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REVIEW ARTICLE

Etiology of an emerging disease: bakanae of rice

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Abstract
Bakanae disease caused by *Fusarium fujikuroi* Nirenberg is reported from almost all the rice growing countries of the world and it has emerged as a major problem in Asian countries. The typical and distinguished symptoms of the disease are elongation and rotting of rice plants. *F. fujikuroi* produces broad spectrum secondary metabolites, pigments and mycotoxins resulting quantitative and qualitative losses to rice crop. Recent changes in climate and cropping patterns have aggravated this disease. In this article, the information on disease etiology and management has been discussed.

Keywords Bakanae · Rice · *Fusarium fujikuroi* · Symptoms · Management

Historical perspective

The bakanae disease of rice is known to be present from 1828 in Japan (Ito and Kimura 1931), but the disease was first described by Hori (1898). He named the pathogen as *Fusarium heterosporum* Nees. Sawada (1917), identified the perfect stage of the pathogen and named it as *Lisea fujikuroi* Saw. The name of pathogen was changed later to *Gibberella fujikuroi* Sawada (Ito and Kimura 1931) and the imperfect stage was changed to *Fusarium moniliforme* Sheld. Current name of the pathogen is *F. fujikuroi* (Nirenberg 1976) and the name *F. moniliforme* is no longer used. Bakanae effect of pathogen on plant was described by Kurosawa (1926), where he observed that pathogen is producing a chemical which may be responsible for the stimulation of elongation of stems and suppression of chlorophyll content in infected plants. This finding attracted the different scientists from the fields of plant Physiology, Biochemistry, etc., to know the chemical responsible for disease development. Yabuta and Hayashi (1939) discovered gibberellins from the bakanae disease pathogen *F. moniliforme*.

The name bakanae is a Japanese word which refers to 'bad' or 'foolish' seedlings for the specific elongation symptoms of the disease. The disease is known by different names in different parts of the world. In Japan it is known as *otoke nae* (male seedling), in China white stalk and Fusariosis, in British Guiana *palay lalake* (man rice), in French Equatorial foot rot and bakanae, in India foolish plant or foot rot (Singh and Sunder 1997). It is also known as white head disease and root rot also (Saremi et al. 2008).

Geographical distribution of bakanae disease

The bakanae disease has been reported from all over the globe in all the rice producing countries like Turkey, Pakistan, Thailand, Japan, European countries, America, African countries, California, Philippines, Nepal, Bangladesh, Cameroon, Nigeria, Vietnam, Indonesia, Malaysia, Sri Lanka, Ivory Coast, Uganda, Brazil, Spain, China, Trinidad, Iran, Venezuela, Mexico, etc. (Surek 1997; Khokhar 1990; Kanjanasoon 1965; Desjardins et al. 2000; Nelson et al. 1993; Cumagun et al. 2011). Karov et al. (2009) reported bakanae disease for first time in Macedonia. The disease is emerging as a major problem in the area of South and South East Asia including India, Nepal, Thailand, Indonesia and Japan due to change in cultivation conditions (Bashyal et al. 2016a; Saremi 2005; Webster and Gunnell 1992; Desjardins et al. 2000; Kini et al. 2002). In India, the disease was reported first time by Thomas (1931). This disease has been reported from different parts of country like Uttar Pradesh (Pavgi and Singh 1964), Bihar, Andhra Pradesh (Vidyasekaran et al. 1967), Assam, Maharashtra (Parate and Lanjewar 1987),

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Punjab (Bedi and Dhaliwal 1970), West Bengal (Hajra et al. 1994), Tripura (Sarkar 1986), Odisha (Kauraw 1981), etc. In India bakanae disease is more prevalent in basmati growing states and high disease incidence (Fig. 1) was recorded in different districts of Haryana, Punjab and Uttar Pradesh (Bashyal and Aggarwal 2013; Bashyal et al. 2014, 2016a).

Economic importance of disease

The reduction in crop production due to bakanae disease changes under different locations and at same location under different period of time of crop production. In congenial environmental conditions the disease is known to cause a yield reduction of as much as 70% in different corners of the world (Hajra et al. 1994; Singh et al. 1996). Yield loss of 25% has been reported in Bangladesh (Hossain et al. 2007). Desjardins et al. (2000) reported about 40% reduction in crop yield in Nepal. Bakanae disease is responsible for 20–50% reduction in crop production in Japan while 3.7–14.7% yield reduction has been reported in Thailand (Kanjanasoon 1965; Ito and Kimura 1931). The disease is known to cause a yield loss of 10–50% in Pakistan (Bhalli et al. 2001; Ghazanfar et al. 2013; Khokhar and Jaffrey 2002). In India, bakanae disease has been reported to be more prevalent and more severe in varieties of basmati rice (Bashyal et al. 2014; Gupta et al. 2014). The reduction in crop production of 15–25% have been recorded from different states of India (Pavgi and Singh 1964; Rathaiah et al. 1991; Sunder et al. 2014; Pannu et al. 2012). The disease is known to cause both qualitative as well as quantitative losses to crop produce. The pathogen has been reported to be associated with grains of various basmati rice genotypes (Butt et al. 2011; Bashyal and Aggarwal 2013; Bashyal et al. 2016b) and is having a huge impact on quality of rice grains.

Symptoms

Bakanae disease of rice caused by *F. fujikuroi* is known to produce various kind of symptoms ranging from rotting of seedlings prior to emergence to infection of grains at ripening, seedling blight, crown rot, rotting of root, stunting of plants, etiolation, excessive or abnormal elongation of plants or hypertrophy, sterility and discoloration of grains and production of empty panicles under different climatic conditions around the world (Sun and Snyder 1981; Ou 1985; Webster and Gunnell 1992; Desjardins et al. 2000). The disease is known to appear in main crop as well as ratoon in Japan (Sasaki 1976).The pathogen growth is visible at the coleoptiles just above the soil and also at the joint of lemma and palea in the grains affected by the pathogen (Thomas 1931). The seedlings starts dying 1 week after the sowing in wet nurseries. The infected plants are known to show brown discoloration when the nodal tissues are split opened. Initially the brown discoloration is limited to lower nodes but during later stages the upper nodes also show brown discoloration. Mycelial masses bearing conidia are known to be present inside the hollow internodes. During the high incidence of disease the fungal growth appears on the surface of the nodes and produces pink or white colour on plant surface (Surek and Gumustekin 1994). Thomas (1931) reported adventitious roots development from the lower part of culm as a one of the disease symptom from India. The pathogen forms lesions on the surface of leaves of rice plants (Sasaki 1976). The infected plants are known to exhibit yellowish flag leaves. Some plants may survive up to maturity but they produce tall, lanky and thin tillers. Different types of symptoms are visible in highly susceptible variety Pusa Basmati 1121 in India which includes above ground symptoms as (1) elongated pale yellow seedlings, (2) elongated green plant, (3) elongated and rotted plant, (4) normal and rotted plant, (5) rotting in few tillers, (6) completely rotted plants, (7)

Fig. 1 Field view of bakanae disease in rice variety Pusa Basmati 1121 at different growth stage. **a** elongation; **b** rotting at maximum tillerring stage, **c** empty panicles at panicle emergence stage

elongated plant bearing empty panicles, (8) adventitious root formation (Fig. 2). It produces underground symptoms like (i) rotting and blackening of roots and (ii) adventitious roots (Fig. 3).

The pathogen

The bakanae disease is caused by *F. fujikuroi* Nirenberg but some other species of *Fusarium* such as *F. proliferatum* (Mats.) Nirenberg and *Fusarium verticillioides*

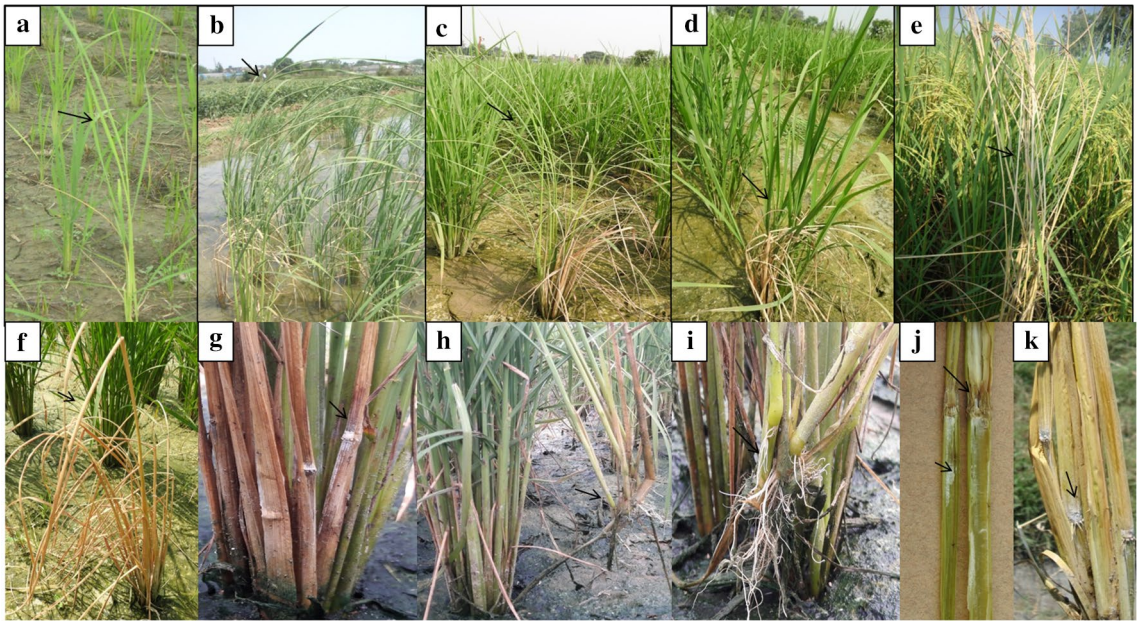

Fig. 2 Different types of above ground symptoms of bakanae disease observed in rice variety Pusa Basmati 1121 **a** elongated pale yellow seedlings; **b** elongated green plant; **c** elongated and rotted plant; **d** normal and rotted plant; **e** elongated plant bearing empty panicles; **f** completely rotted plant; **g** rotting in few tillers; **h**, **i** adventitious root formation; **j** white mycelium in diseased plant; **k** colonization of pathogen in nodal area

Fig. 3 Different types of underground symptoms of bakanae disease observed in rice variety Pusa Basmati 1121. **a** healthy roots; **b** adventitious roots; **c** rotting and blackening of roots

(Sacc.) Nirenberg are also found to be associated with this disease (Amoah et al. 1995; Desjardins et al. 2000). *Gibberella fujikuroi* Sawada is sexual stage for species of genus *Fusarium* under the Liseola section (O'Donnell et al. 1998; Leslie and Summerell 2006). The pathogen *Gibberella fujikuroi* is filamentous fungi which comes under Phylum Ascomycota of Fungi kingdom. The fungi belong to class Sordariomycetes, Hypocreales Order and Nectriaceae family. The pathogen is known to produce ascus and ascospores. The pathogen is known to produce mycelium of white colour. Generally sporodochia are not produced but if present they are pale orange in colour. Asci are produced under perithecia or ascocarps with oval to spherical shape and a size of 250–330 × 220–280 µm. Asci are 4–8 spored piston shaped cylindrical with a size of 90–102 × 7–9 µm. The pathogen is known to have both macro and micro conidiophores bearing macro and micro conidia, respectively. Three to five septate apically tapered and slightly slender macroconidia and 0–1 septate oval or club shaped with flattened base microconidia are produced by the pathogen. Polyphialides produces false heads which after proliferation forms monophialides, and chlamydospores are not formed (Leslie and Summerell 2006).

The disease is known to be caused by species of *Gibberella fujikuroi* species complex which is divided into 10 different fully fertile mating populations (MP A-J) (Kvas et al. 2009; Bashyal et al. 2012). Three different mating populations (A, C and D) from *Gibberella fujikuroi* species complex are associated with the bakanae disease in rice. The conidial stage of MP-A is *F. verticillioides,* of MP-C is *F. fujikuroi* and conidial stage for MP-D is *F. proliferatum* (Amoah et al. 1995; Desjardins et al. 2000). Hseieh et al. (1977) first identified Mating population C (MP-C) from the strains of pathogen infecting rice in Taiwan. In Italy also this mating population has been discovered to be associated with the bakanae disease (Amatulli et al. 2010). Two mating populations A and D were isolated from the rice plant infected with bakanae disease from Australia, USA and Africa, whereas, MP-D has been identified from bakanae infected rice of Asia (Amoah et al. 1995; Desjardins et al. 1997). Among all the species associated with the bakanae disease of rice, *F. fujikuroi* has been found most abundant and most virulent by most of the researchers in their studies all around the world (Nancy 2002; Zainudin and Salleh 2010; Zainudin et al. 2008a, b; Amatulli et al. 2010; Bashyal et al. 2016a). On the other hand, some other *Fusarium* spp. namely, *F. andiyazi, F. moniliforme, F. subglutinans* and *F. sacchari* have been identified to be related with bakanae disease from different rice growing nations by various researchers like India, Bangladesh, Malaysia, Nepal, Pakistan, Italy, Indonesia and Iran (Bashyal and Aggarwal 2013; Quazi et al. 2013; Khokhar 1990; Desjardins et al. 2000; Pra et al. 2010; Saremi and Farrokhi 2004; Wulff et al. 2010; Zainudin et al. 2008a, b).

Three different *Fusarium* species viz. *F. fujikuroi, F. verticillioides* and *F. Proliferatum* were identified to be associated with bakanae disease of rice in India (Bashyal and Aggarwal 2013; Bashyal et al. 2016b). *Gibberella fujikuroi* species complex were reported to be infecting 1–24% of rice seeds in India (Bashyal and Aggarwal 2013). These *Fusarium* spp. varied in bakanae disease symptom production and pathogenicity. Bakanae disease elongation symptoms were produced by *F. fujikuroi* while, crown and stem rot was induced by *F. verticillioides* (Bashyal and Aggarwal 2013). Bashyal et al. (2016b) studied the single and combined effect of three pathogenic *Fusarium* spp. *F. fujikuroi* (Ff), *F. proliferatum* (Fp) and *F. verticillioides* (Fv) on bakanae disease severity on susceptible rice genotype Pusa Basmati 1121. In single pathogen inoculation *F. fujikuroi* was most virulent with disease severity of more than 70% while disease severity was 43% for *F. proliferatum* and 62% for *F. verticillioides.* Disease severity was maximum when rice plants were co-inoculated with Fv + Ff (75%) followed by Ff + Fv + Fp (70%), Ff + Fp (63%) and Fv + Fp (48%). Bashyal et al. (2016a) conducted extensive survey for the bakanae disease in different basmati rice growing states of India and observed high disease incidence (up to 20%) in Karnal and Mathura district of Haryana and Uttar Pradesh, respectively. Out of one hundred twenty-six *Fusarium* spp. isolates collected from symptomatic bakanae diseased rice plants 99.2% isolates were identified as *F. fujikuroi.* On the basis of virulence isolates were further categorized as highly virulent (28.6%), virulent (34.1%) and moderately virulent (37.3%).

Bakanae epidemiology

Fusarium fujikuroi inciting bakanae disease in rice is mainly seed borne in nature but the pathogen also survives in debris of plants and soil. The main source of primary inoculum inciting disease is seeds infected with the pathogen (Watanabe 1974; Anderson and Webster 2005) as the inoculum present in soil is reduced quickly after decomposition of host debris in field situations (Ou 1985; Sun 1975; Kanjanasoon 1965). In harsh conditions the pathogen is known to survive in the form of spores on seed coat and as macroconidia or thick walled hyphae in plant debris in the soil (Watanabe 1974; Saremi and Farrokhi 2004; Ou 1987). Sun (1975) discovered that the pathogen can survive in the soil for a period of 100–120 days in the form of macroconidia or thick wall hyphae. Karov et al. (2009) recorded the very low incidence of bakanae disease when the fields with previous records of disease occurrence were planted with clean and healthy seeds. Puyam et al. (2017)

also investigated the survival of *F. fujikuroi* in the soil and concluded that bakanae pathogen is weak soil inhabitant and survival of the pathogen under field conditions reduces with time. Wind and water are the main source for dissemination of conidia. The seeds are infected by the air borne ascospores produced during flowering of the crop or by the contamination of seeds by conidia at the time of seed harvesting, which after germination infect the seedlings (Sun 1975). In seed pathogen was observed in husk, embryo and endosperm with the maximum colonization in husk region. Embryo infection ranged from 2 to 41% in different cultivars. The isolation frequency of *G. fujikuroi* from infected, untreated rice seeds were 75, 15 and 25% from the hulls, embryo and endosperm, respectively (Manandhar 1999). The fungus is known to become systemic in plants but it is not reported to infect the panicles systemically. The pathogen was observed inside xylem vessels of host plants by Nisikado and Kimura (1941). Conidial germination of the pathogen was maximum in root tissue followed by stem (Sunani et al. 2017).

The best suitable temperature for the infection of pathogen is 27–30 °C while the most suitable temperature for the development of the disease is 35 °C which is best suited for the growth of plant too. The incidence of disease was reduced when the temperature was reduced (Burgess et al. 1996; Saremi and Farrokhi 2004). Mandal and Chaudhuri (1988) observed the reduced population of the pathogen in soil on the application of nitrogenous fertilizers in high dose. More disease was observed in the rice plants which were transplanted as compared to the plants which grown from broadcasting the seeds (Saremi and Farrokhi 2004). Higher disease incidence was recorded in summer crop, dry nurseries under high temperature and high relative humidity conditions. Kanjanasoon (1965) reported that the disease incidence was less in the presoaked seeds as compared to dry seeds.

Genomics of *F. fujikuroi*

During the last one decade whole genomes of the multiple *Fusarium* spp. were sequenced and improved the understanding of host–pathogen interaction including virulence/defence mechanism along with the pathways involved for the same (King et al. 2015). Till now thirteen genomes of *F. fujikuroi* are published from different countries (Bashyal et al. 2017; Niehaus et al. 2017; Chiara et al. 2015; Wiemann et al. 2013; Jeong et al. 2013) as described in Table 1. Based on the genome sequence of *F. fujikuroi* isolate IMI58289, Wiemann et al. (2013) identified a polyketide synthase gene (PKS19) and another that includes a non-ribosomal peptide synthetase gene (NRPS31) are unique to *F. fujikuroi*. Niehaus et al. (2017) sequenced the genome of eight *F. fujikuroi* isolates from different geographic locations and observed the differences in the type of asexual spores (microconidia and/or macroconidia), size of chromosomes and expression profile of secondary metabolite gene clusters. Further, based on secondary metabolite profiling and symptoms produced (rotting and stunting) isolates were characterized as two distinct pathotypes. Bashyal et al. (2017) identified 1194 secretory proteins in the "F250" isolate of *F. fujikuroi.* Out of 356 carbohydrate active enzymes (CAZymes) genes identified, glycoside hydrolase (GH) families like GH3 and GH5 involved in cellulose and hemicelluloses degradation were predominant. Further, α-galactosidases encoding CAZymes GH67 and GH36 deficient in other plant pathogens, were present in *F. fujikuroi*. Pectin degrading enzyme families (GH28, GH78, CE8, PL3, PL1 and PL9) involved in root

Table 1 Whole genomes of *F. fujikuroi* sequenced from different countries

Strain	Species	Country of origin and host	Genome size (MB)	References
F250	*F. fujikuroi*	India	42.4	Bashyal et al. (2017)
IMI58289	*F. fujikuroi*	Taiwan, rice	43.9	Wiemann et al. (2013
FGSC 8932	*F. fujikuroi*	Taiwan, rice	43.0	Chiara et al. (2015
KSU 3368	*F. fujikuroi*	Thailand, rice (1990)	43.1	Chiara et al. (2015)
KSU X-10626	*F. fujikuroi*	Konza Prairie (USA), *Schizachyrium scoparium* (1997)	43.1	Chiara et al. (2015)
B14	*F. fujikuroi*	South Korea, rice	44.0	Jeong et al. (2013)
m567	*F. fujikuroi*	Japan, infected rice	44.0	Niehaus et al. (2017)
MRC2276	*F. fujikuroi*	Philippines, infected rice	45.0	Niehaus et al. (2017)
C1995	*F. fujikuroi*	Taiwan, infected rice	45.8	Niehaus et al. (2017)
E282	*F. fujikuroi*	Italy, infected rice	46.1	Niehaus et al. (2017)
FSU48	*F. fujikuroi*	Germany, maize	46.1	Niehaus et al. (2017)
NCIM 1100	*F. fujikuroi*	India, infected rice	45.3	Niehaus et al. (2017)
B20	*F. fujikuroi*	South Korea, infected rice	44.3	Niehaus et al. (2017)

tissue colonization were abundant in *F. fujikuroi* genome. Phylogenetic analysis conducted based on the whole genome of the 5 isolates (IMI58289, B14, KSU 3368, FGSC 8932 and KSU X-10,626) of different geographic locations indicated that the Indian isolate "F250" is closer to the Taiwan isolate "IMI58289" (Fig. 4). Further, through comparative analysis 12,240 common clusters were identified between the different genomes of *F. fujikuroi*.

Disease management

Ma et al. (2008) evaluated rice genotypes carrying dwarf and semi dwarf genes under field conditions and identified genotypes carrying sd6 of sdq(t) and d2q genes as resistant while genotypes carrying d1 as a susceptible against the bakanae disease. Lu (1994) identified moderately resistant genotype Qingxi 96 at seedling stage was resistant at adult stage, while, seedling stage resistant genotype Longjiao 86074-6 was moderately resistant at adult stage and some genotypes Zupei 7, Dongrong 84-21, G-6, Sui 89-17 were stable and showing moderately resistant reaction at both the stage indicating the bakanae disease resistance may be growth stage specific. Studies on varietal resistance screening revealed that aromatic germplasm and cultivars are more susceptible to bakanae disease as compared to non-scented rice cultivars (Sunder and Singh 1998; Bashyal et al. 2017; Fiyaz et al. 2014, Pannu et al. 2012; Ghazanfar et al. 2013; Gupta et al. 2014). Currently, the high disease severity was observed in cultivars viz., Pusa Basmati 1121, and Pusa Basmati 1509 in Northern part of India, however, other basmati rice varieties viz., Pusa 2511, CSR 30, Pusa Basmati 1401, Pakistani basmati and Dehradun basmati were also susceptible with 0.5–15% incidence in India under field conditions (Bashyal et al. 2016a, 2017; Gupta et al. 2014). Rice genotypes C 4-64 (green base), Karjat x 13-21, BR 4363-8-11-4-9, BR 1067-84-1-3-2-1, IR 58109-109-1-1-3, BR 1257-31-1-1, HKR 96-561, HKR 96-565, HKR 07-40, HKR 07-53, HKR 08-13, HKR 08-22, HKR 08-21, PAU 3456-46-6-1-1, MAUB 2009-1, PNR 600 and RDN 01-2-10-9 were identified resistant by Sunder and Singh (1998). Fiyaz et al. (2014) identified

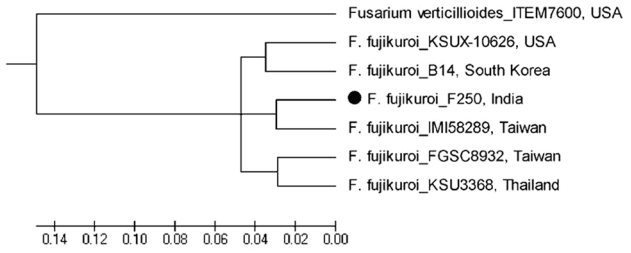

Fig. 4 Whole genome phylogenetic analysis of *F. fujikuroi* sequences. *F. verticillioides* was used as outgroup

rice genotypes C101A51, Athad apunnu, IR 58025B, Chandana, PAU 201, Pusa 1342, Panchami and Varun Dhan as highly resistant, whereas, BPT 5204, Himju, Peeli Badam and Suphala as resistant to bakanae disease. Ghazanfar et al. (2013) screened various rice germplasm through and identified KKS-133 and IR-6 as resistant with 19.82% and 18.80% plant infection. Saremi et al. (2008), Saremi and Farrokhi (2004) identified cultivars Shafagh Fajr, Kadous, Shafagh and Sahel as moderately resistant and cultivar Binam as highly resistant against the foot rot disease. Aggarwal et al. (2017) reported Pusa 1342, IR6582 and Calrose as promising genotype against bakanae disease.

Bakanae disease resistance is identified as monogenic as it was dominant in cv. KS 282 and recessive in cv. IR 6 (Khan et al. 1999). Yang et al. (2006) identified two quantitative trait loci (QTLs) viz., *qB1* in chromosome 1 and *qB10* in chromosome 10 using japonica/indica double haploid population (Chunjiang 06 and TN1). Both the QTLs showed additive effect with almost 13% phenotypic variation by each. Hur et al. (2015), identified a major QTL, named as *qBK1*, on the long arm of chromosome 1 using near-isogenic lines (NILs) derived from a cross between the highly resistant *indica* variety Shingwang and the susceptible *japonica* variety Ilpum, explaining 65% of the phenotypic. Fiyaz et al. (2016) analyzed the RIL population of Pusa Basmati 1121 and Pusa 1342 for the bakanae disease resistance QTLs using QTL IciMapping software and through Interval mapping (IM) identified four QTLs located on chromosomes 1 (*qBK1.1, qBK1.2* and *qBK1.3*) and chromosome 3 (*qBK3.1*). Two QTLs detected on chromosome 1 viz. *qBK1.2* and *qBK1.3* were novel QTLs. The QTL *qBK1.2* was designated as a major QTL and was mapped in 0.26 Mb region between RM10153 and RM5336 where almost 55 annotated genes were identified.

Lee et al. (2018) identified QTL $qBK1^{WD}$ in *japonica* variety Wonseadaesoo accounting for 20.2% of the total phenotypic variation. Further, QTLs qBK^{WD} and *qBK1* were combined (QTLs pyramiding) and the effect of two QTLs together on bakanae disease reistance was 80.2%, which was significantly higher than the individual effect of each QTL.

The most common and widely accepted practice for the management of bakanae disease is the seed treatment with fungicides (Gupta et al. 2015; Bashyal et al. 2016c). Fungicidal seed treatment with thiram, benomyl, thiram + benomyl, thiram + carboxim, thiram + carbendazim, thiophanate-methyl, mancozeb, fludioxonil, prochloraz, iprodione + triticonazole, ipconazole, @ 1–2% of seed weight was effective in different countries viz., Taiwan, Japan, Korea, Iran, Turkey, Pakistan, India, Bangladesh, Nepal and Italy (Ou 1987; Tateishi et al. 1998; Bagga and Sharma 2006; Bagga et al. 2007; Karov et al. 2009; Ora et al. 2011). Propiconazole, triflumizole, prochloraz and ipconazole were also effective against benomyl resistant

strains (Tateishi et al. 1998; Karov et al. 2009). Seedling dip treatments with benlate, carbendazim and topsin were highly effective against the disease (Javed et al. 1996). Benzimidazole fungicide nursery soil drenching @ 0.2% found to be effective against the bakanae disease of rice (Bhalli et al. 2001). Seedling treatment with carbendazim or benlate, (0.1%) for 6 and 8 h reduced the disease incidence significantly and improved the grain yield also (Bagga and Sharma 2006). Tilt 25 EC @ 0.05% was observed effective, but phytotoxic also as it reduced plant height and grain yield under field conditions. The hot water immersion method (Hayasaka et al. 2001), and combination of antagonistic yeasts and thermotherapy was reported effective against the bakanae disease (Matic et al. 2014). Immersing the rice seeds in distilled water and irradiation with plasma reduced the bakanae disease severity from 18.1 to 7.8% depending on the duration of plasma irradiation (Ochi et al. 2016). Out of eleven fungicides evaluated as seed treatment against the bakanae disease Bavistin, Nativo, Carzeb and Sunphanate at 2.5 g/L concentration completely inhibited the growth of the pathogen and significantly reduced the seedling infection (Hossain et al. 2015). Seed treatment and carbendazim-sand mix application @ 1 g/m^2 in nursery beds along with seedling dip for 3 h in 0.1% carbendazim was also observed effective against the disease. Reduction in bakanae disease incidence up to 73.9–35.0% was observed when the foliar spray of carbendazim was given at flowering stage (Sunder et al. 2014). Kumar et al. (2016) observed the foliar spray of Tebuconazole 250 EC reduced the bakanae disease incidence and increased the grain yield.

The treatment of rice rhizosphere by the suspension of *Bacillus oryzicola* (YC7007) @ 2.0×10^7 cfu/ml reduced bakanae severity up to 78% (Hossain et al. 2016). The surfactin-producing *Bacillus* (SPB) strains NH-217 and NH-100 and purified surfactin from them reduced the bakanae disease incidence up to 80% (Sarwar et al. 2018). *Trichoderma asperellum* SKT-1 (Eco-hope, Kumiai Chemical Industry Co.) and *Talaromyces flavus* SAY-Y-94-01 (Tough-block, Idemitsu Kosan Co.) have been registered as biofungicides in Japan for the control of Bakanae disease (Kato et al. 2012). The seed treatment of biocontrol agent *Talaromyces* sp. isolate (KNB-422) was observed effective against bakanae disease of rice (Tateishi et al. 2006). *Talaromyces flavus* application reduced bakanae disease severity and incidence by 70–75% in India and increased aboveground biomass, grains/panicle and yield of rice (Rawat et al. 2016; Bashyal et al. 2016c). Integrated management module against the bakanae disease of rice which is helpful to reduce 95% incidence of bakanae disease of rice was developed. Effect of nursery drenching with Carbendazim was evaluated against bakanae disease of rice. Eighteen days old seedlings of rice variety Pusa Basmati 1121 were drenched with different concentration of carbendazim and transplanted after 5 days of treatment. Minimum disease incidence was observed in 0.2% carbendazim. Seeds of each treatment were subjected to residue analysis. Results indicated that the use of 0.2% carbendazim as nursery drenching is safe without any residual effect (Anonymous, 2018).

Future perspective

Bakanae disease is emerging as a potential threat in rice cultivation worldwide including India where it is responsible for the tremendous loss in basmati varieties. New effective sources for bakanae resistance need to be identified for resistance breeding for alternative disease control measures. As highlighted by different studies, *F. fujikuroi* is highly variable in nature therefore, identification of pathotypes/races and resistance sources against them is of utmost important. Identification of differential hosts will be helpful to characterize the pathogen in specific group. As pathogen is seed borne in nature, development of field based, easy and reliable diagnostics will be helpful to reduce the primary inoculums source. Study on the manipulation of different cultural practices to decrease pathogen population needs to be conducted. Integrated disease management modules needs to be developed and validated under field conditions. Further scope is there to develop and evaluate the effective fungicide/chemical molecule/biopesticide and its need based application against bakanae disease.

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