



Exploring New Sources of Resistance for Insect Pest and Diseases of Rice

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SUMMARY

In the present scenario of rice pest management, host plant resistance is playing a pivotal role. It is the easiest way to reduce pesticide load in rice ecosystems as well as to mitigate pest problem under adverse environmental conditions. With the development of nitrogen responsive high yielding rice varieties and hybrids, several insect pests and diseases assumed major status. Significant effort has been made in the past to develop resistant varieties against different pests, particularly, brown plant hopper, gall midge, blast and bacterial blight with identified resistant genes. But gradually, most of the developed varieties have lost their resistance resulting in more frequent and severe pest outbreaks. Therefore, again the search has begun for new resistant donors of different pests from the existing vast germplasm collection of the country including those identified in the past. The mechanism of resistance in identified genotypes has to be studied by assessing its effect on pest biology and behavior or disease infection pattern. Molecular marker analysis of resistant genotypes (donors) will give an indication of the presence of a known or new gene effective against the particular pest. A set of donors should always be in place to be utilized in resistance breeding programme for the development of pest resistant varieties, which will benefit rice farmers of the country.

1. Introduction

Productivity of rice is facing severe threat from biotic stresses, particularly insect pests and diseases, causing huge yield loss. Among the biotic stresses, insect pests like yellow stem borer (YSB), gall midge, brown plant hopper (BPH), white backed plant hopper (WBPH), and leaf folder are the major problems whereas among the diseases, blast, brown spot, bacterial blight (BB) and sheath blight (ShB) are most destructive to the crop. Recently, insects and diseases like case worm, swarming caterpillar, mealybug, gundhi bug, false smut, bakanae and sheath rot have emerged as the major problem in many rice growing areas of the country. Stored grain pests also are gaining significant importance in causing post harvest losses among which the rice weevil and angoumois grain moth are considered to be the most common pests. Moreover, rapid change in the virulence characteristics of plant pathogen/ insect populations pose continuous threat to existing popular rice varieties as well as for development of a virulent pathotype or biotype. Pesticide application has been followed by farmers as the major option for pest management which in turn, is creating



environmental pollution as well as health hazards by contaminating the food chain. Host plant resistance has the potential to be an alternative for effective, economic and ecofriendly means of pest management in rice independent of pesticide use. The resistance of rice plant to biotic stresses may be an inherited one (Resistant through donor) or it may be induced by application of an elicitor, activating the defense mechanism of the plant.

Resistant sources/donors are most important as they are the key to success of resistance breeding for developing pest resistant varieties. Keeping in view of the emerging pest problems in rice and the role of resistant donors in controlling these pests, the main objective should be to identify resistant donors against insect pests and diseases from the vast gene pool of the country. This can be achieved by evaluating large number of genotypes through standard screening techniques, supported by study on their mechanism of resistance. Mechanism of plant resistance against insects can be assured by biochemical analysis of the plant for its resistance-imparting contents such as sugar, silica, phenol *etc.* as well as antixenosis, antibiosis and tolerance studies. The resistance mechanism against diseases is to be ascertained through study of virulence patterns. Molecular characterization of identified resistant donors is necessary to look for the presence of resistance genes using reported markers or identification of new genes, if any. In the case of induced resistance, identification of effective elicitor/s is the prime need for inducing resistance in a popular but susceptible rice variety.

2. Host plant resistance

Plant resistance is an inherited characteristic of a host that lessens the attack of a pest, may it be the insect, disease, nematode or other organisms. As per the recent pest management strategy through IPM, the use of resistant varieties should be the major or syncing with other control measures. Host plant resistance provides an efficient, economical, ecologically acceptable and safe means of crop protection. Resistant cultivars are the most durable, economical and practical means of tackling pest problems, being compatible with all other components of IPM. Besides constitutive resistance, the plant resistance to pests can also be induced either by endogenous or exogenous signaling molecules. Silicon, chitosan, plant growth promoting rhizobacteria (PGPRs), jasmonic acid (JA), jasmonoyl-isoleucine (JA-Ile), salicylic acid (SA) and ethylene (ET) are some of the well known elicitors inducing plant to put forth its resistance. These exogenous material or inducers are not directly toxic or inhibitory to the pests but cause the plant to increase its level of resistance. Though several donors have been identified in the past against several insects and diseases and many varieties were developed by utilizing them, most of these donors as well as varieties have lost their resistance in the present day scenario either due to continuous exposure to the pest or due to development of more virulent population. Screening data of released resistant varieties at National Rice Research Institute (NRRI) gave an indication of gradual breaking down of their resistance.

The genotypes, still retaining the resistance are not popular among farmers due to low yield or cooking quality or taste or are not utilized to develop new varieties due to



their poor combining ability. Hence, identification of donors, resistant to different rice pests, should be a continuous process to keep enough of such genotypes in store so that the development of pest resistant varieties will be sufficient and continuous to combat the pest situation in rice successfully. Further, the future challenge is to exploit the elicitors of induced defense in rice for pest management especially for borer pests. There is also a need to test the effect of foliar application of silicon on natural enemy foraging and impact. The research should focus on studying the integration of cultivar resistance and cultural controls, especially soil silicon amendment, against the entire pest complex in rice.

3. STATUS OF RESEARCH

3.1. Host plant resistance against insect pests

3.1.1. Brown plant hopper: The International Rice Research Institute, Philippines initiated studies on varietal resistance to BPH in 1966 with efficient mass- screening techniques. The basic technique has been introduced in Japan, Korea, Taiwan, India, Thailand, Sri Lanka, Indonesia and Solomon Island. The BPH resistant selections, IR 26 and IR 1561-228-3, were grown widely in the Philippines during 1974 and 1975. Both cultivars have *Bph1* gene for resistance. IR36 and IR38 which have the *bph2* gene for resistance to BPH were released by the Philippine Government during 1976. Varieties ASD 7 and Mudgo were resistant in the Philippines, Japan, Korea, Taiwan, Thailand and Indonesia, but susceptible in India. The different reaction is due to biotype formation. Biotype 1 in Southeast Asia (Philippines, China, Japan, Korea, Malaysia, Taiwan, Thailand); Biotype 2 in Philippines, Solomon Island, Vietnam; Biotype 3 in Southeast Asian countries (Philippines, Taiwan); Biotype 4 in South Asian countries of India, Bangladesh and Sri Lanka are widely distributed. Afterwards, though many resistant gene/QTLs were identified in different genotypes (Fujita et al. 2013), most of them have already lost their resistance against BPH population of India.

Following extensive damage by BPH during mid 70s, breeding for resistance was intensified in India which culminated in release of varieties like Jyothi in Kerala, Sonasali, Vajram, Chaitanya in AP, Neela and Udaya in Orissa and Manasarovar across the country. Some common donors were Ptb 33, Manoharsali, Rasi, Ptb 10, Ptb 20 etc. Afterwards, many BPH resistant varieties were released for different ecologies all over India and were released in different states (Krishnamurthy et al. 1995). By 2006, more than 65 varieties were released with resistance/tolerance to the insect. But, most of these varieties were developed keeping higher yield as the primary criteria and were later found to be resistant/tolerant to BPH. Therefore, in most cases after few years, the resistance breaks down and leading to the BPH menace. Several highly resistant donors have been identified at NRRI, Cuttack through green house screening according to the Standard Evaluation System during 2000-2016.

At NRRI, three thousand rice genotypes from NRRI Genetic resources were screened for their resistant reaction to BPH under greenhouse condition during the



years 2001 - 2016. More than 80 genotypes were found highly resistant with score 1. Some of them are – CRRI accession numbers 35677, 35703, 34997, 35003, 35927, 35070, 35155, 35183, 35184, 35228, 35181, 34969, 34993, 34997, 35014, 38448, 38448, 38449, 38450, 38452, 38459, 38469, 38500, 38530, 38552 and 38552C. One hundred lines, evolved from resistance breeding for BPH in the background of resistance from Salkathi (CR.Ac.35181) and Dhobanumberi (CR.Ac.35184), 10 lines were highly resistant with score ‘1’ whereas 36 lines showed resistance of score ‘3’. The lines are : CR 2711-76, CR CR2712-22711-114, CR 2711-139, CR 2711-149, CR2712-2, CR 2712-11-1, CR 2712-11-13, CR 2712-229, CR 2713-8 and CR 2714-2, out of which CR2711-114, CR 2711-76, 2711-139, CR 2711-149 and CR2712-2 were found highly resistant (Jena and Sahu, 2013). Out of seventy entries from IRRI screened at NRRI, IR69726-29-1-2-2-2, IR70454-144-1-1-3-2 and IR72894-35-2-2-2 were found resistant. Out of 220 released varieties, IR-64 MAS and Hazaridhan scored ‘1’ whereas CR-1980-1, Lalat MAS and Satykrishna showed resistance of score ‘3’. Six hundred farmers’ varieties of Odisha were evaluated and 21 were highly resistant (Jena et al. 2006; 2015).

Molecular approach for BPH resistance was initiated at NRRI with a DBT sponsored network project on “Identification and Functional Analysis of Brown Planthopper Resistance Genes in Rice”. Under the programme, mapping population was developed from the cross TN1/Salkathi. Phenotyping was made of 300 RIL populations under artificial infestation conditions and the putative QTLs associated with the resistance to BPH were identified (Mohanty et al. 2017).

The line CR2711-76 is also found to be resistant to multiple pests of rice (AICRIP Report 2012-13) and having the resistant gene Bph 31 (Prahallada et al, 2017). Three accessions of IRRI Philippines, IR 73382-80-9-3-13-2-2-1-3-B (IR 64 x *O. rufipogon*), IR 75870-8-1-2-B-6-1-1-B (IR64 x *O. glaberrima*) and IR77390-6-2-18-2-B (IR69502-6-SRN-3-UBN-1-B x *O. glaberrima*) were found highly resistant against NRRI population of BPH . After being used in popular varieties like MTU 1010 and Swarna, three lines each from F3 lines of MTU1010/Swarna x IR 75870-8-1-2-B-6-1-1-B were highly resistant against BPH. Four genotypes from Assam Rice Collection (ARC), ARC - 333, 356, 11324 and 11309 were also found highly resistant. Two accessions of doubled haploid lines were highly resistant.

3.1.2. White backed planthopper: In general white backed planthopper (WBPH) has not received as much research attention as BPH. However, 14 loci have been identified for WBPH resistance. Since, it mainly occurs as a mixed population with BPH, identification of single resistant donor is as important as identification of common resistant donors for both. At IRRI, two resistant genes, *Wbph7* and *Wbph8* has been identified from *O. officinalis*. Four varieties, IR48, IR52, IR60 and IR62 were reported as moderately resistant. More than 300 cultivars resistant to WBPH have been identified and 80 of them have been analyzed genetically (Brar and Khush, 2009). Four donors (N22, ARC 10239, ADR 52 and Podiwi A8) have been identified at IRRI and used to develop hopper resistant varieties. Several genes/QTLs have been identified for resistance to the pest (Fujita et al. 2013).



In India, *O. officinalis*, *O. punctata*, and *O. latifolia* showed high levels of resistance to the pest. IR 2035-117-3 has been used in breeding programmes for *S. furcifera* resistance (Padmavathi et al. 2007). Antibiotic Mechanisms of resistance to *S. furcifera* include reduction in feeding on the resistant cultivar Rathu Heenati could be attributed to the presence of certain water-soluble inhibitors in the plant. Low chlorophyll, low sugar, low amino acid and high phenol content in the plant had contributed for the resistance.

At NRRI, 167 rice genotypes from NRRI rice genetic resources and Punjab Agricultural University (PAU) were screened under net house condition. The genotypes IR 64 and TN1 were used as resistant and susceptible checks, respectively. The entries IC568061, AC 111, AC 1066, AC 1073, AC 124, AC 1418 were found highly resistant with score '1' whereas 1552(2) and 1552(8) from PAU, IC567998, IC568060, IC568065 and IC568082 were of score '3'. From 65 accessions reported resistant earlier against WBPH at NRRI, only four accessions, i.e., AC 34222, AC 34264, AC 38468 and AC 42425 were highly resistant at present against WBPH.

3.1.3. Yellow stem borer: Out of 17000 accessions screened against YSB at IIRI upto 1987, only about 40 *O. sativa* accessions and 80 wild rice accessions were found to have resistance against yellow stem borer. From India, CO 7, CO 15, CO 21, Ratna, TKM 6 and WC 1263 were identified as donors. Efforts were made to develop resistant/tolerant varieties by using donors such as TKM6, CB 1, CB2 but none were good combiners to produce desired level of resistance. Still, some accessions showed moderate level of resistance which needs further evaluation. TKM 6 was found tolerant against striped stem borer, *Chilo suppressalis* and was utilized in breeding programme. The cultivars IR 36 developed at IIRI and Ratna developed at NRRI were having highest level of resistance.

Thousands of entries have been screened at NRRI against yellow stem borer (YSB). But most of them succumbed to the pest after continuous exposure for 2-3 years. One tropical japonica line WC-152 and a doubled haploid line SS-5 showed zero SES score against YSB in consecutive two years of screening against the susceptible check TN1 with damage score of 5. The inherent capacity of the pest to adopt a variety after 2-3 years exposure as evident from the screening data of NRRI for the past several years has not left avenue till now for choosing a highly resistant donor. Seven hundred and ten rice cultivars from NRRI that were evaluated against YSB in 2007, resistant cultivars with score 1 (below 5% white ear head) were NDR 402, CR 580-5, LPR 256, LPR 85, LPR 14, LPR 96-10, LPR 56-49, LPR 50, Kariawa 4, TCA 12, Bazail 65, Nali Hazara, Janaki, OR 1358-RGA-4, OR 1529-28-2, TKM 6, ARC 10660, Litipiti, Daonara, Chadhei Nakhi, Dahijhil, Brahmanbojni, Mahalakshmi, Jogen, Punshi, Triveni and Saket-4 as against Jaya the susceptible check with score 9 (28.1% WEH). Those are to be screened again for confirmation of resistance.

3.1.4. Gall midge: Wide spread cultivation of some of the resistant varieties carrying a single resistance gene has led to evolution of virulent populations, known to as biotypes, that are capable of overcoming the resistance. Existence and emergence of



new and virulent biotypes of the rice gall midge resulted in the breakdown of resistance in many of the popular gall midge resistant varieties. So far, 11 resistance (R) genes (designated Gm1 through Gm11) have been identified from different rice varieties (Himabindu et al. 2010). Seven distinct gall midge biotypes, differing in their virulence against these R genes have been reported (Vijaya Lakshmi et al. 2006). Using three or four of these sources of resistance, more than 60 gall midge-resistant rice varieties have been developed and released for commercial cultivation since 1975 (Bentur et al. 2003). Improved rice varieties carrying Gm1 or Gm2, however, have lost their resistance against gall midge in most of the rice growing areas. Exceptionally, varieties deriving resistance from Ptb21 have displayed resistance against five of the seven biotypes as per AICRIP report, 2006. Keeping this in view, thorough screening of various available rice germplasm is necessary in order to get new source of resistance.

Systematic evaluation of germplasm by NRRI for gall midge resistance during the 1950s - 1970s at hot spots such as Cuttack and Sambalpur in Odisha and at Warangal in Andhra Pradesh under field conditions resulted identification of sources such as Eswarakora, Ptb 18, Ptb 21, Siam 29, and Leuang 152. Some accessions of wild species of *Oryza* such as *O. brachyantha*, *O. coarctata* (now *Porteresia coarctata*), *O. eichingeri*, *O. granulata*, and *O. ridleyi* were reported to be gall midge resistant. None of the donors displayed resistance against all the six biotypes. Only Orumundakan was resistant against 5 biotypes. Ptb 27, Dhanala 27, Ptb 18, Ptb 21, ARC 5959 and 22 other accessions were reported resistant at NRRI during 1964, 1965 and 1974. Also studies prior to 1975 suggested the prevalence of biotype 1 at NRRI as differentials W1263 (with the *Gm1* gene) and Leuang152 (*Gm2*) were resistant. Subsequently, this population evolved into biotype 2 by acquiring virulence against resistance conferred by the *Gm1* gene. The present study shows resistance of W1263 whereas phalguna and ARC 5984 were susceptible. In recent years, all the known gene differentials of gall midge having resistant genes 1, 2, 3, 4, 5, 6,7, 9,10 and 11 showed susceptible reaction to NRRI gall midge population (Biotype 2), either showing breakdown of resistance or indicating a population change which is a researchable issue.

3.1.5. Leaf folder: The rice leaf folder has recently emerged as an important insect pest of rice in many Asian countries under changed climatic scenario. Management of the pest with insecticides is becoming costly and there are reports of resurgence. So, there is a need for the development of resistant cultivars to minimize the yield losses. In India, the varieties like GEB 24 (a mutant of Konamani) and TKM6, Ptb 33 were reported as resistant to leaf folder (Punithavalli et al. 2013). Similarly, TKM6, GEB24, CO7, PTB33, ARC10982, Shete, Bir-Me-Fen, Kaohsiung Sen Yu 169, *O. rufipogon* and *O. brachyantha* were reported as resistant genotypes. However, Ishaq A. (2014) observed that Kaohsiung Sen Yu 169 was susceptible, TKM6, Ptb 33 and GEB24 were moderately susceptible and only ARC10982 was moderately resistant against leaf folder. Likewise, Genotypes like CR 56-17 and its donor parents GEB-24, CR 190-103 and 294-548, Bundeji, Harisankar, Sunakathi, Surjana, Juli and Sana chinamala and Chandanpedi were identified as resistant varieties at NRRI during 1985 to 1998. Genotypes such as RP 1746-1770-209; RP 2542-179-298; ARC 11281; RP 2543-136-



277; RP 2572-3-340; RP 2572-5-342; RP 2572-24-7 were relatively less susceptible while IR 8, IR 5 and TN 1 were highly susceptible. Three hundred sixty entries screened for resistance against leaf folder under field condition showed AC 42738, IC 569085, IC 569017 with less than 1% leaf damage and Konark, Rudra and Mahalakshmi had less than 5% damage against 12.5% leaf damage in susceptible check TN1. Using the biotechnological tools, two transgenic rice lines, expressing Cry1Ab, CpTI and Cry1Ac showed significantly lower damage at different developmental stages. Further, studies on mechanism of resistance need to be conducted to confirm either a tested rice variety/line is resistant or susceptible to the pest.

3.1.6. Stored grain pests: There is common belief that the aromatic fine rice varieties are more susceptible to insect attack. Khan and Halder (2012) reported Kalijira, an aromatic fine rice variety (locally known as polao rice), to be less infested by the rice weevil. The degree of susceptibility of the rice varieties from the highest to lowest susceptibility was Lata (755) > Nazersail (695) > Minicate (654) > Pariza (482) > Kataribhog (456) > Kalijira (402). Parboiled rice varieties were reported to be more susceptible to stored pest infestation (Islam 2007).

At ICAR-NRRI, out of 20 rice varieties screened against *S. cerealella* multiplication, only Annada showed tolerant reaction upto 90 days. Other varieties like Heera, Kalinga III, Vandana, Sattari, Sneha, Dhaula, Naveen, Jaya, Indira, Saket-4, Tara, Kalinga III, Pooja, Panidhan, Pusa Basmati-1, Basmati 370, Durga and Ratna were susceptible and Tapaswini was highly susceptible to storage insects. So far many scientists in different countries have sorted out countless varieties of cereals resistant against *S. cerealella* to incorporate useful information in breeding programme.

3.1.7. Induced resistance: Silicon amendment conferred resistance to the rice leaf folder (Han et al. 2015), by increased leaf abrasiveness against *Spodoptera exempta* and *Schistocerca gregaria*. Nanosilica and Jasmonic acid were found to be effective in controlling the pests like army worm (Stout et al. 2009). Soil incorporation of Si and K present in fly ash mitigated the incidence of the rice stem borer, soil application of Si reduced the percentage of white head caused by *Chilo partellus* in Parto cultivar (Hosseini et al. 2012) and enhanced plant resistance to BPH (Yang et al. 2017). The induced resistance by JA did not produce any phytotoxicity (Senthil-Nathan et al. 2009). Methyl Salicylate (MeSA) at 100 mg L⁻¹ exhibited greater mortality against rice leaf folder (Kalaivani et al. 2017).

3.2. Host Plant Resistance against Diseases

3.2.1. Blast: Yang et al. (2017) screened 358 rice varieties for the presence of 13 major blast resistance (R) genes against *M. oryzae* using functional markers out of which 259 varieties were having one to seven R genes. Twenty-six SSR markers associated with blast resistance in a set of 276 indica landraces from China and few from different parts of the world were reported. Genome wide association mapping (GWAS) identified 16 LAFBR and 20 resistant cultivars with seventy-four candidate genes, which encode receptor-like protein kinases, transcription factors, and other defense-related proteins (Zhu et al. 2016). The identified markers associated with blast resistance can be



validated for their effectiveness in a variety of genetic backgrounds and can be helpful in the pyramiding of QTLs from different sources through marker-assisted selection.

The genetic diversity for eight resistant genes against rice blast, was assessed in landrace collections of Manipur, India and the presence of six to seven genes in rice accessions from the North Eastern state of Manipur was related to high level of resistance (Mahender et al, 2012). The rice blast resistant *Pi9* gene was analyzed in 47 rice germplasm using the dominant STS marker 195R-1/195F-1 derived from the Nbs2-*Pi9* candidate gene and only six were positive for the *Pi9* gene (Imam et al. 2013). Molecular screening of *Pi2* gene was carried out on 61 landraces of rice using gene based marker NBS2P3 and NBS2R derived from Nbs4-*Pi2* candidate gene that generates a monomorphic band of 1.8 kb. Restriction digestion of PCR product with *EcoRI* enzyme, however, revealed polymorphism between susceptible and resistant lines. Out of 61 landraces, only five landraces had *Pi2* gene type banding pattern. The five landraces positive for *Pi2* gene are from Sikkim and Jharkhand (Alam et al. 2015).

Phenotyping followed by genetic diversity study at NRRI, of eighty rice varieties released by the institute, has been completed using molecular markers linked to twelve major blast resistance (*R*) genes viz. *Pib*, *Piz*, *Piz-t*, *Pik*, *Pik-p*, *Pikm*, *Pik-h*, *Pita/Pita-2*, *Pi2*, *Pi9*, *Pi1* and *Pi5*. Out of which, nineteen varieties (23.75%) showed resistance and twenty one were moderately resistant (Yadav et al. 2017). Among the 1314 germplasm accessions (ICAR-IIRR, NBPGR) evaluated for leaf blast resistance at Hazaribagh, 19 accessions (IC no. 245865, 246277, 246403, 246274, 454167, 121865, 199562, 218270, 245927, 246012, 246228, 246273 and 246659) were highly resistant (SES scores 0, 1, 2).

3.2.2. Bacterial blight: The most effective resistance gene *Xa21* was reported from wild rice by Ikeda et al. (1990), which was effective against all the races of *Xoo* in India. Long-term cultivation of rice varieties carrying single resistance gene has resulted in a significant alter in pathogen-race frequency and consequential breakdown of resistance. An example of this is failure of *Xa4* which was integrated widely in many high yielding varieties of rice via conventional breeding. Extensive cultivation of varieties carrying *Xa4* has lead to the predominance of *Xoo* races that can overcome resistance conferred by this gene. One concrete solution to resistance breakdown is pyramiding of multiple resistance genes in the background of modern high yielding varieties. More than 36 resistance genes have been identified and designated in a series from *Xa1* to *Xa41* till now. The effectiveness of *R* genes varies over locations due to geographical structuring of the pathogen.

Oryza barthii found to have resistance against most of the races of *Xoo* in India especially in the Eastern India. Works at NRRI, reported BR-4-39-51-2, BR-51-49-6, IR3796-14-2, ARC-5925 & ARC 5943 as highly resistant and another 50 lines as resistant to BLB kresek phase. A total of 5000 lines were screened for bacterial blight resistance and 50 were resistant. Some of them are AC 36797, 35799, 36370, 36362, 35720, 36357, 36253, 35734, 36369, 35719, 35740, 36283, 35714 and 36294.

3.2.3. Brown spot: Three QTLs, qBS2, qBS9 and qBS 11 had been identified against the disease in cultivar Tadukan with latest qBS 11 having major effect (Sato et al.



2008). Satija et al. (2005) identified 15 *Oryza sativa* entries out of 124 classified as resistant (less than 5% severity). Conversely, Hossain et al. (2004) identified one resistant line out of 29 entries. Goel and Bala (2006) evaluated 219 wild rice accessions with diverse origin belonging to 15 *Oryza* species encompassing all the six genomes for their resistance to brown leaf spot and found that 15 lines were resistant while 78 lines were moderately resistant.

Synthesis of polyphenols and their oxidation products were observed to be associated with the phenomenon of resistance. A high correlation has been existing between the levels of phenols, lignin, flavonoids, silicon and oxidative enzymes in rice leaf tissue and the susceptibility of rice lines Giza 180 and Arabi to brown spot. However, Katara et al. (2010) identified 10 QTLs, some of which may be common to those of Sato et al.

Work at NRRI revealed that, Out of 573 Assam rice collections (ARC) screened against brown spot disease of rice, only 22 accessions were found moderately resistant. Those are ARC – 5846,5918, 5956, 5550, 6017, 6058, 6101, 6110, 6170, 6622, 7080,7335, 10618, 10670, 10922, 10934, 11206,11434,11566, 11641, 11679 and 12006.

3.2.4. Sheath blight: Many workers employed various methods for testing varietal resistance against this disease including (i) field tests using artificial inoculation (ii) seedling test (iii) inoculation at different stages of plant growth (iv) tests in pots and (v) sheath inoculation test. The results showed that, tall varieties with a few tillers were more resistant than short varieties with many tillers and resistant genes were located in tall varieties. In comparison with field ShB evaluation, the controlled chamber or mist-chamber assays were simple, precise and more reliable methods in tagging sheath blight resistance. Two wild rice species viz. *Oryza australiensis* and *O. nivara* were resistant against *R. solani*. Among different red (*Oryza sativa*) and wild rice (*O. alta*, *O. lativa*, *O. grandiglumis* and *O. glubepatula*) populations, none were found resistant (Santos et al. 2002).

Work at NRRI revealed that, A tolerant donor CR 1014 has been identified for disease, which has been utilized for developing mapping populations and transferring the tolerance gene to mega variety 'Swarna'. So far, out of 604 farmer's varieties from different parts of Odisha were screened by found that 31 varieties were found moderately resistant, 56 varieties showed tolerant reaction. A total of 90 NRRI released varieties were screened and 14 were moderately resistant and 16 were tolerant. Farmers varieties such as Biradia Bankoi, Dhusara, Ganjamgedi, Kalaketiki, Panikoili, Rajamani-K, Latamahu, Kendrapara-Kalama, Pasakathi, Tulasimali, Gangabhalu, Kandhamal-Jhalaka, KanakChampa, K-Balisara-LaktiMarchi, LaxmiVilash, Magra-P, Bolangir-Baidipali-Mahipal found moderately resistant/tolerant and NRRI varieties CR-1014, IR 64 MAS, CR Dhan-306, CR Dhan-601, CR Dhan-701, Kalinga-III, Satyakrishna, Gayatri, Reeta, Utkalprava, Geetanjali, Hanseswari, Binadhan 8, Varsadhan, Wita 9 found moderately resistant/tolerant. During 2012-13, 17 genotypes namely, Tapaswini, Annapurna, Swarna, Swarna sub 1, Tetep, CR 1014, ADT 39, Manasarovar, IET 19346, IET 20443, IET 19790, IET 20252, IET 17885, IET 17886, IET 19140, IET 20755 and IET 20216 were screened against the disease and results showed one genotype, CR 1014



as moderately resistant, four genotypes Tetep, Manasarovar, IET 17886 and IET 20443 as tolerant and rest twelve genotypes were susceptible to highly susceptible.

3.2.5. False smut: The resistance of rice genotypes to false smut under natural disease incidence was reported by various workers. Out of the seven rice genotypes screened, IRAT 170 was highly resistant, Ex-China was resistant (disease severity score < 1% to false smut), ITA 316 was moderately resistant (disease severity score < 5%). Genotype ITA 150 was susceptible, while ITA 315, ITA 335, and FARO 3 were highly susceptible with disease severity scores > 20%. The resistance level of Japonica type ranged from 20.37 to 92.90%, whereas, resistance level of Indica rice ranged from 68.15 to 83.21%. Also hybrid rice showed similar Indica rice behaviour whereas their resistance level ranged from 66.82 to 81.88% (El-Shafey 2013).

Seven varieties viz., Ptb 7, Ptb 23, Ptb 24, Ptb 32, Ptb 36, Ptb 42 and Ptb 46 were free from disease when screened under field condition (Raji et al. 2016). Out of 20 varieties screened, the varieties Harsha and Vaishak were found highly resistant and Makom, Thekkancheera, Pavizham and Karthika were resistant and Kanakom, Revathi and Prathyasha showed moderate resistance to the disease (Rashmi et al. 2016). Works at NRRI revealed that, Ranjit and Luna Suvarna, were free from infection. Whereas CR Dhan 907, CR Dhan 303, Nua Kalajeera, Ketakijoha, Nua Dhusara, Nua Chinikamini have exhibited moderate resistance against false smut pathogen.

3.2.6. Bakanae: Rice materials carrying dwarf (*d1*) and semi-dwarf (*d29*, *sd6* or *sdq(t)*) genes are useful in resistant breeding program. Recent studies have reported thirteen genotypes with moderate or high resistance, five genotypes with medium resistance, and one genotype with moderate resistance, respectively. Fiyaz et al. (2016) reported eight highly resistant, four resistant, thirty-three moderately resistant genotypes through high throughput screening protocol. Moreover, using inclusive composite interval mapping, three quantitative trait loci, *qBK1.1*, *qBK1.2*, and *qBK1.3*, regulating resistance of rice basmati to *Fusarium fujikuroi* were reported. Two quantitative trait loci (QTLs) on chromosome 1 and 10 were found by an *in vitro* evaluation of the Chunjiang 06/TN1 DH population (Yang et al. 2006). Despite of the necessity of identifying resistance genes and the underlying mechanisms of resistant varieties developed, genetic studies on bakanae disease resistance in rice need to be exploited.

3.2.7. Sheath rot: Sixty deep water rice entries were screened to sheath rot disease and reported the cultivars viz., MDR40049, CN 1035-61 and OR-090-3-158 as resistant with less than one percent infection. Of the rest, 32 showed moderate resistant and other 25 showed moderately susceptible reaction. Sahu and Parida (1997) studied the response of 60 rice breeding lines against sheath rot. Out of 60 lines tested, three lines were highly resistant, 18 were resistant and 33 were moderately resistant to the disease. Seed inoculation of rice varieties like BPT-5204, MAS-26 and MAS 946-1 by soaking of seeds in conidial suspension (10^5 conidial ml^{-1}) of *S. oryzae* overnight was standardized by Mahadevaiah et al. (2016). Twenty aromatic rice genotypes were screened against sheath rot of rice. Less disease incidence were recorded viz., Boga Jalsi, Boga Joha, Monika madhuri Joha, Tulsi Joha, Goul poriya Joha, Bokul Joha



Monipuri Joha, Keteki Joha, and higher disease incidence were recorded *viz.*, Kameni Joha, Badshabhog, Jalsa Joha, Krishna Joha (Singh and Das 2015).

Inspite of the efforts at NRRI for last several years, the availability of resistant genotypes for rice pests at present is very scanty except for BPH, blast and BB (Table 1). Therefore, we should continue evaluating genotypes to obtain resistant donors for other pests, particularly for YSB and sheath blight, which are of economic importance. Further, there is a need to evaluate previously identified genotypes against different pest ecotypes, which may vary in reaction.

Table 1. Status of resistant genotypes identified against rice pests at NRRI, Cuttack.

Insect/Disease	Source	R/HR* genotype	MR
BPH	NRRI gene bank, breeding lines of NRRI, IRRI	>60	-
WBPH	NRRI gene bank	07	-
Gall Midge	NRRI gene bank,	10	01
Yellow stem borer	NRRI gene bank	-	03
Bacterial blight	NRRI gene bank	43	-
Rice leaf Blast	NRRI gene bank	35	-
Brown spot	NRRI gene bank	-	03
Sheath blight	NRRI gene bank	-	02
False smut	NRRI gene bank	02	06
Tungro	NRRI gene bank	-	09
Angoumois grain moth	NRRI gene bank	-	01

4. KNOWLEDGE GAPS

Most of the varieties are developed keeping higher yield as the primary criteria and were later found to be resistant/tolerant to pests like BPH. Therefore, in most cases after few years, the resistance break down occurred leading to the havoc of BPH menace. Several resistant donors were identified through screening, but the detail of the mechanism operating for resistance is not worked out properly including molecular basis of resistance. Though several resistance loci have been reported for different pests, most of these are difficult to use during marker-assisted selection due to thorough resolution of some genetic analyses, limited access to donor varieties, and the widespread virulence of insect pests and diseases against certain resistance genes. Resistant donors for most of the necrotrophic pathogens as well as insects such as YSB, leaf folder, case worm and gundhi bug are not yet fully explored. Phenotyping, genotyping, mapping, cloning and characterization of resistance genes against emerging insect pests and diseases are yet to be done. Identification of broad spectrum and durable resistance genes against major insects and diseases are to be continued. Gene pyramiding to combine major R genes against multiple diseases is to be studied properly along with its impact on crop yield. There is a need to understand the relative importance of both physical and biochemical defense mechanism of plant against insect pests and diseases under induced resistance by different plant elicitors



in rice. This is important for the pests where resistant donors are still lacking. Resistance of the rice varieties (Seeds) to the infestation of stored insect pests is to be exploited for reduction of infestation and also for formulating better storage options for susceptible varieties.

5. RESEARCH AND DEVELOPMENT NEEDS

The first and foremost need is to screen a vast number of germplasm against insect pests and diseases under high pressure to identify resistant donors. The mechanism of plant resistance for each identified donor must be understood, particularly against insects through biochemical, antixenosis, antibiosis and tolerance study. Characterization of identified resistant donors for presence of resistance genes using reported markers and identification of new genes, if any. The expression of defense enzymes should be studied in susceptible and resistant lines, particularly, studying the regulation of defense related genes.

The research should be focused to formulate strategies for improving rice pest resistance through genetic studies, plant-pathogen interaction, identification of novel R genes, development of new resistant varieties through marker-assisted breeding for improving rice insect pest and disease resistance in India and worldwide. Genotyping of resistant lines should be attempted by using SSRs, SNPs, and allele mining for major resistance genes. Evaluation of the elicitors must be taken up for induced defense in rice for pest management especially for borer pest and simultaneous identification of genes responsible for defense. There is also a need to test for the effects of foliar deposits of applied silicon on natural enemy foraging and impact. The research should focus on studying the integration cultivar resistance and cultural controls, especially soil silicon amendment, against the entire pest complex in rice. It is necessary to know the resistance/susceptibility of stored rice varieties to the infestation of insect pests, particularly to *Sitophilus oryzae* and *Sitotroga cerealella* (Olivier), their occurrence and damage pattern under different storage conditions. Resistant genotypes may be grown in pest endemic areas to assess their performance under different environmental conditions.

6. WAY FORWARD

Exploring genetic diversity of rice cultivars for the presence of brown plant hopper (BPH) resistance genes through screening of vast germplasm available at NRRI and National Bureau of Plant Genetic Resource (NBPGR) will pave the way for resistance breeding. At the same time, the valuable resistant genotypes already identified through phenotyping and genotyping should be utilized to develop resistant varieties. They are to be tested also for their reaction against other pests to obtain a multiple resistant donor/variety. Since the susceptibility of rice genotypes to the infestation of stored grain pests depends on the combination of many factors like grain hardness, nutritive value, and natural resistance etc., studies are to be undertaken on these areas for different popular varieties which occupy a greater space in national storage system.



In addition, the factors comprising grain size and moisture content in rice might be the reasons of severe infestation by the rice weevil population. These factors should also be studied along with their management strategies. Important pests and diseases like YSB, leaf folder, gundhi bug, sheath blight, brown spot etc., where resistant genotypes are not available yet, induced resistance work should be in progress for immediate protection of the plant.

The gene/QTL conferring resistance should be identified for further utilization in marker assisted selection of resistant varieties which will quicken the process of varietal development. Although incorporation and utilization of resistance to major rice diseases have succeeded globally, with the currently available biotechnological tools, it is feasible to identify major R genes as well as quantitative trait loci (QTLs) conferring high level of partial resistance and achieve nearly complete resistance against the major and emerging rice diseases.

Identification of donors needs a systematic and continuous evaluation of genotypes for ascertaining their durable reaction. The identified donors can be utilized as genotypes themselves or can be utilized in a breeding programme to develop resistant varieties, may be for a single or for multiple pests. This is the most effective and economic way of pest management system in rice to reduce production cost of farmers as well as pesticide load from the environment.

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