
REVIEW

Geographical Distribution, pathogen diversity and host plant resistance in bacterial blight of rice

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Bacterial blight (BB) of rice, caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is one of the major production constraints in India. Analyses of disease survey data for the last 40 years in India revealed that the disease has increased both in terms of geographical distribution and intensity in different rice growing regions of India. Major reasons are changed cultivation practices with heavy dependence on nitrogen fertilizers, apparent changes in climatic parameters, narrow genetic base and complex pathogen population structure due to dynamic nature of the pathogen. *Xoo* is highly dynamic in nature and knowledge on pathogen virulence structure is imperative for designing a scientific resistance breeding program. Analysis of virulence profile of *Xoo* isolates collected from different rice growing regions of India on a set of rice differentials revealed existence of wide diversity in pathogen population structure in India. Molecular analysis of *Xoo* isolates revealed a high level of genetic polymorphism among the isolates. As the chemicals do not provide satisfactory level of protection against the disease, emphasis has been given for the development and deployment of BB resistant rice varieties. Diverse sources of resistance to bacterial blight of rice have been identified and characterized. Using marker assisted backcross breeding, different BB resistance genes have been incorporated in popular rice cultivars and several rice varieties viz., Improved Samba Mahsuri, DRR Dhan 53, DRR Dhan 58, DRR Dhan 59, DRR Dhan 60 and DRR Dhan 62 have been developed and released for commercial cultivation.

Keywords: Bacterial blight, resistance, rice, *Xanthomonas oryzae* pv. *oryzae*, variety

INTRODUCTION

Rice continues to be the most important staple food crop in India and several other countries especially in Asia. It is also an important food crop in tropical areas of Latin America and many African nations. Rice is considered as life for millions of Asians as it has immensely influenced their culture, diets, and economic condition. It is cultivated in diverse ecosystem ranging from wettest areas in the world (e.g. Arakan coast of Myanmar with an average rainfall of more than 5100 mm) to driest deserts and temperate to tropical climate. It is cultivated at sea level on coastal plains to delta region to places at high altitude. About 92% of rice is grown and consumed in Asia where 55% of the world's population lives (Wilson and Talbot, 2009). It has

been reported that China and India alone grow and consume about 50% rice (Muthayya *et al.* 2014).

However, it is estimated that by 2050, the world population will reach about 9.1 billion, 34% higher than today and majority of this population increase will happen in developing countries. There will be increased urbanization and increase in income. To feed this richer and urbanized population, food production must increase by 70%. Annual cereal production will need to rise to about 3 billion tonnes from 2.1 billion today (Anonymous, 2009).

Indian economy is largely dependent on agriculture and undoubtedly, rice crop occupies a central position in Indian agriculture. About 60-65% of the Indian population depends on rice as the primary source of nutrition. Rice production increased from 53.6 million tons in 1980 to 129 million tons in 2021-22 (Anonymous, 2022). Though India is in comfortable position with

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respect to food production, continuous efforts are required to increase the food production to meet the requirements of ever-increasing population while keeping the environment clean and healthy. This has become more challenging because of several factors like accelerating loss of productive rice land to industrialization and human settlement, scarcity of labour and water, increased incidence of several biotic stresses and apparent changes in climatic conditions leading to uncertain monsoon and untimely flood or drought. Over the years, rice cultivation has become more intensive involving excessive use of chemical fertilizers and pesticides, large scale cultivation of few high yielding rice varieties with narrow genetic base and increase in cropping intensity. These changed cultivation practices and apparent changes in climatic conditions have resulted in increased incidences of different pests and diseases (Laha *et al.* 2012). Many rice diseases which were earlier considered a minor disease with sporadic occurrence have become a major one occurring in larger geographical areas e.g. false smut and panicle blast of rice. Bacterial blight of rice caused by *Xanthomonas oryzae* pv. *oryzae*, remains a major production constraint in rice cultivation. In recent years, this disease has been reported to appear in severe form in many areas which were earlier not considered endemic to this disease.

Distribution and Economic Importance of Bacterial Blight

Bacterial blight (BB) of rice caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is one of the most destructive diseases of rice in majority of the rice growing countries especially in Asia. Though the disease has been known in Japan since 1884, its bacterial nature was established in 1922. In India, the first authentic report of typical bacterial blight symptoms was made from Maharashtra where it was reported to be widespread and destructive since 1951. The disease remained localised in Maharashtra until it appeared in an epidemic form in Shahabad district of Bihar in 1963. With widespread cultivation of semi-dwarf, high-yielding and nitrogen-responsive varieties like Taichung Native 1, it spread like wild fire in almost all the major rice-growing regions. In India, bacterial blight is

considered as a serious production constraint especially in irrigated and rainfed lowland ecosystem. In Punjab and Haryana states of India, major epidemics occurred in 1979 and 1980; severe kresak was observed and total crop failure was reported. The disease was again reported in epidemic form during 1998 in Pallakad district of Kerala and since then it has become endemic in that region. Presently, this disease appears regularly in moderate to severe form in major rice growing states of India viz., Punjab, Haryana, plains of Uttarakhand, Western and eastern part of Uttar Pradesh, Bihar, parts of Jharkhand, West Bengal, Parts of Assam, Tripura, Odisha, Chhattishgarh, Andhra Pradesh, parts of Telangana, Coastal part of Tamil Nadu and Kerala, Konkan region of Maharashtra and parts of Karnataka and Gujarat (Laha *et al.* 2023).

Globally, the disease has been reported from most of the Asian countries and many African and Latin American countries (Laha *et al.* 2017). The disease was reported from most parts of East, South and South-east Asian countries viz., China, Korea, Taiwan, India, Sri Lanka, Nepal, Bangladesh, Pakistan, Thailand, The Philippines, Indonesia, Vietnam, Malaysia, Cambodia, Myanmar and Laos (Laha *et al.* 2017). The disease has also been reported from Australia on cultivated rice and on the wild species. The disease was first reported in West Africa in 1979 from Mali. Subsequently, it was reported from many African countries like Senegal, Niger, Nigeria, Madagascar, Gabon, Mauritania, Benin, Burkina Faso, Guinea Bissau, Ghana, Cameroon, Togo, Mozambique, Rwanda, Tanzania and Uganda (Sere *et al.* 2013). The disease was reported from most of the rice growing countries of Caribbean region (Mexico, Costa Rica, Honduras, Salvador and Panama), South America (Colombia, Venezuela, Equador and Bolivia) and North America (Texas and Louisiana).

Bacterial blight of rice is essentially a monsoon season disease of high yielding varieties grown with high dosage of nitrogen fertilizer. Though the disease is reported worldwide, it is of economic importance mainly in Asia and in some parts of Africa (OEPP/EPPO 2007). In India, several workers have reported yield losses due to bacterial blight of rice ranging from 2 to 74 %

depending on varieties, season, weather conditions, stages of infection and nitrogen application. In many African countries like Burkina Faso, Niger and Mali, yield loss due to BB has been reported in the range of 50-90% (Sere *et al.* 2005; Basso *et al.* 2011).

Changes in Rice Bacterial Blight Disease Scenario

BB of rice has remained as one of the most devastating diseases of rice. However, during the last decade or so, the disease has increased both in terms of geographical distribution and intensity and moved to areas which were earlier not considered as endemic for BB. Under AICRPR (All India Coordinated Research Project on Rice), a survey called 'Production Oriented Survey' (POS) is conducted every year in different rice growing regions of India by ICAR-Indian Institute of Rice Research. One of the major areas of the survey is the survey on incidences of different pests and diseases. Using the survey data of POS from 1981 to 2022, a district wise database was created on incidences of bacterial blight disease as low ($\leq 5\%$), low to moderate (6-15%), moderate (16-25%), moderate to severe (26-50%) and severe ($>50\%$). The data were then categorized into four decades *viz.*, 1981-1990, 1991-2000, 2001-2010 and 2011-2022. District wise incidence of BB disease was averaged for each decade. The data were then converted into numerical format by allotting scores in the scale of 1-5 (1-trace; low; 2-low to moderate; 3-moderate, 4-moderate to severe and 5-severe). District wise data points of BB incidence was then geotagged to generate the distribution maps of BB using point symbology of QGIS software (Version 3.2). District level data of rice crop area were collected from Directorate of Economics and Statistics (https://aps.dac.gov.in/APY/Public_Report1.aspx) for the years 1990, 1999, 2009 and 2019 representing each decade to generate rice area map using polygon symbology. Generated decade wise BB distribution maps were overlaid on district level rice area maps to visualize the BB distribution in different rice growing regions of India (Fig.1).

During, 1981-1990, BB was recorded in severe intensity mainly in north western India, Gujarat and

parts of eastern India. During this period, the disease was wide spread in several rice growing districts of Bihar, Punjab, Gujarat and Uttar Pradesh as evidenced by several reports of occurrence of the disease in high intensity in these states (Fig.1 & 2). The disease was also wide spread in moderate intensities in several rice growing regions of undivided Andhra Pradesh, Haryana and Konkan region of Maharashtra with instances of severe occurrence. In rest of India, the disease was either not recorded or was present in sporadic intensities. During 1991-2000, the intensity of the disease increased significantly in states like Haryana, Konkan region of Maharashtra, Punjab, undivided Andhra Pradesh and Tamil Nadu as evidenced by its increased spread (Fig.1) and several instances of occurrence in high intensity (Fig. 2). Compared to previous decade *i.e.* 1981-1990, the intensity of the disease increased significantly in Assam, Odisha and West Bengal (Fig. 1). In the next decade (2001-2010), intensity and spread of the disease increased significantly in many rice growing regions of India. The intensity and distribution of the disease increased significantly in coastal Andhra Pradesh and parts of Royalseema, parts of Gujarat, Haryana, Konkan region of Maharashtra, parts of Kerala, Odisha, Puducherry, Punjab, Tamil Nadu and Uttar Pradesh and there were many instances of its occurrence in high intensity (Fig. 1 & 2). In the last decade (2011-2022), the intensity and geographical spread of the disease further increased especially in southern India as evidenced by several reports of occurrence of the disease in high intensity (Fig.1 & 2; Table.1). The disease appeared in severe form in several parts of Andhra Pradesh in 2010 and 2013 especially on rice variety Samba Mahsuri (Yugander *et al.* 2014). The disease appeared in epidemic form in Khammam district of Telangana in 2017 and 2021 (Laha *et al.* 2021a). Interestingly, in the last decade, the BB disease intensity significantly came down in Punjab and Haryana (Fig. 2).

Disease Symptoms and Disease Development

This is a vascular disease and has two typical phases of symptoms, *viz.*, leaf blight phase and kresek phase. Another phase of symptoms called

'Pale Yellow Phase' has been reported from Philippines. Some of the youngest leaves in a clump may become pale yellow or whitish. The diseased leaves later wither, turn yellowish brown and dry up. The pale-yellow phase has not been reported from other countries.

Leaf Blight Phase: Leaf blight phase is most common (Fig.3h). The symptom starts as water-soaked lesions on the tip of the leaves and increases in length downwards (Fig. 3a). Initially, the lesions are pale green in colour and later turn into yellow to straw-coloured stripes with wavy margins. The lesions adjoining the healthy part show water soaking. Lesions may start at one or both the edges of the leaves (Fig.3b, 3c). Occasionally, the linear stripes may develop anywhere on the leaf lamina or along the midrib with or without marginal stripes (Fig.3d). As the disease advances, the lesion covers the entire leaf blade (Fig. 3e), turns white and later becomes greyish or blackish due to growth of various saprophytic fungi. In humid areas, on the surface of the young lesions, yellowish, opaque and turbid drops of bacterial ooze may be observed during early morning (Fig.3f). They dry up to form small, yellowish, spherical beads on the lesions.

Kresek Phase: The most destructive phase of the disease in the tropics is 'kresek' or wilt phase (Fig.3g) resulting from early systemic infection in the nursery or from seed infection. The leaves roll completely, droop, turn yellow or grey and ultimately the tillers wither away. In severe cases, the affected hills may be completely killed.

Though seed infection can be observed especially in tropical regions in India, several studies have shown that such seeds may not produce diseased plants. Thus, seed transmission is not considered likely under normal conditions. The bacterium cannot survive in soil and field water from season to season in single cropped areas but the ratoons and self-sown plants in low lands constitute the primary source of inoculum in some parts of the country. In double cropped areas, infected straw and stubble, infected wild rice, living rice plants growing in ponds, ditches and irrigation canals during the off season serve as a source of inoculum. Infected straw, when applied in nursery soil or near an irrigation canal,

serves as the primary source of inoculum. Infected straw piled on the bunds serve as one of the major sources of primary inoculum. Staggered sowings and transplanting results in overlapping of crops and in such cases the spread of the disease is very easy and fast. The pathogen may survive on some grasses like *Leersia hexandra*, *Cyperus rotundus* (motha grass), *Panicum repens* as an epiphyte and forms the source of primary inoculum. Irrigation water, contaminated with bacteria flowing through the fields also provides the primary inoculum.

Several factors influence the development of the disease. High humidity (>80%), rain and cloudy condition accelerate the disease development. A moderate amount of rainfall evenly distributed during the crop season can bring about an epidemic. Reduced duration of sunshine or cloudy condition favours the disease development. Flooding and water logging conditions, strong winds or cyclone accompanied with rains accelerate the disease development and horizontal spread of the disease. Excess of nitrogen and late top dressing increases the disease.

The Pathogen

Bacterial blight of rice is caused by *Xanthomonas oryzae* pv. *oryzae* (Ishiyama) Swings *et al.* According to the new classification system, the bacterium has been placed in the family Xanthomonadaceae, order Xanthomonadales, class Gammaproteobacteria and phylum proteobacteria in the domain Bacteria. *Xoo* is a gram negative, non-spore forming and rod-shaped bacterium with a single polar flagellum (Fig. 4b). The bacterium can be readily isolated from infected leaf samples on culture medium like modified Wakimoto's medium. The bacterium is a slow grower and after 4-5 days of incubation at 28±2°C, pinhead sized *Xoo* colonies can be observed in culture plates which can be further purified by sub-culturing. Colonies on agar culture medium are round, convex, mucoid and yellow in colour (Fig. 4a) due to production of a non-diffusible yellow pigment called xanthomonadin (a brominated, aryl polyene pigment), characteristics of the genus. Very rarely the pigment deficient albino form of the pathogen is

detected (Fig.4c). The pathogenicity of the isolated bacterium can be easily confirmed by inoculating the culture in a susceptible rice variety like Taichung Native 1. Alternatively, the identity of the pathogen can also be confirmed using specific molecular markers (Sakthivel *et al.* 2001; Lang *et al.* 2010).

Xoo is a highly variable pathogen and the dynamic nature of its pathogenicity is demonstrated by the continuous appearance of new pathogenic variants. Knowledge on the virulence profile of the pathogen is essential for a successful resistance breeding programme. Pathogen population structure can be monitored by inoculating the *Xoo* isolates on a set of differential rice varieties and recording their reactions. Initially, rice varieties having differential reaction were used to characterize the *Xoo* isolates (Gupta *et al.* 1986; Reddy and Reddy 1992). With the advance in knowledge in the genetics of BB resistance and availability of different BB resistance genes (*Xa/xa* genes) and their various combination in a common genetic background IR 24, analysis of virulence profile of *Xoo* isolates is mostly done on these near isogenic lines (commonly referred to as IRBB lines). Several workers from India analyzed the *Xoo* population from different rice growing regions of India both through phenotyping (using the IRBB lines) and molecular markers and showed the existence of different pathotypes/races and also diversity in their genetic makeup (Shanti *et al.* 2001; Singh *et al.* 2003, Lore *et al.* 2011; Mishra *et al.* 2013; Yugander *et al.* 2014; Mondal *et al.* 2014; Pandey *et al.* 2014; Yugander *et al.* 2022). *Xoo* employ an array of compounds and mechanisms to cause disease in rice. Most important mechanism is Type III secretion system which translocates the effector proteins that can suppress the host defences. TAL (Transcription activator-like) effectors constitute the major group of effectors that suppresses the host defence by targeting some host susceptibility genes or SWEET (Sugars Will Eventually be Exported Transporters) genes like SWEET11, SWEET13 or SWEET14 (Oliva *et al.* 2019). *Xoo* also employs some non-TAL effectors like Xop (Xanthomonas outer protein) effectors like Xop R, XopF and others during pathogenesis (Mondal, 2017). Additionally, *Xoo* also employ several amino acids (Li *et al.* 2019) and xyloglucan

depolymerization machinery (Vieira *et al.* 2021) during pathogenicity and pathogen establishment.

Disease Management

The strategy for management of the disease should be directed in such a manner that various sources of inoculum are avoided and spread of the disease in field is checked. As chemical management of the disease is not as successful as in fungal diseases of rice, much importance has been given on host plant resistance. Cultural practices, host nutrition and limited chemical control measures help in the reduction of the initial inocula and the secondary spread of the disease.

Host Plant Resistance

Development and deployment of rice varieties resistant to BB (possessing one or more BB resistance gene) is the most effective approach for managing the disease. Extensive genetic studies of diverse germplasm have been conducted in last 2 decades to decipher the genetics of BB resistance. Till date 48 BB resistance genes have been identified from diverse sources (Table. 2). However, the effectiveness of these resistance genes varies due to difference in virulence profile of the pathogen isolates in different geographical regions. Majority of these genes have been identified from cultivated rice *Oryza sativa*; but some are from related wild species like *O. longistaminata*, *O. rufipogon*, *O. minuta*, *O. officinalis* and *O. nivara*. Some of the BB resistance genes are dominant in nature (e.g. *Xa21*) while some are recessive in nature (e.g. *xa13*). Some of the 'R' genes provide wide spectrum resistance against multiple isolates/strains (e.g. *xa13*, *Xa21*, *Xa23*) while others are narrow in their protective activity (e.g. *Xa1*). Sixteen BB resistance genes have been cloned (*Xa1*, *Xa2/Xa31*, *Xa3/Xa26*, *Xa4*, *xa5*, *Xa7*, *Xa10*, *xa13*, *Xa14*, *Xa21*, *Xa23*, *xa25*, *Xa27*, *xa41*, *Xa45* and *Xa47*) (Yang *et al.* 2022; Lu *et al.* 2022). Some of the BB resistance genes are receptor-like kinase (RLK) genes (*Xa4*, *Xa21*), some are SWEET genes (Sugar Will Eventually be Exported Transporter) (*xa13*, *xa25*, *xa41*), some are executor genes (*Xa10*, *Xa23*, *Xa27*) and some are other types of genes (*Xa1*, *xa5*) (Jiang *et al.*

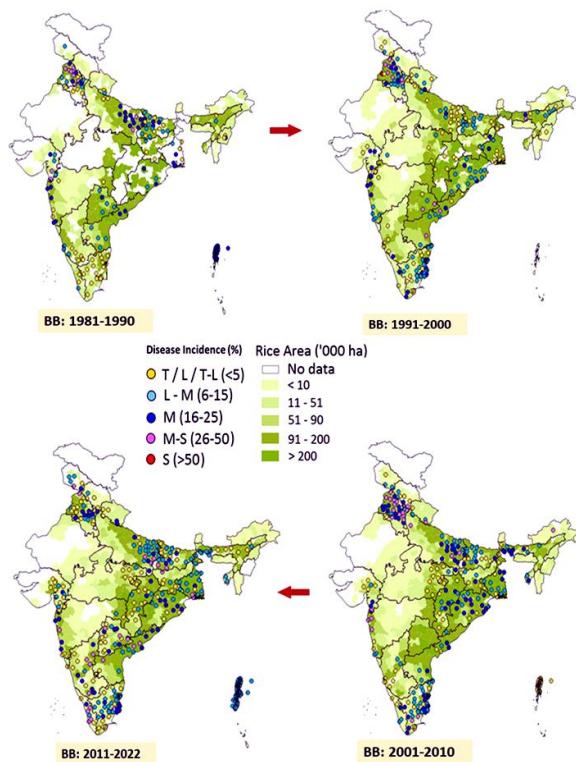


Fig. 1: Map showing the changes in distribution and intensity of bacterial blight disease of rice in different rice growing regions of India in last four decades

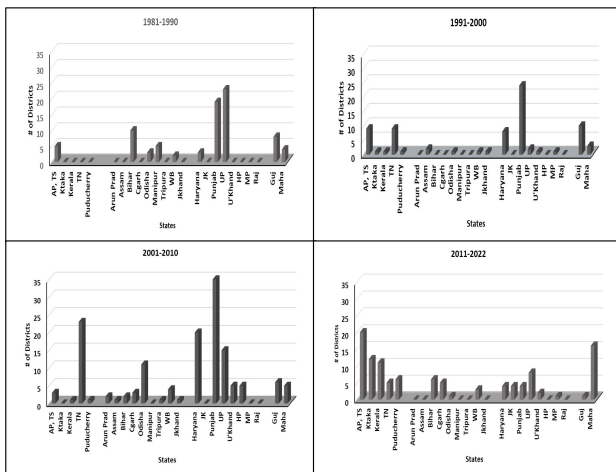


Fig. 2: Number of districts in different states of India which showed severe Bacterial blight incidence in four decades

2020). Among the BB resistance genes identified, only few genes, viz. *Xa4*, *xa5*, *Xa7*, *xa13*, *Xa21*, *Xa23*, *Xa27*, *Xa33* and *Xa38*, have been used for marker-assisted selection (MAS) breeding.

BB resistance breeding started in IRRI and elsewhere through conventional plant breeding approach and BB resistant rice varieties like IR 20 and IR 22 were released from IRRI in 1969.



Fig. 3: Symptoms of bacterial blight disease of rice; (a) initial symptoms of bacterial blight disease; (b) Lesion on one edge of the leaf blade; (c) lesion on both the edges of leaf blade; (d) lesion along midrib without marginal stripes; (e) Advanced stages of symptom development showing total drying of leaves; (f) bacterial ooze on infected leaves; (g) kresak or wilt phase of the disease; (h) severe bacterial blight disease under field condition

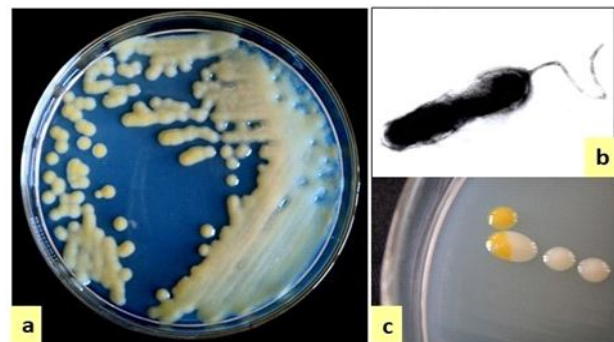


Fig. 4: The bacterial blight pathogen, *Xanthomonas oryzae* pv. *oryzae*: (a) Characteristic colonies of *Xoo* on culture plate; (b) Transmission electron microscopical view showing single cell of *Xoo* with single polar flagellum; (c) Albino colony of *Xoo*

Following this, many BB resistant rice varieties mostly possessing BB resistance gene *Xa4* were released from different rice growing countries including India in 1970s and 1980s. However, due to wide spread cultivation of these varieties, there was a shift in the *Xoo* population structure and majority of these varieties became moderately to highly susceptible to BB. Subsequently, plant breeders started incorporating other BB resistance genes like *xa5* and *Xa7*. Significant development in BB resistance breeding program took place with the identification of *Xa21*, a major dominant BB resistance gene from *Oryza longistaminata*. Because of dynamic nature of the pathogen, the resistance conferred by single BB resistance gene is short-lived. Therefore, the best way to ensure the durability of BB resistance is

Table 1: Occurrence of bacterial blight in epidemic form in south Indian states in last one and half decade

Year	State/District	Affected Rice variety	Extent of damage
2010	Andhra Pradesh (Kurnool District)	Samba Mahsuri	Wide spread occurrence of bacterial blight in about 10,000 acres of Samba Mahsuri
2013	Andhra Pradesh (Guntur District)	Samba Mahsuri	30-70% BB incidence in about 70% rice area
2014	Tamil Nadu (Thanjavur)	BPT 5204 and ADT 43	-
2014	Andhra Pradesh (East and West Godavari)	Samba Mahsuri and Prabhat	30-80% incidence in majority of the rice fields
2014	Kerala (Alapuzzha)	Uma	About 1250 ha rice crop was very severely affected
2015	Tamil Nadu (Trichy)	-	Epidemic occurrence of bacterial blight
2017	Telangana (Khammam)	Samba Mahsuri, Chintu	~ 80% BB incidence in large areas in Khammam district
2018	Telangana (Nizamabad)	Samba Mahsuri	70-80% incidence in large areas in Nizamabad district
2021	Telangana (Khammam)	Samba Mahsuri	Up to 100% BB incidence in part of Khammam

Source: POS (2010-2022)

to pyramid multiple BB resistance genes (preferably with diverse gene mechanisms) in a single cultivar using marker assisted selection (MAS) (Sundaram *et al.* 2008). In 2007, first MAS derived BB resistant rice variety Improved Pusa Basmati 1 possessing two BB resistance genes viz., *xa13* and *Xa21* was released from ICAR-Indian Agricultural Research Institute (Gopalakrishnan *et al.* 2008) followed by release of Improved Samba Mahsuri possessing three BB resistance genes viz., *xa5*, *xa13* and *Xa21* from ICAR-Indian Institute of Rice Research in 2008 (Sundaram *et al.* 2008). Improved Samba Mahsuri exhibited excellent BB resistance in farmers' fields and occupied a large area under cultivation. Another rice variety called DRR Dhan 53 possessing four BB resistance genes viz., *xa5*, *xa13*, *Xa21* and *Xa38* was developed and released from ICAR-Indian Institute of Rice Research for commercial cultivation (Yugander *et al.* 2018a,b; Laha *et al.* 2021b). The variety exhibited very high level of BB resistance and high yield in farmers' fields. This was followed by release of several BB resistant rice varieties viz., DRR Dhan 58 possessing three BB resistance genes viz., *Xa21*, *xa13* and *xa5* and seedling stage salinity tolerance (*Saltol*), DRR Dhan 59 possessing newly identified BB resistance gene *Xa33*, DRR Dhan 60 possessing three BB resistance genes viz., *Xa21*, *xa13* and *xa5* and low soil phosphorous tolerance (*Pup1*) and DRR Dhan 62 possessing three BB resistance genes viz., *Xa21*, *xa13* and *xa5* and two blast resistance genes viz., *Pi2* and *Pi54* (IIRR annual Report

2021). In addition, bacterial blight resistance was improved in several hybrid parental lines viz., DRR 17B, RPHR 1005 and APMS6B (Balachiranjeevi *et al.* 2015; AbhilashKumar *et al.* 2017; Yugander *et al.* 2018).

Chemical Management

In spite of extensive testing of various chemicals and antibiotics, none of them was found to provide sufficient level of protection against the disease in India. Some of these chemicals may offer partial protection against the disease especially when the disease pressure is low. Though seed transmission is not common, infected seeds can introduce the bacterium in new area and environment. Therefore, eradication of seed inoculum is very important. Overnight soaking of infected seeds in 100 ppm streptomycin (streptomycin 12% + chlorotetracycline hydrochloride 1.5%) solution can effectively eradicate the seed infection. It has been reported that spraying twice with 250 ppm of Agrimycin 100 can effectively reduce the disease intensity and secondary spread of the disease (Laha *et al.* 2009). It is reported that five sprays (at 12-day interval) of Agrimycin 100 and Fytolan (copper oxychloride) (50:500) or 665 ppm of Agrimycin 500 (streptomycin sulphate 1.75 % + terramycin 0.17 % + tribasic copper sulphate 42.4 %) can significantly reduce the intensity of the disease. Combination of one spray of 2,4-D ethyl ester (1.0 ml/l) with two sprays of streptomycin (200 mg/l) + copper oxychloride (2.5 g/l) was

Table 2: List of genes conferring resistance to bacterial blight of rice

R gene	Dominant/ Recessive	Chromo- some	Donor	Source	References
<i>Xa1</i>	Dominant	4	Kogyoku, Java 14	Japan	Lee <i>et al.</i> , 2003
<i>Xa2/Xa31</i>	Dominant	4	Rantaimas II, Tetep	Vietnam	
<i>Xa3 (Xa-w)/Xa26/Xa4b/Xa6/Xa9</i>	Dominant	11	Wase Aikoku 3, Semora Mangga, Zenith,M. Sungsong, Sateng, Minghui 63, Java-14, Chugoku-45, Cempocolek	Japan	Xiang <i>et al.</i> , 2006 Chukwu <i>et al.</i> , 2019;
<i>Xa4 (Xa4a)</i>	Dominant	11	TKM6, IR20, IR22 , IR72	India	
<i>xa5</i>	Recessive	5	DZ192, IR1545 -339, DV 85, DV 86, DZ 78	Bangladesh	Kumar <i>et al.</i> , 2020;
<i>Xa7</i>	Dominant	6	DV 85, DV 86, DZ78,	Bangladesh	
<i>xa8</i>	Recessive	7	PI231129	USA	Kant <i>et al.</i> , 2021;
<i>Xa10</i>	Dominant	11	Cas 209	Philippines	
<i>Xa11</i>	Dominant	3	IR8, IR944-102	Philippines	Fiyaz <i>et al.</i> , 2022;
<i>Xa12</i>	Dominant	4	Kogyoku, Tetep, Java 14	Japan	
<i>xa13 (SWEET 11)</i>	Recessive	8	BJ1, ChinsurahBoro II	India	Yang <i>et al.</i> , 2022
<i>Xa14</i>	Dominant	4	TN1	China	
<i>xa15</i>	Recessive	ND	M41 (a mutant line of Harebare)	Japan	
<i>Xa16</i>	Dominant	ND	Tetep	Vietnam	
<i>Xa17</i>	Dominant	ND	Asominori	South Korea	
<i>Xa18</i>	Dominant	ND	Toyonishiki, Milyang 23, IR24	Philippines, Japan	
<i>xa19</i>	Recessive	ND	XM5 (mutant of IR 24)	Philippines	
<i>xa20</i>	Recessive	ND	XM6 (mutant of IR 24)	Philippines	
<i>Xa21</i>	Dominant	11	Wild rice (<i>O. longistaminata</i>)	Africa, Mali	
<i>Xa22</i>	Dominant	11	Zhachanglong	China	
<i>Xa23</i>	Dominant	11	<i>O. rufipogon</i> , CBB23, IRBB 23	China/ Cambodia	
<i>xa24</i>	Recessive	2	DV86, DV85, Aus 295	Bangladesh	
<i>xa25 (SWEET 13)</i>	Recessive	12	Minghui 63	China	
<i>Xa25(t)</i>	Dominant	4	HX3 (Somaclonal mutant)	China	
<i>xa26(t)</i>	Recessive	ND	Nep Bha Bong To	Vietnam	
<i>Xa27</i>	Dominant	6	<i>O. minuta</i> , IRGC 101141, IRBB 27	Philippines	
<i>Xa28(t)</i>	Recessive	ND	Lota sail	Bangladesh	
<i>Xa29(t)</i>	Dominant	1	<i>Oryza officinalis</i> (B5)	-	
<i>Xa30(t)</i>	Dominant	11	<i>Oryza rufipogon</i> (Y 238)	India	
<i>xa31(t)</i>	Recessive	4	Zhachanglong	China	
<i>Xa32(t)</i>	Dominant	11	<i>Oryza australiensis</i> (C4064)	-	
<i>xa32(t)</i>	Recessive	12	Germplasm Y76 (somatic hybridization between wild wart grain rice and cultivated rice)	China	
<i>Xa33</i>	Dominant	7	<i>O. nivara</i> (Acc. No. 105710)	India	
<i>xa33(t)</i>	Recessive	6	Indica rice cultivar Ba7	Thailand	
<i>xa34(t)</i>	Recessive	1	Sri Lanka variety BG1222	Sri Lanka	
<i>xa34(t)</i>	Recessive	ND	<i>O. branchyantha</i>	India	
<i>Xa35(t)</i>	Dominant	11	<i>Oryza minuta</i> (Acc. No.101133)	Philippines	
<i>Xa36(t)</i>	Dominant	11	C4059	China	
<i>Xa38</i>	Dominant	4	<i>Oryza nivara</i> , IRGC81825	India	
<i>Xa39</i>	Dominant	11	FF329	China, Philippines	
<i>Xa40(t)</i>	Dominant	11	indica rice IR65482-7-216-1-2	Korea	
<i>xa41 (SWEET 14)</i>	Recessive	11	<i>Oryza barthii</i> and <i>Oryza glaberrima</i>	Africa, Mali	
<i>xa42</i>	Recessive	3	XM14, a mutant of IR 24	Japan	
<i>xa42(t)</i>	Recessive	6	Baixiangzhan	China	
<i>Xa43(t)</i>	Dominant	11	P8 (IRGC: 126,955)	Japan	
<i>xa44(t)</i>	Recessive	11	P6 (IR73571-3B-11-3- K3 //lpum)	Philippines, Korea	
<i>Xa45</i>	Dominant	4	AXO1947, T7174	-	
<i>xa45(t)</i>	Recessive	8	<i>O. glaberrima</i> , IRGC 102600B	India	Neelam <i>et al.</i> , 2019
<i>Xa46(t)</i>	Dominant	11	Mutant H120 derived from the japonica line Lijiangxintuanheigu	China	Chen <i>et al.</i> , 2020
<i>Xa47(t)</i>	Domonant	11	Introgression line derived from Yuanjiang common wild rice, <i>Oryza rufipogon</i>	China	Xing <i>et al.</i> , 2021
<i>Xa48(t)</i>	Dominant	11	Introgression line, IR 75084-15-3-B-B, derived from <i>Oryza officinalis</i>	India	Sinha <i>et al.</i> , 2023

ND: Not Determined

effective in reducing the intensity of BB disease (Singh *et al.*, 2012).

Several cultural practices like use of disease resistant/tolerant rice varieties, removal of infected

plant debris, self-sown rice plants, avoiding field to field irrigation, keeping the fields weeds free, use of healthy seeds and seeds collected from disease free plots, judicious application of nitrogenous fertilizers with required level of

potassic fertilizers have been found to reduce the initial inoculum and spread of the disease under field condition. Regular surveillance of the fields and adoption of the available control measures will certainly keep the disease below the economic threshold level.

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DECLARATIONS

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