bacterial leaf blight of rice caused by *Xanthomonas oryzae* (Uyeda et Ishiyama) Dowson. Special Report of the Plant Disease and Insect Pests Forecasting Service 10. Mini. Agric. Fores., Japan, pp: 112.
37. Srinivasan, M.C., M.J. Thirumalachar and M.K. Patel, 1959. Bacterial blight disease of rice. Curr. Sci., 28: 469-470.
38. Srivastava, D.N. and Y.P. Rao, 1966. Can taichung native 1 stand up to bacterial blight? Ind. Farm., 16: 15-17.
39. Mew, T.W., 1987. Current status and future prospects of research on bacterial blight of rice. Ann. Rev. Phytopathol., 25: 359-382.
40. Ou, S.H., 1985. Rice Diseases. Commonwealth Mycological Institute, Kew, UK., pp: 109-201.
41. Singh, G.P., M.K. Srivastava, R.V. Singh and R.M. Singh, 1997. Variation and qualitative loses caused by bacterial blight in different rice varieties. Ind. Phytopathol., 30: 180-185.
42. Sonti, R.V., 1998. Bacterial leaf blight of rice: New insights from molecular genetics. Curr. Sci., 74: 206-206.
43. Srinivasan, B. and S. Gnanamanickam, 2005. Identification of a new source of resistance in wild rice, *Oryza rufipogon* to bacterial blight of rice caused by Indian strains of *Xanthomonas oryzae* pv. *oryzae*. Curr. Sci., 88: 1229-1231.
44. Zhai, W.X. and L.H. Zhu, 1999. Rice bacterial blight resistance genes and their utilization in molecular breeding. Adv. Biotechnol., 19: 9-15.
45. Gnanamanickam, S.S., V.B. Priyadarisini, N.N. Narayanan, P. Vasudevan and S. Kavitha, 1999. An overview of bacterial blight disease of rice and strategies for its management. Curr. Sci., 77: 1435-1444.
46. Singh, S., J.S. Sidhu, N. Huang, Y. Vikal and Z. Li *et al*., 2001. Pyramiding three bacterial blight resistance genes (xa5, xa13 and Xa21) using marker-assisted selection into indica rice cultivar PR106. Theor. Applied Genet., 102: 1011-1015.
47. Mew, T.W., C.M. Vera Cruz and E.S. Medalla, 1992. Changes in race frequency of *Xanthomonas oryzae* pv. *oryzae* in response to rice cultivars planted in the Philippines. Plant Dis., 76: 1029-1032.
48. Mundt, C.C., 1990. Probability of mutation to multiple virulence and durability of resistance gene pyramids. Phytopathology, 80: 221-223.
49. Khush, G.S., E. Bacalangco and T. Ogawa, 1990. A New Gene for Resistance to Bacterial Blight from *O. longistaminata*. Rice Genet. News, 7: 121-122.
50. Song, W.Y., G.L. Wang, L.L. Chen, H.S. Kim and L.Y. Pi *et al*., 1995. A receptor kinase-like protein encoded by the rice disease resistance gene, *Xa21*. Science, 270: 1804-1806.
51. Zeng, L.X., S.H. Huang and S.Z. Wu, 2002. The resistance of IRBB21 (Xa21) against 5 races of Guangdong province. Acta Phytopathol. Sin., 29: 97-100.
52. Zhang, Q., 2009. Genetics and improvement of bacterial blight resistance of hybrid rice in China. Rice Sci., 16: 83-92.
53. Tanksley, S.D., N.D. Young, A.H. Paterson and M.W. Bonierbale, 1989. RFLP mapping in plant breeding: New tools for an old science. Nat. Biotechnol., 7: 257-264.
54. Shanti, M.L., G.L. Devi, G.N. Kumar and H.E. Shashidhar, 2010. Molecular marker-assisted selection: A tool for insulating parental lines of hybrid rice against bacterial leaf blight. Int. J. Plant Pathol., 1: 114-123.
55. Shanti, L.M. and V.V. Shenoy, 2005. Evaluation of BB resistance genes and their pyramids against rice bacterial leaf blight pathogen *Xanthomonas oryzae* pv. *oryzae*. Oryza, 42: 169-193.
56. Brar, D.S. and G.S. Khush, 2003. Utilization of Wild Species of Genus *Oryza* in Rice Improvement. In: Monograph of Genus *Oryza*, Nanda, J.S. and S.D. Sharma (Eds.). Science Publishers, Inc., UK., pp: 283-310.
57. Sun, C.Q., X.K. Wang, Z.C. Li, A. Yoshimura and N. Iwata, 2001. Comparison of the genetic diversity of common wild rice (*Oryza rufipogon* Griff.) and cultivated rice (*O. sativa* L.) using RFLP markers. Theor. Applied Genet., 102: 157-162.

58. Brar, D.S. and G.S. Khush, 1997. Alien introgression in rice. Plant Mol. Biol., 35: 35-47.
59. Zhang, Q., S.C. Lin, B.Y. Zho, C.L. Wang and W.C. Yang *et al*., 1998. Identification and Tagging a new gene for resistance to bacterial blight (*Xanthomonas oryzae* pv. *oryzae*) from *O. rufipogon*. Rice Genet. Newslett., 15: 138-142.
60. Zhang, Q., C.L. Wang, K.J. Zhao, Y.L. Zhao and V.C. Caslana *et al*., 2001. The effectiveness of advanced rice lines with new resistance gene Xa23 to rice bacterial blight. Rice Gen. Newslet., 18: 71-72.
61. Zhou, Y.L., V.N. Uzokwe, C.H. Zhang, L.R. Cheng and L. Wang *et al*., 2011. Improvement of bacterial blight resistance of hybrid rice in China using the Xa23 gene derived from wild rice (*Oryza rufipogon*). Crop Prot., 30: 637-644.
62. Jin, X., C. Wang, Q. Yang, Q. Jiang, Y. Fan and G. Liu, 2007. Breeding of near-isogenic line CBB30 and molecular mapping of Xa30(t), a new resistance gene to bacterial blight in rice. Scient. Agric. Sin., 40: 1094-1100.
63. Tan, G.X., X. Ren, Q.M. Weng, Z.Y. Shi, L.L. Zhu and G.C. He, 2004. Mapping of a new resistance gene to bacterial blight in rice line introgressed from *Oryza officinalis*. Yi Chuan Xue Bao., 431: 724-729, (In Chinese).
64. Zheng, C.K., C.L. Wang, Y.J. Yu, Y.T. Liang and K.J. Zhao, 2009. Identification and molecular mapping of Xa32(t), a novel resistance gene for bacterial blight (*Xanthomonas oryzae* pv. *oryzae*) in rice. Acta Agron. Sin., 35: 1173-1180.
65. Guo, S., D. Zhang and X. Lin, 2010. Identification and mapping of a novel bacterial blight resistance gene Xa35 (t) originated from *Oryza minuta*. Scient. Agric. Sin., 43: 2611-2618.
66. Gu, K., D. Tian, F. Yang, L. Wu and C. Sreekala *et al*., 2004. High-resolution genetic mapping of Xa27 (t), a new bacterial blight resistance gene in rice, *Oryza sativa* L. Theor. Applied Genet., 108: 800-807.
67. Ruan, H.H., C.Q. Yan, D. An, R.H. Liu and J.P. Chen, 2008. Identifying and mapping new gene xa32(t) for resistance to bacterial blight (*Xanthomonas oryzae* pv. *oryzae*, Xoo) from *Oryza meyeriana* L. Acta Agric. Boreal. Sin., 17: 170-174.
68. Kumar, P.N., K. Sujatha, G.S. Laha, K.S. Rao and B. Mishra *et al*., 2012. Identification and fine-mapping of Xa33, a novel gene for resistance to *Xanthomonas oryzae* pv. *oryzae*. Phytopathology, 102: 222-228.
69. Cheema, K.K., N.K. Grewal, Y. Vikal, R. Sharma and J.S. Lore *et al*., 2008. A novel bacterial blight resistance gene from *Oryza nivara* mapped to 38 kb region on chromosome 4L and transferred to *Oryza sativa* L. Genet. Res., 90: 397-407.
70. Bhasin, H., D. Bhatia, S. Raghuvanshi, J.S. Lore and G.K. Sahi *et al*., 2012. New PCR-based sequence-tagged site marker for bacterial blight resistance gene Xa38 of rice. Mol. Breed., 30: 607-611.
71. Sundaram, R.M., S. Chatterjee, R. Oliva, G.S. Laha, C.V. Cruz, J.E. Leach and R.V. Sonti, 2014. Update on bacterial blight of rice: Fourth international conference on bacterial blight. Rice, Vol. 7. 10.1186/s12284-014-0012-7.
72. Kim, S.M., J.P. Suh, Y. Qin, T.H. Noh, R.F. Reinke and K.K. Jena, 2015. Identification and fine-mapping of a new resistance gene, Xa40, conferring resistance to bacterial blight races in rice (*Oryza sativa* L.). Theor. Applied Genet., 128: 1933-1943.
73. Hutin, M., F. Sabot, A. Ghesquière, R. Koebnik and B. Szurek, 2015. A knowledge-based molecular screen uncovers a broad-spectrum Os SWEET 14 resistance allele to bacterial blight from wild rice. Plant J., 84: 694-703.
74. 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. Applied Genet., 131: 2733-2743.
75. Kim, S.M. and R.F. Reinke, 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, Vol. 14, No. 2. 10.1371/journal.pone.0211775.
76. Neelam, K., R. Mahajan, V. Gupta, D. Bhatia and B.K. Gill *et al*., 2020. High-resolution genetic mapping of a novel bacterial blight resistance gene xa-45 (t) identified from *Oryza glaberrima* and transferred to *Oryza sativa*. Theor. Applied Genet., 133: 689-705.
77. Sun, X., Z. Yang, S. Wang and Q. Zhang, 2003. Identification of a 47-kb DNA fragment containing Xa4, a locus for bacterial blight resistance in rice. Theor. Applied Genet., 106: 683-687.
78. Gu, K., B. Yang, D. Tian, L. Wu, D. Wang and C. Sreelekha, 2005. R gene expression induced by a type-III effector triggers disease resistance in rice. Nature, 435: 1122-1125.
79. Petpisit, V., G.S. Khush and H.E. Kauffman, 1977. Inheritance of resistance to bacterial blight in rice 1. Crop Sci., 17: 551-554.
80. Sidhu, G.S., G.S. Khush and T.W. Mew, 1978. Genetic analysis of bacterial blight resistance in seventy-four cultivars of rice, *Oryza sativa* L. Theor. Applied Genet., 53: 105-111.
81. Singh, K., Y. Vikal, S. Singh, H. Leung, H.S. Dhaliwal and G.S. Khush, 2002. Mapping of bacterial blight resistance gene *xa8* using microsatellite markers. Rice Genet. Newslett., 19: 94-97.
82. Ogawa, T., L. Lin, R.E. Tabien and G.S. Khush, 1987. A new recessive gene for resistance to bacterial blight of rice. Rice Genet. Newslett., 4: 98-100.
83. Nakai, H., K. Nakamura, S. Kuwahara and M. Saito, 1988. Genetic studies of an induced rice mutant resistant to multiple races of bacterial leaf blight. Rice Genet. Newslett., 5: 101-113.
84. Ogawa, T., 1996. Monitoring race distribution and identification of genes for resistance to bacterial leaf blight. Proceedings of the 3rd International Rice Genetics Symposium, October 16-20, 1995, International Rice Research Institute, Manila, Philippines, pp: 456-459.
85. Taura, S., T. Ogawa, A. Yoshimura, R. Ikeda and T. Omura, 1991. Identification of a recessive resistance gene in induced mutant line XM5 of rice to rice bacterial blight. Jpn. J. Breed., 41: 427-432.

86. Taura, S., T. Ogawa, A. Yoshimura, R. Ikeda and N. Iwata, 1992. Identification of a recessive resistance gene to rice bacterial blight of mutant line XM6, *Oryza sativa* L. Jpn. J. Breed., 42: 7-13.
87. Khush, G.S. and E.R. Angeles, 1999. A new gene for resistance to race 6 of bacterial blight in rice, *Oryza sativa* L. Rice Genet. Newslett., 16: 92-93.
88. Liu, Y., Y. Wang, J. Fan, B. Lu, D. Qin, P. Wang and D. Xu, 2011. Application of marker-assisted selection of *Xa23* gene in enhancing bacterial leaf blight resistance in rice. Acta Agriculturae Zhejiangensis, 23: 248-251.
89. Lee, K.S., S. Rasabandith, E.R. Angeles and G.S. Khush, 2003. Inheritance of resistance to bacterial blight in 21 cultivars of rice. Phytopathology, 93: 147-152.
90. Wang, C., G. Wen, X. Lin, X. Liu and D. Zhang, 2009. Identification and fine mapping of the new bacterial blight resistance gene, *Xa31(t)*, in rice. Eur. J. Plant Pathol., 123: 235-240.
91. Korinsak, S., S. Sriprakhon, P. Sirithanya, J. Jairin, A. Vanavichit and T. Toojinda, 2009. Identification of microsatellite markers (SSR) linked to a new bacterial blight resistance gene *Xa33(t)* in rice cultivar 'Ba7'. Maejo Int. J. Sci. Technol., 3: 235-247.
92. Chen, S., X. Liu, L. Zeng, D. Ouyang, J. Yang and X. Zhu, 2011. Genetic analysis and molecular mapping of a novel recessive gene xa*34*(t) for resistance against *Xanthomonas oryzae* pv. *oryzae*. Theor. Applied Genet., 122: 1331-1338.
93. Busungu, C., S. Taura, J.I. Sakagami and K. Ichitani, 2016. Identification and linkage analysis of a new rice bacterial blight resistance gene from XM14, a mutant line from IR24. Breed. Sci., 66: 636-645.
94. Yoshimura, S., U. Yamanouchi, Y. Katayose, S. Toki and Z.X. Wang *et al*., 1998. Expression of *Xa1*, a bacterial blight-resistance gene in rice, is induced by bacterial inoculation. Proc. Natl. Acad. Sci. USA., 95: 1663-1668.
95. Sun, X., Y. Cao, Z. Yang, C. Xu, X. Li, S. Wang and Q. Zhang, 2004. Xa26, a gene conferring resistance to *Xanthomonas oryzae* pv. oryzae in rice, encodes an LRR receptor kinase-like protein. Plant J., 37: 517-527.
96. Xiang, Y., Y. Cao, C. Xu, X. Li and S. Wang, 2006. Xa3, conferring resistance for rice bacterial blight and encoding a receptor kinase-like protein, is the same as Xa26. Theor. Applied Genet., 113: 1347-1355.
97. Iyer, A.S. and S.R. McCouch, 2004. The rice bacterial blight resistance gene xa5 encodes a novel form of disease resistance. Mol. Plant-Microbe Interact., 17: 1348-1354.
98. Jiang, G.H., Z.H. Xia, Y.L. Zhou, J. Wan and D.Y. Li *et al*., 2006. Testifying the rice bacterial blight resistance gene *xa5* by genetic complementation and further analyzing *xa5* (*Xa5*) in comparison with its homolog *TFIIAγ1*. Mol. Genet. Genom., 275: 354-366.
99. Tian, D., J. Wang, X. Zeng, K. Gu and C. Qiu *et al*., 2014. The rice TAL effector-dependent resistance protein XA10 triggers cell death and calcium depletion in the endoplasmic reticulum. Plant Cell, 26: 497-515.
100. Chu, Z., B. Fu, H. Yang, C. Xu and Z. Li *et al*., 2006. Targeting *xa13*, a recessive gene for bacterial blight resistance in rice. Theoret. Applied Genet., 112: 455-461.
101. Wang, C., X. Zhang, Y. Fan, Y. Gao and Q. Zhu *et al*., 2015. XA23 is an executor R protein and confers broad-spectrum disease resistance in rice. Mol. Plant, 8: 290-302.
102. He, Q., D. Li, Y. Zhu, M. Tan, D. Zhang and X. Lin, 2006. Fine mapping of *Xa2*, a bacterial blight resistance gene in rice. Mol. Breed., 17: 1-6.
103. Ingvardsen, C.R., B. Schejbel and T. Lubberstedt, 2008. Functional Markers in Resistance Breeding. In: Progress in Botany, Luttge, U., W. Beyschlag and J. Murata (Eds.). Springer-Verlag, Berlin, Germany, ISBN: 978-3-540-72954-9, pp: 61-87.
104. Yeam, I., B.C. Kang, W. Lindeman, J.D. Frantz, N. Faber and M.M. Jahn, 2005. Allele-specific CAPS markers based on point mutations in resistance alleles at the *pvr1* locus encoding eIF4E in *Capsicum*. Theoret. Applied Genet., 112: 178-186.
105. Tommasini, L., N. Yahiaoui, P. Srichumpa and B. Keller, 2006. Development of functional markers specific for seven *Pm3* resistance alleles and their validation in the bread wheat gene pool. Theoret. Applied Genet., 114: 165-175.
106. Iyer-Pascuzzi, A.S. and S.R. McCouch, 2007. Recessive resistance genes and the *Oryza sativa*-*Xanthomonas oryzae* pv. *oryzae* pathosystem. Mol. Plant-Microbe Interact., 20: 731-739.
107. Chu, Z., M. Yuan, J. Yao, X. Ge and B. Yuan *et al*., 2006. Promoter mutations of an essential gene for pollen development result in disease resistance in rice. Genes Dev., 20: 1250-1255.
108. Perumalsamy, S., M. Bharani, M. Sudha, P. Nagarajan and L. Arul *et al*., 2010. Functional marker-assisted selection for bacterial leaf blight resistance genes in rice (*Oryza sativa* L.). Plant Breed., 129: 400-406.
109. Kou, Y. and S. Wang, 2012. Toward an understanding of the molecular basis of quantitative disease resistance in rice. J. Biotechnol., 159: 283-290.
110. Boyd, L.A., C. Ridout, D.M. O'Sullivan, J.E. Leach and H. Leung, 2013. Plant-pathogen interactions: Disease resistance in modern agriculture. Trends Genet., 29: 233-240.
111. Harlan, H.V. and M.N. Pope, 1922. The use and value of back-crosses in small-grain breeding. J. Heredity, 13: 319-322.
112. Stoskopf, N.C., D.T. Tomes and B.R. Christie, 1993. Plant Breeding: Theory and Practice. Westview Press Inc., Oxford, UK., ISBN-13: 9780813317649, Pages: 531.

113. Allard, R.W., 1960. Principles of Plant Breeding. 2nd Edn., Wiley, New York, USA., ISBN-13: 9780471023104, Pages: 485.
114. Becker, H., 1993. Pflanzenzüchtung. Verlag Eugen Ulmer, Stuttgart, Germany, ISBN-13: 9783825217440, Pages: 327.
115. Babu, R., S.K. Nair, B.M. Prasanna and H.S. Gupta, 2004. Integrating marker-assisted selection in crop breeding-prospects and challenges. Curr. Sci., 87: 607-619.
116. Sakaguchi, S., 1967. Linkage studies on the resistance to bacterial leaf blight, *Xanthomonas oryzae* (Uyeda et Ishiyama) Dowson, in rice. Bull. Natl. Inst. Agric. Sci. Ser., D16: 1-18.
117. Yoshimura, S., R. Nelson, A. Y oshimura, T.W. Mew and N. Iwata, 1992. RFLP mapping of the bacterial blight resistance genes *Xa-3* and *Xa-4*. Rice Genet. Newslett., 9: 136-138.
118. Yoshimura, S., Y. Umehara, N. Kurata, Y. Nagamura, T. Sasaki, Y. Minobe and N. Iwata, 1996. Identification of a YAC clone carrying the Xa-1 allele, a bacterial blight resistance gene in rice. Theoret. Applied Genet., 93: 117-122.
119. Ezuka. A., O. Horino, K. Toriyama, H. Shinoda and T. Morinaka, 1975. Inheritance of resistance of rice variety Wase Aikoku 3 to *Xanthomonas oryzae*. Bull. Tokai-Kinki Natl. Agric. Exp. Stat., 8: 124-130.
120. Yoshimura, S., A. Yoshimura, N. Iwata, S.R. McCouch and M.L. Abenes *et al*., 1995. Tagging and combining bacterial blight resistance genes in rice using RAPD and RFLP markers. Mol. Breed., 1: 375-387.
121. Sidhu, G.S., G.S. Khush and T.W. Mew, 1979. Genetic analysis of resistance to bacterial blight in seventy cultivars of rice, *Oryza sativa* L., from Indonesia. Crop Improv., 6: 19-25.
122. Blair, M.W. and S.R. McCouch, 1997. Microsatellite and sequence-tagged site markers diagnostic for the rice bacterial leaf blight resistance gene xa-5. Theoret. Applied Genet., 95: 174-184.
123. Sidhu, G.S. and G.S. Khush, 1978. Dominance reversal of a bacterial blight resistance gene in some rice cultivars. Phytopathology, 68: 461-463.
124. Kaji, R. and T. Ogawa, 1995. Identification of the located chromosome of the resistance gene, *Xa-7*, to bacterial leaf blight in rice. Breed. Sci., 45: 79-79.
125. Porter, B.W., J.M. Chittoor, M. Yano, T. Sasaki and F.F. White, 2003. Development and mapping of markers linked to the rice bacterial blight resistance gene *Xa7*. Crop Sci., 43: 1484-1492.
126. Chen, S., Z. Huang, L. Zeng, J. Yang, Q. Liu and X. Zhu, 2008. High-resolution mapping and gene prediction of *Xanthomonas oryzae* pv. *oryzae* resistance gene *Xa7*. Mol. Breed., 22: 433-441.
127. Vikal, Y., H. Chawla, R. Sharma, J.S. Lore and K. Singh, 2014. Mapping of bacterial blight resistance gene *xa8* in rice (*Oryza sativa* L.). Indian J. Genet. Plant Breed., 74: 589-595.
128. Singh, R.J., G.S. Khush and T.W. Mew, 1983. A new gene for resistance to bacterial blight in rice. Crop Sci., 23: 558-560.
129. Mew, T.W., V. Cruz and R.C. Reyes, 1982. Interaction of *Xanthomonas campestris* pv. *oryzae* and a resistant rice cultivar. Phytopathology, 72: 786-789.
130. Yoshimura, A., T.W. Mew, G.S. Khush and T. Omura, 1983. Inheritance of resistance to bacterial blight in rice cultivar Cas 209. Phytopathology, 73: 1409-1412.
131. Gu, K., J.S. Sangha, Y. Li and Z. Yin, 2008. High-resolution genetic mapping of bacterial blight resistance gene *Xa10*. Theoret. Applied Genet., 116: 155-163.
132. Ogawa, T. and T. Yamamoto, 1986. Inheritance of resistance to bacterial blight in rice. Proceedings of the International Rice Genetics Symposium, May 27-31, 1985, Manila, Philippines, pp: 471-480.
133. Goto, T., T. Matsumoto, N. Furuya, K. Tsuchiya and A. Yoshimura, 2009. Mapping of bacterial blight resistance gene *Xa11* on rice chromosome 3. Jpn. Agric. Res. Quart., 43: 221-225.
134. Yamamoto, T., R.H. Hartini, M. Machmud, T. Nishizawa and D.M. Tantera, 1977. Variation in pathogenicity of *Xanthomonas oryzae* (Dyeda et Ishiyama) Dowson and resistance of rice varieties to the pathogen. Contrib. Cent. Res. Inst. Agric. Bogor, 28: 1-22.
135. Ogawa, T., T. Morinaka, K. Fujii and T. Kimura, 1978. Inheritance of resistance of rice varieties Kogyoku and Java 14 to bacterial group V of *Xanthomonas oryzae*. Jpn. J. Phytopathol., 44: 137-141.
136. Zhang, G.Q., E.R. Angeles, M.L.P. Abenes, G.S. Khush and N. Huang, 1996. RAPD and RFLP mapping of the bacterial blight resistance gene xa-13 in rice. Theoret. Applied Genet., 93: 65-70.
137. Sanchez, A.C., L.L. Ilag, D. Yang, D.S. Brar and F. Ausubel *et al*., 1999. Genetic and physical mapping of xa13, a recessive bacterial blight resistance gene in rice. Theoret. Applied Genet., 98: 1022-1028.
138. Taura, S., T. Ogawa, R.E. Tabien, G.S. Khush, A. Yoshimura and T. Omura, 1987. The specific reaction of Taichung Native 1 to Philippine races of bacterial blight and inheritance of resistance to race 5 (PXO112). Rice Genet. Newslett., 4: 101-102.
139. Bao, S., M. Tan and X. Lin, 2010. Genetic mapping of a bacterial blight resistance gene *Xa14* in rice. Acta Agron. Sin., 36: 422-427.
140. Tan, Z., Q. Zhang, L. Zhu and C. Wang, 1998. RFLP mapping of a rice bacterial blight resistance gene *Xa-14*. Hereditas, 20: 30-33.
141. Ogawa, T., 1993. Methods and strategy for monitoring race distribution and identification of resistance genes to bacterial leaf blight (*Xanthomonas campestris* pv. *oryzae*) in rice [*Oryza sativa*]. Jpn. Agric. Res. Quart., 27: 78-80.

142. Noda, T. and A. Ohuchi, 1989. A new pathogenic race of *Xanthomonas campestris* pv. *oryzae* and inheritance of resistance of differential rice variety, Te-tep to it. Jpn. J. Phytopathol., 55: 201-207.
143. Ogawa, T., H. Kaku and T. Yamamoto, 1989. Resistance gene of rice cultivar, Asominori to bacterial blight of rice. Jpn. J. Breed., 39: 196-197.
144. Ronald, P.C., B. Albano, R. Tabien, L. Abenes, K.S. Wu, S. McCouch and S.D. Tanksley, 1992. Genetic and physical analysis of the rice bacterial blight disease resistance locus, *Xa21*. Mol. Gen. Genet., 236: 113-120.
145. Zhai, W., X. Li, W. Tian, Y. Zhou and X. Pan *et al*., 2000. Introduction of a rice blight resistance gene, *Xa21*, into five Chinese rice varieties through an *Agrobacterium*-mediated system. Sci. China Ser. C: Life Sci., 43: 361-368.
146. Harushima, Y., M. Yano, A. Shomura, M. Sato and T. Shimano *et al*., 1998. A high-density rice genetic linkage map with 2275 markers using a single F_2 population. Genetics, 148: 479-494.
147. Lin, X.H., D.P. Zhang, Y.F. Xie, H.P. Gao and Q. Zhang, 1996. Identifying and mapping a new gene for bacterial blight resistance in rice based on RFLP markers. Phytopathology, 86: 1156-1159.
148. Wang, C., M. Tan, X. Xu, G. Wen, D. Zhang and X. Lin, 2003. Localizing the bacterial blight resistance gene, *Xa22*(t), to a 100-kilobase bacterial artificial chromosome. Phytopathology, 93: 1258-1262.
149. Zhang, Q., 2005. Highlights in identification and application of resistance genes to bacterial blight. Chin. J. Rice Sci., 19: 453-459.
150. Wang, C.L., H.X. Qi, H.J. Pan, J.B. Li, Y.L. Fan, Q. Zhang and K.J. Zhao, 2005. EST-markers flanking the rice bacterial blight resistance gene *Xa23* and their application in marker-assisted selection. Sci. Agric. Sin., 38: 1996-2001.
151. Mir, G.N. and G.S. Khush, 1990. Genetics of resistance to bacterial blight in rice cultivar DV 86. Crop Res., 3: 194-198.
152. Wu, X., X. Li, C. Xuand S. Wang, 2008. Fine genetic mapping of xa24, a recessive gene for resistance against *Xanthomonas oryzae* pv. *oryzae* in rice. Theoret. Applied Genet., 118: 185-191.
153. Chen, H., S. Wang and Q. Zhang, 2002. New gene for bacterial blight resistance in rice located on chromosome 12 identified from Minghui 63, an elite restorer line. Phytopahtology, 92: 750-754.
154. Gao, D.Y., A.M. Liu, Y.H. Zhou, Y.J. Cheng, Y.H. Xiang, L.H. Sun and W.X. Zhai, 2005. Molecular mapping of a bacterial blight resistance gene Xa-25 in rice. Acta Genet. Sinica, 32: 183-188.
155. Miao, L., C. Wang, C. Zheng, J. Che and Y. Gao *et al*., 2010. Molecular mapping of a new gene for resistance to rice bacterial blight. Scientia Agric. Sinica, 43: 3051-3058.
156. Zhang, F., D.L. Zhuo, F. Zhang, L.Y. Huang and W.S. Wang *et al*., 2015. Xa39, a novel dominant gene conferring broad spectrum resistance to *Xanthomonas oryzae* pv. *oryzae* in rice. Plant Pathol., 64: 568-575.
157. Foolad, M.R. and A. Sharma, 2005. Molecular markers as selection tools in tomato breeding. Acta Hortic., 695: 225-240.
158. Beckmann, J.S. and M. Soller, 1986. Restriction fragment length polymorphisms and genetic improvement of agricultural species. Euphytica, 35: 111-124.
159. Mohler, V. and C. Singrun, 2004. General Consideration: Marker Assisted Selection. In: Biotechnology in Agriculture and Forestry: Molecular Marker Sytems in Plant Breeding and Ropomprovement, Lorez, H. and G. Wenzel (Ed.)., Vol. 55, Springer, Berlin, pp: 305-318.
160. Collard, B.C.Y. and D.J. Mackill, 2008. Marker-assisted selection: An approach for precision plant breeding in the twenty-first century. Philos. Trans. R. Soc. London B: Biol. Sci., 363: 557-572.
161. Semagn, K., A. Bjornstad and M.N. Ndjiondjop, 2006. An overview of molecular marker methods for plants. Afr. J. Biotechnol., 5: 2540-2568.
162. Neeraja, C.N., R. Maghirang-Rodriguez, A.Pamplona, S. Heuer and B.C.Y. Collard *et al*., 2007. A marker-assisted backcross approach for developing submergence-tolerant rice cultivars. Theor. Applied Genet., 115: 767-776.
163. Jiang, G.L., 2013. Plant marker-assisted breeding and conventional breeding: Challenges and perspectives. Adv. Crop Sci. Technol., Vol. 1. 10.4172/2329-88631000e106.
164. Holland, J.B., 2004. Implementation of molecular markers for quantitative traits in breeding programs-challenges and opportunities. Proceedings of the 4th Internationl Crop Science Congress, September 26-October 1, 2004, Brisbane, Australia.
165. Hospital, F. and A. Charcosset, 1997. Marker-assisted introgression of quantitative trait loci. Genetics, 147: 1469-1485.
166. Schulthess, A. and A.R. Schwember, 2013. Improving durum wheat (*Triticum turgidum* L. var *durum*) grain yellow pigment content through plant breeding. Int. J. Agric. Natural Resour., 40: 475-490.
167. Hospital, F., 2003. Marker-Assisted Breeding. In: Plant Molecular Breeding, Newbury, H.J. (Ed.)., Blackwell Publishing and CRC Press, Oxford and Boca Raton, pp: 30-59.
168. Takeuchi, Y., T. Ebitani, T. Yamamoto, H. Sato and H. Ohta *et al*., 2006. Development of isogenic lines of rice cultivar Koshihikari with early and late heading by marker-assisted selection. Breed. Sci., 56: 405-413.
169. Tanksley, S.D., 1983. Molecular markers in plant breeding. Plant Mol. Biol. Rep., 1: 3-8.

170. Melchniger, A.E., 1990. Use of molecular markers in breeding for oligogenic disease resistance. Plant Breed., 104: 1-9.
171. Ribaut, J.M. and D. Hoisington, 1998. Marker-assisted selection: New tools and strategies. Trends Plant Sci., 30: 236-239.
172. Salina, E., O. Dobrovolskaya, T. Efremova, I. Leonova and M.S. Röuder, 2003. Microsatellite monitoring of recombination around the *Vrn* B1 locus of wheat during early backcross breeding. Plant Breed., 122: 116-119.
173. Hospital, F., 2005. Selection in backcross programmes. Philosophical Trans.: Biol. Sci., 360: 1503-1511.
174. Frisch, M., M. Bohn and A.E. Melchinger, 1999. Comparison of selection strategies for marker-assisted backcrossing of a gene. Crop Sci., 39: 1295-1301.
175. Visscher, P.M., C.S. Haley and R. Thompson, 1996. Marker-assisted introgression in backcross breeding programs. Genetics, 144: 1923-1932.
176. Frisch, M., M. Bohn and A.A. Melchinger, 1999. Minimum sample size and optimal positioning of flanking markers in marker assisted backcrossing for transfer of a target gene. Crop Sci., 39: 967-975.
177. Huyen, L.T.N., L.M. Cuc, L.H. Ham and T.D. Khanh, 2013. Introgression the SALTOL QTL into Q5DB, the elite variety of Vietnam using Marker-Assisted-Selection (MAS). Am. J. BioSci., 1: 80-84.
178. Ribaut, J.M., M. Banziger, J. Betran, C. Jiang, G.O. Edmeades, K. Dreher and D. Hoisington, 2002. Use of Molecular Markers in Plant Breeding: Drought Tolerance Improvement in Tropical Maize. In: Quantitative Genetics, Genomics and Plant Breeding, Kang, M.S. (Ed.)., CABI., Wallingford, UK., pp: 85-99.
179. Sreewongchai, T., T. Toojinda, N. Thanintorn, C. Kosawang, A. Vanavichit, D. Tharreau and P. Sirithunya, 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.
180. Koide, Y., A. Kawasaki, M.J. Telebanco-Yanoria, A. Hairmansis and N.T.M. Nguyet *et al*., 2010. Development of pyramided lines with two resistance genes, *Pish* and *Pib*, for blast disease (*Magnaporthe oryzae* B. Couch) in rice (*Oryza sativa* L.). Plant Breed., 129: 670-675.
181. Srikanth, S., M.K. Pandey, B.C. Chiranjeevi, S.K. Hajira and S.V. Kumar *et al*., 2016. Introgression of major bacterial blight and blast resistant genes into vallabh basmati 22, an elite basmati variety. Int. J. Dev. Res., 6: 8366-8370.
182. Sanchez, A.C., D.S. Brar, N. Haung, Z. Li and G.S. Khush, 2000. Sequence tagged site marker-assisted selection for three bacterial blight resistance genes in rice. Crop Sci., 40: 792-797.
183. Shanti, M.L., M.L.C. George, C.M.V. Cruz, M.A. Bernardo and R.J. Nelson *et al*., 2001. Identification of resistance genes effective against rice bacterial blight pathogen in Eastern India. Plant Dis., 85: 506-512.
184. Bharathkumar, S., R.D. Paulraj, P.V. Brindha, S. Kavitha and S.S. Gnanamanickam, 2008. Improvement of bacterial blight resistance in rice cultivars Jyothi and IR50 via marker-assisted backcross breeding. J. Crop Improv., 21: 101-116.
185. Perez, L.M., E.D. Redoña, M.S. M endioro, C.M.V. Cruz and H. Leung, 2008. Introgression of *Xa4*, *Xa7* and *Xa21* for resistance to bacterial blight in thermosensitive genetic male sterile rice (*Oryza sativa* L.) for the development of two-line hybrids. Euphytica, 164: 627-636.
186. Rajpurohit, D., R. Kumar, M. Kumar, P. Paul and A. Awasthi *et al*., 2011. Pyramiding of two bacterial blight resistance and a semidwarfing gene in type 3 Basmati using marker-assisted selection. Euphytica, 178: 111-126.
187. Suh, J.P., J.U. Jeung, T.H. Noh, Y.C. Cho and S.H. Park *et al*., 2013. Development of breeding lines with three pyramided resistance genes that confer broad-spectrum bacterial blight resistance and their molecular analysis in rice. Rice, Vol. 6. 10.1186/1939-8433-6-5.
188. Pradhan, S.K., D.K. Nayak, S. Mohanty, L. Behera and S.R. Barik *et al*., 2015. Pyramiding of three bacterial blight resistance genes for broad-spectrum resistance in deepwater rice variety, Jalmagna. Rice, Vol. 8. 10.1186/s12284-015-0051-8.
189. Singh, V.K., A. Singh, S.P. Singh, R.K. Ellur and D. Singh *et al*., 2013. Marker assisted simultaneous but stepwise backcross breeding for pyramiding blast resistance genes *Piz5* and *Pi54* into an elite Basmati rice restorer line 'PRR 78'. Plant Breed., 1324: 486-495.
190. Liu, Y., L. Chen, Y. Liu, H. Dai and J. He *et al*., 2016. Marker assisted pyramiding of two brown planthopper resistance genes, *Bph3* and *Bph27* (t), into elite rice cultivars. Rice, Vol. 9. 10.1186/s12284-016-0096-3.
191. Gopalakrishnan, S., R.K. Sharma, K.A. Rajkumar, M. Joseph and V.P. Singh *et al*., 2008. Integrating marker assisted background analysis with foreground selection for identification of superior bacterial blight resistant recombinants in Basmati rice. Plant Breed., 127: 131-139.
192. Dokku, P., K.M. Das and G.J.N. Rao, 2013. Pyramiding of four resistance genes of bacterial blight in Tapaswini, an elite rice cultivar, through marker-assisted selection. Euphytica, 192: 87-96.
193. Dokku, P., K.M. Das and G.J.N. Rao, 2013. Genetic enhancement of host plant-resistance of the Lalat cultivar of rice against bacterial blight employing marker-assisted selection. Biotechnol. Lett., 35: 1339-1348.
194. Pandey, M.K., N.S. Rani, R.M. Sundaram, G.S. Laha and M.S. Madhav *et al*., 2013. Improvement of two traditional Basmati rice varieties for bacterial blight resistance and plant stature through morphological and marker-assisted selection. Mol. Breed., 31: 239-246.

195. Salgotra, R.K., B.B. Gupta, R.J. Millwood, M. Balasubramaniam and C.N. Stewart Jr., 2012. Introgression of bacterial leaf blight resistance and aroma genes using functional marker-assisted selection in rice (*Oryza sativa* L.). Euphytica, 187: 313-323.
196. Gidamo, G.H. and N. Kumaravadivel, 2015. Marker-assisted introgression of broad spectrum bacterial blight resistance gene xa33 to co43, a salt and alkaline soil tolerant indica rice variety. 2136. Trends Biosci., 8: 2136-2142.
197. Basavaraj, S.H., V.K. Singh, A. Singh, D. Singh and M. Nagarajan *et al*., 2009. Marker aided improvement of Pusa 6B, the maintainer parent of rice hybrid Pusa RH10, for resistance to bacterial blight. Indian J. Genet., 69: 10-16.
198. Dash, A.K., R.N. Rao, G.J.N. Rao, R.L. Verma and J.L. Katara *et al*., 2016. Phenotypic and marker-assisted genetic enhancement of parental lines of rajalaxmi, an elite rice hybrid. Front. Plant Sci., Vol. 7. 10.3389/fpls.2016.01005.
199. Bustamam, M., R.E. Tabien, A. Suwarno, M.C. Abalos and T.S. Kadir *et al*., 2002. Asian Rice Biotechnology Network: Improving Popular Cultivars Through Marker Assisted Backcrossing by the NARES. In: Proceedings of International, Rice Congress, NARC. (Ed.)., NARES., Beijing, China.
200. Luo, Y.C., S.H. Wang, C.Q. Li, D.Z. Wang, S. Wu and S.Y. Du, 2003. Breeding of the photo-period-sensitive genetic male-sterile line 3418S resistant to bacterial blight in rice by molecular m a rker-assisted selection. Acta Agron. Sin., 29: 402-407.
201. Luo, Y.C., S.H. Wang, C.Q. Li, S. Wu, D.Z. Wang and S.Y. Du, 2004. Improvement of resistance to bacterial blight by marker-assisted selection in a wide compatibility restorer line of hybrid rice. Rice Sci., 11: 231-237.
202. Cao, L.Y., J.Y. Zhuang, S.J. Yuan, X.D. Zhan, K.L. Zheng and S.H. Cheng, 2003. Hybrid rice resistant to bacterial leaf blight developed by marker assisted selection. Rice Sci., 11: 68-70.
203. Luo, Y., J.S. Sangha, S. Wang, Z. Li, J. Yang and Z. Yin, 2012. Marker-assisted breeding of *Xa4*, *Xa21* and *Xa27* in the restorer lines of hybrid rice for broad-spectrum and enhanced disease resistance to bacterial blight. Mol. Breed., 30: 1601-1610.
204. Xu, J., J. Jiang, X. Dong, J. Ali and T. Mou, 2012. Introgression of Bacterial Blight (BB) resistance genes *Xa7* and *Xa21* into popular restorer line and their hybrids by molecular Marker-Assisted Backcross (MABC) selection scheme. Afr. J. Biotechnol., 11: 8225-8233.
205. Pinta, W., T. Toojinda, P. Thummabenjapone and J. Sanitchon, 2013. Pyramiding of blast and bacterial leaf blight resistance genes into rice cultivar RD6 using marker assisted selection. Afr. J. Biotechnol., 12: 4432-4438.
206. Guvvala, L.D., P. Koradi, V. Shenoy and L.S. Marella, 2013. Improvement of resistance to bacterial blight through marker assisted backcross breeding and field validation in rice (*Oryza sativa*). Res. J. Biol., 1: 52-66.
207. Jain, B.T., A.K. Sarial and P. Kaushik, 2018. Stability analysis utilizing AMMI model and regression analysis for grain yield of Basmati rice (*Oryza sativa* L.) genotypes. J. Exp. Biol. Agric. Sci., 6: 522-630.
208. Jain, B.T., A.K. Sarial and P. Kaushik, 2019. Understanding G×E interaction of elite basmati rice (*Oryza sativa* L.) genotypes under North Indian conditions using stability models. Applied Ecol. Environ. Res., 17: 5863-5885.
209. Saini, D.K., P. Devi and P. Kaushik, 2020. Advances in genomic interventions for wheat biofortification: A review. Agronomy, Vol. 10. 10.3390/agronomy10010062
210. Sharma, V., D.K. Saini, A. Kumar and P. Kaushik, 2019. A review of important QTLs for biofortification traits in rice. Preprints, 10.20944/preprints201912.0158.v1.
211. Devi, P., P. Kaushik and D.K. Saini, 2019. QTLs identified for biofortification traits in wheat: A review. Preprints. 10.20944/preprints201908.0120.v1.