Received: 12 Jan 2026 | Revised: 27 Mar 2026 | Accepted: 28 Mar 2026

Electronic Journal of Plant Breeding

Research Note

Marker-assisted confirmation and BLB reaction profiling of donor and recipient parents in a multi-gene introgression program

Bharti Singh[1], Abhinav Sao[1], Ritu R. Saxena[1], Hemant Sahu[2], P. K. Tiwari[3], Zenu Jha[2], Santram Sahu[3], Sunil K. Verma[2], Karishma[1], Devarchan Nirala[1], and M.V.S.K. Rohit[1]

[1]Department of Genetics and Plant Breeding, College of Agriculture,Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh
[2]Department of Plant Molecular Biology and Biotechnology, College of Agriculture,Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh
[3]Department of Plant Pathology, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh
***E-Mail:** bhartisinghparmar84@gmail.com

Abstract
Bacterial leaf blight (BLB) caused by *Xanthomonas oryzae* pv. *oryzae* is a major constraint to rice productivity, necessitating the deployment of durable resistance genes. The present study evaluated donor and recipient parents for introgression of BLB resistance genes *xa5*, *xa13* and *Xa21* into the susceptible but widely cultivated rice varieties Mahamaya and Swarna. Phenotypic screening using a virulent Raipur isolate revealed high susceptibility in Mahamaya (SES score 9) and Swarna (score 7), whereas donor parents Improved Samba Mahsuri and DRR Dhan-62 exhibited strong resistance (SES score 1). Molecular validation using seven gene-specific and linked markers showed clear polymorphism between donors and recipients for most loci, with resistant alleles consistently amplified in donor genotypes. Markers RM31, *xa13/xa13pro*, pTA248 and RM21 were highly informative for allele discrimination. Combined phenotypic and molecular analyses confirmed the suitability of these parental combinations for pyramiding multiple BLB resistance genes through marker-assisted breeding.

Keywords: Rice, Bacterial leaf blight (BLB), parental validation, *Xanthomonas oryzae* pv *oryzae,* gene pyramiding, MAS

Rice (*Oryza sativa* L.) is a major staple food supporting more than half of the global population, with Asia contributing nearly 90 % of world rice production (Bandumula, 2018; Fukagawa and Ziska, 2019). However, rising demand, shrinking resources and increasing biotic pressures threaten its sustainable cultivation. Among these constraints, bacterial leaf blight (BLB), caused by *Xanthomonas oryzae* pv. *oryzae*, remains one of the most destructive diseases, causing yield losses ranging from 50–80 % depending on cultivar susceptibility and environmental conditions (Srinivasan and Gnanamanickam, 2005; Prasad *et al*., 2018; Shekhar *et al*., 2020). The disease is widespread in major rice-growing states, including Chhattisgarh, where high-yielding but BLB-susceptible varieties such as Swarna and Mahamaya occupy a significant share of the cultivated area.

Chemical and cultural methods offer limited and inconsistent control of BLB (Mew *et al*., 1993; Nino-Liu *et al*., 2006), making host plant resistance the most effective and sustainable management strategy.

The resistance genes *xa5*, *xa13* and *Xa21* have been shown to provide broad-spectrum and long-lasting protection and their deployment through Marker-Assisted Selection (MAS) has been successfully demonstrated in several improved cultivars, including Improved Samba Mahsuri and enhanced versions of Pusa Basmati 1 and IR64 (Sundaram *et al*., 2008; Gopalakrishnan *et al*., 2008 and Pradhan *et al*., 2015).

Accurate molecular and phenotypic validation of parental lines is a critical first step in any gene pyramiding program to ensure the correct deployment of genes in subsequent generations. The present study focuses on the marker-assisted confirmation and BLB reaction profiling of donor and recipient parents involved in a multi-gene introgression program aimed at improving Swarna and Mahamaya for durable BLB resistance.

The experiment was conducted during *rabi,* 2022–23 at the Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur, Chhattisgarh. Molecular analysis was carried out at the R.H. Richharia Laboratory, CoA, IGKV, Raipur, and BLB screening was performed using the virulent Raipur isolate obtained from the Department of Plant Pathology, IGKV, Raipur. Swarna and Mahamaya were used as recurrent parents, while Improved Samba Mahsuri and DRR Dhan-62, carrying *xa5*, *xa13* and *Xa21* genes, served as donor parents. Genomic DNA was isolated from young leaf tissue of donor and recipient parents using the CTAB method as described by Murray and Thompson (1980), with minor modifications. DNA concentration and purity were assessed using a NanoDrop ND-1000 spectrophotometer at 260 and 280 nm, and samples with an OD_{260}/OD_{280} ratio of ~1.8 were used for further analysis. Working DNA was standardized to 40 ng/µl using TE buffer and stored at −20°C. PCR amplification was carried out in a 10 µl reaction mixture containing template DNA (1.5 µl), PCR master mix (5.0 µl), primers (0.5 + 0.5 µl) and sterile water (2.5 µl) using an Applied Biosystems thermal cycler Amplified products were resolved by polyacrylamide gel electrophoresis (PAGE).

During the *kharif*, 2022, the rice varieties Mahamaya, Swarna, Improved Sambha Mahsuri and DRR Dhan-62 were evaluated under field conditions for their response to bacterial leaf blight using *Xanthomonas oryzae* pv. *Oryzae,* Raipur isolate obtained from Department of Plant Pathology, Indira Gandhi Krishi Vishwavidyalaya, College of Agriculture, Raipur, (C.G.). The parental lines were inoculated at the maximum tillering stage using the clip inoculation method as described by Kauffman *et al*. (1973), conducted during the early morning hours. On an average, 4 to 5 leaves were inoculated per plant. From each parental line, five plants were inoculated and average score was noted.

Phenotypic screening of parental lines for BLB resistance: The results of phenotypic screening of parental lines revealed that, both the varieties *viz*., Mahamaya and Swarna exhibited a high level of susceptibility for the inoculated Raipur isolate, with a SES scale score of 9 and 7, respectively, whereas both the donors having three BLB resistance genes (*xa5*, *xa13* and *Xa21*), Improved Sambha Mahsuri and DRR Dhan-62 demonstrated high level of resistance to the disease with a SES scale score of 1 (**Plate 1**). Consequently, following crosses were made during *rabi,* 2022-23, *viz*., Mahamaya (♀) x Improved Sambha Mahsuri (♂), Mahamaya (♀) x DRR Dhan-62 (♂), Swarna (♀) x Improved Sambha Mahsuri (♂) and Swarna (♀) x DRR Dhan-62 (♂). The parental lines were further re-evaluated for bacterial leaf blight resistance under field conditions during the screening of the segregating populations.

Sahu (2021), conducted a study on diversity of *Xoo* isolates of Chhattisgarh where, out of four examined isolates-Mahasamund isolate, Ambikapur isolate, Dhamtari isolate and Raipur isolate, Raipur isolate was found to be the most virulent and the BLB resistance gene pyramided line Improved Sambha Mahsuri (*xa5*, *xa13* and *Xa21*)

a. Development of BLB symptoms on parental lines

(b) BLB score of parental lines as per SES scale (IRRI, 2013)

Plate 1. (a) and (b) Phenotypic screening of parental lines for BLB resistance

was found to be resistant against this Raipur isolate. The high level of resistance shown by Improved Sambha Mahsuri is due to presence of *xa5*, *xa13* and *Xa21* genes (Sundaram *et al*., 2008) which was developed by marker assisted introgression of BLB resistance in Sambha Mahsuri using a donor near isogenic line SS1113 possessing three BLB resistance genes, *Xa21*, *xa13* and *xa5* (Singh *et al*., 2001). DRR Dhan-62 is cultivar developed and released with inherent *xa5*, *xa13* and *Xa21* genes along with introgression of *Pi2* and *Pi54* for blast resistance in the genetic background of Improved Samba Mahsuri (IIRR Progress Report, 2019 and Badri *et al*., 2022). Improved Samba Mahsuri has been used as a successful donor for BLB resistance in number of rice varieties Nellore Mahsuri (Dasari *et al*., 2022) and into elite restorer RP5933-1–19-2R (Bandela *et al*., 2025).

Validation of parental lines for BLB resistance through gene specific markers: Genomic DNA of the resistant parents (Improved Samba Mahsuri and DRR Dhan-62) and the susceptible parents (Mahamaya and Swarna) was amplified with seven gene specific SSR markers, *xa5R*, *RM13* and *RM31* (for *xa5*), *xa13* and *xa13pro* (for *xa13*) and *pTA248* and *RM21* (for *Xa21*) to assess polymorphism between the parental genotypes. Among the markers linked to the *xa5* gene, the marker *xa5R* amplified a resistant band of 165 bp only in Improved Samba Mahsuri, while no amplification was observed in DRR Dhan-62, Mahamaya, or Swarna. The marker RM13 produced a resistant band of 125 bp in Improved Samba Mahsuri and 140 bp in DRR Dhan-62 whereas Mahamaya and Swarna exhibited a susceptible band of 150 bp. The marker RM31 amplified a resistant band of 140 bp in Improved Samba Mahsuri and DRR Dhan-62 while Mahamaya and Swarna showed a 160 bp susceptible band, indicating clear polymorphism for the *xa5* locus.

For the *xa13* gene, both markers *xa13* and *xa13pro* amplified a resistant allele of 470 bp in the donor parents, while the susceptible parents Mahamaya and Swarna exhibited a 270 bp band, confirming the absence of the resistance allele in the recurrent parents. Similarly, the markers linked to the *Xa21* gene also showed clear polymorphism between donor and recurrent parents. The marker pTA248 amplified a resistant band of 1000 bp in the donor parents, whereas Mahamaya and Swarna showed a susceptible band of 780 bp. The marker RM21 produced a 150 bp band in the donor parents, while the recurrent parents amplified a 175 bp band, further confirming polymorphism between resistant and susceptible genotypes (**Table 1 & Plate 2**).

The clear polymorphism observed among the parental genotypes indicated that the markers xa5R/RM31 for *xa5*, xa13/xa13pro for *xa13* and pTA248/RM21 for *Xa21* can be effectively used for foreground selection in segregating populations On the basis of parental polymorphism studies using gene specific markers, it has been deduced that employment of *xa5R* or *RM31* (for *xa5* gene), *xa13* or *xa13pro* (for *xa13* gene) and *pTA248* or *RM21* (for *Xa21* gene) gene-based or gene-linked markers exhibited clearcut polymorphism between the parents. These markers can be reliably used in different segregating populations to identify individuals carrying the target resistance alleles, thereby facilitating marker-assisted selection (MAS) for pyramiding multiple bacterial leaf blight resistance genes into the recurrent parent background.

Selection for the *xa5* was carried out using the gene-based markers *xa5R* and *RM31, xa13* using *xa13-pro* and *Xa21* using *pTA248 and RM21.* which showed clear polymorphism between the parental lines. These markers have been extensively utilized for the introgression of *xa13* and *Xa21* genes into the parental lines of the rice hybrid *Pusa RH 10* (Basavraj *et al*., 2010) and the Basmati rice varieties PB1121 and PB6 (Ellur *et al*., 2016 a, 2016 b), Improved Pusa Basmati 1 carrying *xa13+Xa21* (Joseph *et al*., 2004 and Gopalakrishnan *et al*., 2008) and for introgression of *xa5*, *xa13* and *Xa21* in Improved Samba Mahsuri possessing *xa5+xa13+Xa21* (Sundaram *et al*., 2008), in ASD16 and ADT43 (Vidya and Ramalingam, 2018), in Populations Derived from Karma Mahsuri x IRBB 59 (Kotasthane and Gaikwad, 2021), in HUBR 2-1 (Malviya Dhan 2-1) using Improved Pusa Basmati 1, carrying *xa13+Xa21* (Khare *et al*., 2021), in PR-106 (Singh *et al*, 2001), in rice variety Pratikshya (Pradhan *et al*., 2023) and in an elite rice cultivar, Tapaswini (Dokku *et al*., 2013). Noor Ahmed *et al*. (2021) conducted genotyping of three key bacterial leaf blight resistance genes (*xa5*, *xa13*, and *Xa21*) in black rice accessions from North-East India using functional markers namely *xa5FP*, *xa13 promoter* and *pTA248*, respectively.

Pradhan and Bastia, (2022) conducted a similar study and detected the *xa5* gene band at 240 bp using the *RM122* marker, the *xa13* gene band at 500 bp with the *xa13 prom* marker, and the *Xa21* gene band at 1000 bp using the *pTA248* marker in the donor parent *Swarna MAS*. In contrast, no corresponding bands were observed in the susceptible parent *Pratikshya*. Sundaram *et al*. (2008) also used *pTA248* for *Xa21* gene and observed a resistance band in donor at 939 bp and a susceptible band in recurrent parent at 831 bp. Sagar (2018) while pyramiding genes for resistance to bacterial blight and blast into an elite rice variety *Pusa Basmati 1509* via MAS used *pTA248* marker for gene *Xa21and* obtained a resistance band of 950 bp in donor and susceptible band of 500 bp in recurrent parent. *xa13 pro* marker was used for targeting *xa13* gene and similar band sizes of 250 bp (susceptible band) and 500 bp (resistant band) in recurrent and donor parent, respectively were obtained.

Kotasthane and Gaikwad (2021) also utilized *RM13* and *RM122* marker for interogression of *xa5* gene in breeding populations derived from *Karma Mahsuri x IRBB 59* and the markers *xa5R* and *xa5S*, specific to the resistant and

Table 1. Results of parental polymorphism study using gene specific and SSR markers

S. No.	Primer	Parent	Product size (bp)	Allele type	Linked gene	Polymorphic pair
1.	*xa5R*	1. Improved Samba Mahsuri	165	R	*xa5*	Mahamaya x ISM Swarna x ISM
		2. DRR Dhan-62	-	-		
		3. Mahamaya	-	-		
		4. Swarna	-	-		
2.	*RM13*	1. Improved Samba Mahsuri	125	R	*xa5*	Mahamaya x ISM Swarna x ISM
		2. DRR Dhan-62	140	R		
		3. Mahamaya	150	S		
		4. Swarna	150	S		
3.	*RM31*	1. Improved Samba Mahsuri	150	R	*xa5*	Mahamaya x ISM Mahamaya x DRR Dhan-62 Swarna x ISM Swarna x DRR Dhan-62
		2. DRR Dhan-62	150	R		
		3. Mahamaya	160	S		
		4. Swarna	160	S		
4.	*xa13*	1. Improved Samba Mahsuri	470	R	*xa13*	Mahamaya x ISM Mahamaya x DRR Dhan-62 Swarna x ISM Swarna x DRR Dhan-62
		2. DRR Dhan-62	470	R		
		3. Mahamaya	270	S		
		4. Swarna	270	S		
5.	*xa13 pro*	1. Improved Samba Mahsuri	470	R	*xa13*	Mahamaya x ISM Mahamaya x DRR Dhan-62 Swarna x ISM Swarna x DRR Dhan-62
		2. DRR Dhan-62	470	R		
		3. Mahamaya	270	S		
		4. Swarna	270	S		
6.	*pTA248*	1. Improved Samba Mahsuri	1000	R	*Xa21*	Mahamaya x ISM Mahamaya x DRR Dhan-62 Swarna x ISM Swarna x DRR Dhan-62
		2. DRR Dhan-62	1000	R		
		3. Mahamaya	780	S		
		4. Swarna	780	S		
7.	*RM21*	1. Improved Samba Mahsuri	150	R	*Xa21*	Mahamaya x ISM Mahamaya x DRR Dhan-62 Swarna x ISM Swarna x DRR Dhan-62
		2. DRR Dhan-62	150	R		
		3. Mahamaya	175	S		
		4. Swarna	175	S		

ISM= Improved Samba Mahsuri

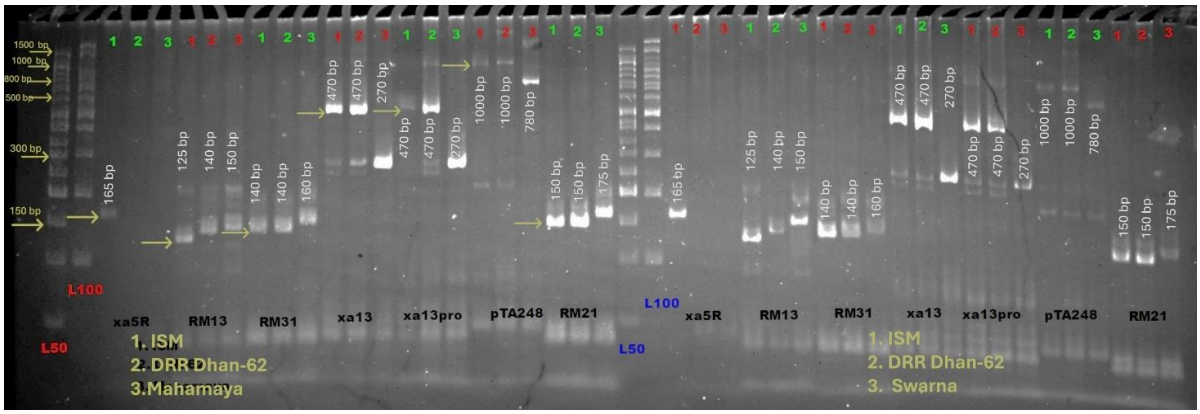

Plate 2. Gel picture presenting parental polymorphism among donor and recipient parents on basis of genetic markers, where ISM= Improved Samba Mahsuri, L_{50}/L_{100}= Ladder

susceptible alleles of the *xa5 gene*, along with *xa13Pro* for the *xa13 gene* and *pTA248* for the *Xa21* gene were also employed in the study for marker-assisted selection (MAS). In the present study, the marker *RM31*, which is linked to the *xa5* gene conferring resistance to bacterial leaf blight, was utilized. It is located at a genetic distance of 17.7 cM from the *xa5* locus on chromosome 5, as reported by Rao *et al*. (2003). The expected amplification product for the *xa5* gene using this marker is 150 bp (Rao *et al*., 2003) which is similar to the present study.

Phenotypic screening of parental lines was performed using the Raipur isolate of *Xanthomonas oryzae* pv. *oryzae*. The results revealed that Mahamaya and Swarna were highly susceptible to the disease, with Standard Evaluation System (SES) scores of 9 and 7, respectively. In contrast, both donor parents, Improved Samba Mahsuri and *DRR Dhan-62*, showed high resistance with a score of 1. Molecular validation through seven gene-specific and gene-linked SSR markers-*xa5R*, *RM13*, *RM31* (for *xa5*), *xa13* and *xa13pro* (for *xa13*) and *pTA248* and *RM21* (for *Xa21*)-revealed clear polymorphism between donor and recipient parents, confirming their suitability for gene introgression.

REFERENCES

Badri, J., Lakshmidevi, G., JaiVidhya, L.R.K., Prasad, M.S., Laha, G.S., Lakshmi, V.J., Isetty, S.R., Padmashree, R., Balakrishnan, D., Varanasi, Y.V.P. and Jukanti, A.K. 2022. Multiparent-derived, marker-assisted introgression lines of the elite Indian rice cultivar,'Krishna Hamsa'show resistance against bacterial blight and blast and tolerance to drought. *Plants*, **11**(5): 622. [Cross Ref]

Bandela, E., Vuppu, G., Thota, S., Bhargavi, M., Laha, G., Raman, M.S. and Ponnuswamy, R. 2025. Improving Parental lines for Bacterial Blight Resistance: Accelerating Rice Hybrid Development through Marker-Assisted Backcross Breeding (MABB). *Cereal Res. Commun*.: 1-11. [Cross Ref]

Bandumula, N. 2018. Rice Production in Asia: Key to Global Food Security. *Proc. Natl. Acad. Sci., India, Sect. B Biol. Sci.,* **88**: 1323–1328. [Cross Ref]

Basavaraj, S.H., Singh, V.K., Singh, A., Anand, D., Yadav, S., Ellur, R.K., Singh, D., Gopalakrishnan, S., Nagarajan, M., Mohapatra, T., Prabhu, K.V. and Singh, A. K. 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. [Cross Ref]

Dasari, A., Vemulapalli, P., Gonuguntla, R., Thota, D.K., Elumalai, P., Muppavarapu, K., Butam, L.P., Kulkarni, S.R., Sinha, P., Gunukula, H. and Kale, R.R. 2022. Improvement of bacterial blight resistance of the popular variety, Nellore Mahsuri (NLR34449) through marker-assisted breeding. *J. Genet*., **101**(1): 7. [Cross Ref]

Dokku, P., Das, K.M. and Rao, G.J.N. 2013. Pyramiding of four resistance genes of bacterial blight in Tapaswini, an elite rice cultivar, through marker-assisted selection. *Euphytica*, **192**: 87–96. [Cross Ref]

Ellur, R. K., Khanna, A., Yadav, A., Pathania, S., Rajashekara, H., Singh, V. K., Gopalakrishnan, S., Bhowmick, P. K., Nagarajan, M., Vinod, K. K., Prakash, G., Mondal, K. K., Singh, N. K., Prabhu, K. V. and Singh A. K. 2016a. Improvement of Basmati rice varieties for resistance to blast and bacterial blight diseases using marker assisted backcross breeding. *Plant Sci,* **242**: 330−341. [Cross Ref]

Ellur, R. K., Khanna. A., Gopalakrishnan. S., Bhowmick, P. K., Vinod, K. K., Nagarajan, M., Mondal, K. K., Singh, N. K., Singh, K., Prabhu, K. V. and Singh, A. K. 2016b. 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 . [Cross Ref]

Fukagawa, N. K. and Ziska, L. H. 2019. Rice: Importance for Global Nutrition. *J. Nutri. sci. and Vitaminol*., **65**(Supplement), S2–S3. [Cross Ref]

Gopalakrishnan, S., Sharma, R.K., Anand Rajkumar, K., Joseph, M., Singh, V.P., Singh, A.K., Bhat, K.V., Singh, N.K. and Mohapatra, T. 2008. Integrating marker assisted background analysis with foreground selection for identification of superior bacterial blight resistant recombinants in Basmati rice. *Plant Breed*, **127**(2):131–139. [Cross Ref]

ICAR-Indian Institute of Rice Research. Progress Report, 2019, Varietal Improvement; India Coordinated Rice Improvement Project, ICAR-Indian Institute of Rice Research, Rajendranagar, Hyderabad-30, TS; ICAR-Indian Institute of Rice Research: New Delhi, India, 2020; Volume 1: 683

Joseph, M., Gopalakrishnan, S., Sharma, R.K., Singh,V.P., Singh, A. K. and Singh, N.K. 2004. Combining bacterial blight resistance and Basmati quality characteristics by phenotypic and molecular marker-assisted selection in rice. *Mol. Breed*., **13**: 377–387. [Cross Ref]

Kauffman, H.E., Reddy, A. P. K., Hsieh, S. P. Y. and Merca, S. D. 1973. An improved technique for evaluating resistance of rice varieties to *Xanthomonas oryzae pv. oryzae*, *Plant Dis. Rep*., **57**: 537- 541

Khare, M., Singh, R. P., Ram, T., Yadav, A. K. and Sharma, A. 2021. Improvement of rice cultivar for bacterial blight disease through marker assisted breeding approach. *Elec. Jr. Plant Breed*., **12**(1): 28 - 36. [Cross Ref]

Kotasthane, A. J. and Gaikwad, N. J. 2021. Marker Assisted Selection of *xa5*, *xa13* and *Xa21* Gene in Breeding Populations Derived from Karma Mahsuri x IRBB 59. *Plantae Scientia*, **4**(1):108–116. [Cross Ref]

Mew, T. W., Alvarez, A. M., Leach, J. E. and Swings, J. 1993. Focus on bacterial blight of rice. *Plant Dis.*, **77**(1): 5–12. [Cross Ref]

Murray, M.G. and Thompson, W.F. 1980. Rapid isolation of high molecular weight plant DNA. *Nucleic Acids Research*, **8:** 4321-4325. [Cross Ref]

Nino-Liu, D.O., Ronald, P.C. and Bogdanove, A.J. 2006. *Xanthomonas oryzae pathovars*: model pathogens of a model crop. *Mol. Plant Pathol.*, **7**(5): 303 324. [Cross Ref]

Noor Ahmed, S., Madhav, M.S., Padma, V. and Satish, Y. 2021.Validation of linked markers of blast and blight resistance genes among black rice accessions of North East India, *Biological Forum*, **13**(2): 293-297

Pradhan, M. and Bastia, D.N. 2022. Validation of linked markers of bacterial leaf blight resistance genes in rice variety of Odisha (*Oryza sativa*). *J. Pharm. Innov.*, **11**: 446-448.

Pradhan, M., Bastia, D., Samal, K.C., Manasi, D. and Sahoo, J. P. 2023. Pyramiding resistance genes for bacterial leaf blight (*Xanthomonas oryzae pv. Oryzae*) into the popular rice variety, Pratikshya through marker assisted backcrossing. *Mol. Biol. Rep.* **50**, 9047–9060. [Cross Ref]

Pradhan, S.K., Nayak, D.K., Mohanty, S., B., Lambodar, Barik, S.R., Pandit, E., Lenka, S. and Anandan, A. 2015. Pyramiding of three bacterial blight resistance genes for broad-spectrum resistance in deepwater rice variety, Jalmagna. *Rice,* **8**,: 19. [Cross Ref]

Prasad, D., Singh, R. and Deep, S. 2018. In-vitro and In-vivo efficacy of antibacterial compounds against *Xanthomonas oryzae pv. oryzae*, A Cause of bacterial leaf blight of rice. Int. *Jr. of Curr. Microbiol. Sci.*, **7**(5): 2960-2969. [Cross Ref]

Rao, K. K., Jena, K. K. and Lakshminarasu, M. 2003. Molecular tagging of a new bacterial blight resistance gene in rice using RAPD and SSR markers. *Plant breed,* **209**: 16-17

Sagar, V. 2018. Marker assisted pyramiding of genes for resistance to bacterial blight and blast into an elite rice variety Pusa Basmati 1509. Ph. D. thesis. ICAR-Indian Agricultural Research Institute, New Delhi

Sahu, Neelu Ram. 2021. Diversity Analysis and Integrated Disease Management of *Xanthomonas oryzae pv. oryzae* causing Bacterial Leaf Blight of Rice (*Oryza sativa* L.). Ph. D. Thesis. Indira Gandhi Krishi Vishwavidyalaya, Raipur

Shekhar, S., Sinha, D. and Kumari, A. 2020. An overview of bacterial leaf blight disease of rice and different strategies for its management. *Int. J. Curr. Microbiol. App. Sci.,* **9**(4): 2250-2265. [Cross Ref]

Singh, S., Sidhu, J. S., Huang, N., Vikal, Y., Li, Z., Brar, D. S., Dhaliwal, H. S. and G. S. Khush. 2001. Pyramiding three bacterial blight resistance genes (*xa5*, *xa13* and *Xa21*) using marker-assisted selection into indica cultivar PR 106. *Theor. Appl. Genet.*, **102**: 1011-1015. [Cross Ref]

Srinivasan, B. and Gnanamanickam, S.S. 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*. *Current Science*, **88**(8): 1229-1231

Sundaram, R.M., Vishnupriya, M.R., Biradar, S.K., Laha, G.S., Reddy, G.A., Rani, N.S., Sarma, N.P. and Sonti, R.V., 2008. Marker assisted introgression of bacterial blight resistance in Samba Mahsuri, an elite indica rice variety. *Euphytica*, **160**(3): 411–4. [Cross Ref]

Vidya, V. and Ramalingam, J. 2018. Marker assisted selection for sheath blight, blast and bacterial blight resistance in two popular rice varieties. *Madras Agricultural Journal*, **105**: 127-134. [Cross Ref]