

Managing the Imminent Danger of Rice Blast (*Pyricularia oryzae* Cav.) and Sheath Blight (*Rhizoctonia solani* Kühn) Disease: A Critical Review Article

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Abstract: Rice is one of the most important crop planted on earth. It provide food and employment for thousands of persons daily through out the world. In Guyana the rice industry is one of the largest user of agricultural lands and contributies more than 20% to the country gross domestic product (GDP). The rice crop is known to suffer from several biotic and abiotic factors. Of which rice blast (*P. oryzae*) and sheath blight (*R. solani*) disease identified as two of the most devastating disease affecting the rice cultivation in Guyana. In this context, the present critical review article entitled 'Managing the imminent danger of Rice Blast (*Pyricularia oryzae* Cav.) and Sheath Blight (*Rhizoctonia solani* Kühn) Disease' was taken up to look at the most practical disease management approaches available and can be utilized to mitigate the imminent threat pose by the rice blast and sheath blight disease. The review will focus on: disease resistant screening and understand the genotype and environment interactions; study the expression pattern of proteins in resistant and susceptible genotypes against blast pathogen (*P. oryzae*); examine the efficacy of botanicals, biocontrol agents and new generation fungicides against blast and sheath blight disease under different conditions. This will form a foundation for the exploration of the various disease management strategies for blast and sheath blight disease.

Keywords: Rice Blast Disease, Sheath Blight, Resistant, Genotype by Environment, Protein, Plant Extracts, Bioagents, New Generation Fungicides

1. Introduction

1.1. Global Scenario of Rice Cultivation

The rice plant (*Oryza sativa* L.) has been cultivated as a major cereal crop for over 7,000 years in many parts of the world [54]. It has been considered as one of the most important plants on earth and a major staple food crop for humankind [137, 154, 65]. The total rice cultivation of the world occupied an area of ~162.72 million hectares, with a total production of ~ 741.48 million tonnes in 2014 [33].

Rice provides more that 35-75% of the calorie and a high percentage of protein intake for nearly 520 million people living below poverty in Asia [93, 71]. It accounts for 20% of the global calorie intake [147]. In African, Latin American and

Caribbean countries, there has been a steady increase in the daily consumption of rice, which fulfill at least one third of the dietary intake of close to one billion people [135]. The cultivation of rice also provides employment for over 200 million households and it is one of the primary sources of income for persons across the countries in the developing world [93]. More than 114 countries grow rice and more than 50 have an annual production of 100,000 tonnes. India is the second largest producer of rice after China, with about 90 million tonnes of rice produced and consumed in Asia [80, 71, 169].

The world population continued to grow at the rate of 1.12% and increase at very rapid rate; therefore, the rice production must also increase by more than forty percent to feed the growing population without adversely affecting the resource base. On the other hand, a number of abiotic (problem soils,

high temperature, flooding, salt water intrusion, drought) and biotic (viruses, bacteria, fungi, nematodes, insects) factors known to adversely affect the cultivation of rice crop [100, 71, 42]. To overcome these challenges and to ensure food security, it is most necessary to cultivate stable high yielding rice varieties that are tolerant to biotic and abiotic stresses [71, 154, 50].

Of the several factors that destabilize the rice yield, diseases are most important ones that accounts for crop losses of varying extent. More than 70 diseases caused by viruses, bacteria, nematodes, and fungi have been recorded in rice with a yield loss of 20-70% [107, 84]. During the period from 2001 to 2003, [104] studied yield loss worldwide caused by various pests. The researcher reported that an estimated yield loss caused by rice disease ranged between 7 and 16% for the 19 regions of the world. An actual 10.8% yield loss is caused by various rice pathogens, in spite of accepted disease management practices carried out during the commercial production of rice crop. These rice pathogens can attack the rice plant at all the growth stages, right from the nursery to harvest of the crop. The disease incidence also varied within the different geographical area and from season to season [108]. In case of rice production, rice blast and sheath blight causes an estimated annual yield loss of more than 37% and 25%, respectively worldwide [104, 105].

1.2. Rice Industry in Guyana

In Guyana, the rice industry is one of the most important agricultural industries and attracts more than US\$ 200 million annually, which amounts to approximately 10% of the country's export earnings [103]. It is also one of the largest users of agriculture lands in Guyana with an area of ~92,694.5 ha being double cropped annually, with a total production of ~977,280 tonnes, and produce an estimated yield of approximately 52,715 Hg/ha in 2014 [33]. The rice industry have about 12,000 farmers and supports at least 10% of Guyanese population directly or indirectly. It also contributes to more than 20% of the country's agricultural GDP [103, 169]. In Guyana, rice is grown primarily within five administrative regions of the country (regions number 2, 3, 4, 5 and 6), and recently a new expansion started with some quantity of rice cultivation in region number 9. In the different geographical regions, the rice crop is suffered by numerous diseases. These include blast, sheath blight, brown spot and sheath rot which are the most important diseases affecting rice industry. These diseases threaten the sustainable production and cause great economic yield losses in Guyana.

2. Materials and Methods

This critical review article was focused on two of the major rice diseases. It was done by consulting various published available research articles on blast and sheath blight disease and all relevant reports. The information collected was arranged and findings from them are summarized and presented under different headings with

conclusions. All article consulted were properly cited in the reference section of this paper.

3. Critical Reviews and Discussion

3.1. Importance of Blast Disease Management in Rice Cultivation

Blast disease caused by the fungal pathogen (Teleomorph: *Magnaporthe grisea*; *Magnaporthe oryzae*; Anamorph: *Pyricularia oryzae*; *Pyricularia grisea*) is one of the most serious constraints for rice production at the global level. It is one of the most devastating diseases in at least 85 countries worldwide [108]. The disease has been reported to destroy sufficient rice that can fulfill the dietary needs for over 60 million persons on an annual basis [125]. The blast fungus, *P. oryzae* often overcomes the resistance conferred by major R-genes after a few years of intensive agricultural use due to the rapid genetic evolution of the fungal pathogen. The host plant resistance has played a key role in sustainable rice production and productivity in many parts of the world, therefore it is considered as an important tool in the management of blast disease [32, 148]. Even though host plant resistance plays a key role in the management of blast disease, there are still challenges exist with the management of this pathogen. Many researchers [59, 27] reported the limited success in development of cultivars with durable resistance, which is complicated by the excessive level of variation in the blast pathogen. *P. oryzae* exhibited a high degree of genetic variability, thus capable of forming new pathogenic variants that can infect previously resistant host plants. The formation of new pathogenic variants or races of *P. oryzae* at an alarming frequency in an intensive rice cultivation system resulted in the break-down of resistance [23]. Regular break-down of blast resistance and frequent epidemics in India and Japan over the last ten years have been reported to cause yield losses of 20-100% [70, 134]. Effective management of such pathogens requires constant breeding efforts for development of resistant cultivars. The seed banks and germplasms consist of a rich stock of genetic diversity are still under-explored. Based on the foregoing, it is clear that among other efforts, the risk of catastrophic loss due to blast must be reduced in order to ensure food security for the first quarter of the current century both locally and globally.

In Guyana, the rice industry is facing the similar challenges to battle against rice blast. The blast disease is reported as most devastating to threaten the sustainability and survival of the rice industry [45]. Over the years, rice farmers have been reporting that there has been an increase in the susceptibility of some of the current popular cultivars under cultivation within the different rice growing regions of Guyana. Therefore, the need for breeding and screening of blast resistance require continuous efforts to identify new source of resistant genotypes to enrich the reservoir of the blast resistant genes. This is also required to strategically manage the continuously evolving and geographically

diverse blast pathogenic race. However, in the past, no systematic research efforts have been undertaken to identify novel genotypes that are resistant and/or possess donor level resistance. Also, no work was done to date at molecular level to unravel the mechanisms involved in thwarting the blast pathogen by resistant genotypes. Similarly, a large number of plant extracts, biocontrol agents have been reported against blast and sheath blight disease, yet no attempt have ever been made in Guyana to develop these as alternative management strategies for the control of blast. In addition, there has been a dependency on particular fungicide for the control of blast disease. This may contribute to a number of problems such as pathogen resistance, over use, failure to give adequate disease control. Therefore, there is a need to identify the new generation fungicides that can be used in the event of an epidemic or a disastrous disease situation should arise.

3.2. Important of Sheath Blight Management in Rice Cultivation

Sheath blight disease (Teleomorph: *Thanatephorus cucumeris* (A. B. Frank) Donk.] Anamorph: *Rhizoctonia solani*) in rice is considered the second most important disease next to blast in many Asian countries [124, 141, 14]. Sheath blight was first reported in rice from Japan [86]. It was later reported from other rice growing regions around the world. It has become a severe concern especially in intensified rice production systems. Yield losses ranged from 1 to 50.0% due to sheath blight disease. Under severe disease conditions, it was reported up to 90% [108, 144, 35]. The loss and level of severity is depends on the environmental conditions, the growth stage at which the plant becomes infected, the degree of infection, and the rice varieties grown. However, the soil-borne nature of the pathogen and long survival of its sclerotia makes the controlling this disease especially difficult.

The employment of host resistance against sheath blight has little scope as no commercial rice cultivar has been found to be possessing donor level resistance [124, 83, 114, 78, 160]. Similarly, in Guyana none of the popular cultivars under cultivation is completely resistant. Under these circumstances, the identification of resistant and/or slow sheath blighting rice cultivars can play a major role in averting the losses caused by the sheath blight disease. Similarly, a number of plant extract, biocontrol agents and new generation fungicides have been reported against *R. solani*. However, a feasible technology for the field use is yet to be developed.

3.3. Resistance Screening in Rice Against Major Diseases

3.3.1. Blast Resistance

Rice blast disease is not only one of the most widely distributed, but also one of the earliest known plant diseases that can infect almost all parts of the rice plant (leaf, stem, neck, node, panicle, grains and of recent reports of infection occurring on roots) at all the stages of growth. The destructiveness of the rice blast is known in every region of

the world where rice is grown and the blast disease known to cause great economic losses. The negative impact of this disease is predicted to further increase due to the impact of climate change at a global level. Increased temperatures and unpredictable weather pattern are likely to change the geographical pathogen distribution [115]. Milus *et al.* [84] found that wheat rust pathogens can cause more economical damages to the crop in warmer temperature which was previously unfavorable to that pathogen. Thus, the weather pattern might likely to result in changes of the effectiveness of present resistance genes in the various species of crop. Many pathogens, like the blast disease pathogen, *Magnaporthe oryzae* are quickly evolving and can overcome the resistance govern by major resistant (R) genes in plants, which can lead to heavy disease outbreak or epidemic [148, 36, 143]. Nevertheless, the ‘break-down’ of true resistance to blast was very ‘unexpected and shocking’, it begun to occur only few years after the release of the varieties, thus having the tendency to being unreliable, with resistance often failing, or ‘breaking-down’, under field conditions [30, 72]. Many years of genetic breeding and research have shown that genetic resistance to blast in favorable environments is short lived, rarely being effective for more than two to three years, sometimes even before the breeding line reach the farmer’s field [146]. In Korea, the resistance of “Tongil” varieties for blast was effective for a five-year period. In Colombia, resistant varieties to blast released during 1969-1986 lasted only for a year or two before being overcome by previously unidentified virulent races [4]. In Japan, the longevity of resistant varieties was reported as three years [81]. In Guyana, blast resistance in BG 60-47, Variety N and G 9502, lasted for 2, 2-3 and 2 years, respectively; while the tolerance to blast in Rustic lasted only one year [112].

The behaviour of these pathogens are also influenced by several factors such as environmental and weather conditions, presence of virulent inoculum and disease pressure, as well as stability of the pathogen genome. As mentioned earlier, the rice blast pathogen are no different. Therefore, it becomes necessary to have a continuous breeding and screening program for identification of new sources of host disease resistance against continuously geographically diverse and changing races of this pathogen. Thus, the rice crop germplasm collections maintained in gene banks at Guyana Rice Development Board (GRDB), Rice Research Station (RRS), Burma has several traditional cultivars, landraces, and wild species collected from various Institutions such as Interantional Center for Tropical Agriculture (CIAT), Iternational Rice Research Iinstitute (IRRI), Latin American Fund for Irrigated Rice (FLAR) and many other rice gene banks from various countries. These germplasms are also from numerous geographical origins such as Suriname, Brazil, Columbia, Philippines, USA and many other parts of the world. Many wild rice species and landraces that may not have the ideal plant type, height, yield potentials or may not have all the suitable agronomic traits that fits it into the modern breeding programs, but may have the genes for specific traits, such as tolerance or resistance

against various abiotic and biotic stresses. For example, a broad spectrum rice blast R gene *Pi9* was identified in *Oryza minuta* [120].

The international collaboration on breeding for blast resistance in rice has started since 1960. This has played an important role in developing cultivars with blast resistance. The International Network for Genetic Evaluation of Rice (INGER) facilitates the collaboration and exchange of germplasms since 1975. Over 3000 germplasms were evaluated in 31 countries at 126 test sites from 1975 to 1992. A total of 522 entries of the International Rice Blast Nursery (IRBN) were utilized in hybridization programme across 18 countries from 1984 to 1992 [4].

At IRRI, Philippines, donors such as Ram Tulsi, *Oryza nivara*, Dawn, Tetpe, Carreom, Zenith, Gam pai 15, Pankhari 203 and a number of improved plant types are used on a regular basis as parents in blast resistant breeding programs. In West Africa, some of the improved resistant donors used are ITA 414, ITA 416, ITA 12, ITA 239, ITA 302, ITA 324, WIAT 3, WAB 56-50, WAB 56-104, IAC 257, Tox 3118-47-1-1-2-3, Tox 3226-5-2-2-2, TAC 84-4, IR 36, IR 72, LAC 23, IRAT 10, and Moroberekan [139].

In India, Persaud [111, 112] found genotypes such as Bala, 5173, RR166-645, RR345-2, IR71677-106-1-5, IR71693-197-4-1, WAB 56-50, IR64, B6144-F-MR-6-0-0, Moroberekan, IR42221-145-2-3-2, RI207-257-5-274-1, VL16, C101 A51, G9502, IR42221-145-2-3-2, 5173, B6441-F-MR-6-0-0, F7 10 and BR 240 possess high level of resistance to blast. In another blast screening trial in India, 91 advance germplasms were tested. Of which, AE258, AE279, AE280, E408 and the resistant check NLR 145 showed complete resistant reaction to leaf blast in seedling stage. The germplasms viz. AE257, AE259, AE275, AE278, AE281, BE325 and E409 showed resistant reaction with score 2 (Ravikumar 2014). In Guyana, cultivars viz. BR 240, F 710, BR 444, Diwani, G96 -196, G98-30-3, G 98-135, GRDB 9, GRDB 10, GRDB 11, GRDB 12, GRDB 13, and GRDB 14 in cultivation were released as blast resistant. Also recently the results of all seasons and all three locations showed the consistent expression of high resistance by genotype FL 127 followed by FG12-08 and FG12-273 [174].

In China (Jiangxi province), out of 50 rice genotypes 72.0% showed resistance to leaf blast; 20.0% showed medium resistance and 8.0% were moderately susceptible [75]. In Iran, Pasha et al. [110] use blast isolate IA-82 to screen rice germplasm and found IRBL5-M, IRBLZ5-CA, B40, CT18235-3-9-1-2-3-4 and CT18617-6-2-2-3-1 genotypes were highly susceptible; CT18615-1-5-1-2-1, IRBL12-M, CT18232-5-9-1-2-6-3, IRBLZT-T, and IR33225-45-3-1-1 genotypes were moderately resistant and also 48 other genotypes were resistant to IA-82 isolate. Of recent, there has been a renewed interest by rice breeders and plant pathologist to study partial resistance because of the belief that partial resistance was more stable and long lasting. Mohaptra et al. [89] in two season testing found 12 and 19 genotypes among the 42 genotypes tested to possess partial resistance in two different clusters. RoyChowdhury [126] studied the resistance

at molecular level in 167 germplasms employing SSR markers and pathogenicity assays and reported the presence of *Pib* blast resistant gene in 109 germplasms. The other 52 germplasms were observed with differential responses to the blast races IB54, IE1k, and IB1. From this, it is inferred that the germplasms may possess *R* gene (s) other than *Pib* gene. Likewise, Sharma [133] has reported the identification and cloning of more than 85 and 14 blast resistant genes, respectively. He also cloned a resistant gene, *Pi-kh* (now designated *Pi54*) from rice line Tetep.

3.3.2. Sheath Blight Resistance and Slow Blighting

The use of resistance is known to be the most environment friendly and economical way of managing the sheath blight disease [79]. A major breeding goal for many rice growing countries is the development of high yielding cultivars combined with resistance to sheath blight. An extensive research has been done over the years to identify source of resistance in rice germplasms [138, 58, 28]. In India (Hyderabad, Andhra Pradesh) one hundred elite advanced breeding rice lines were screened for resistant reactions to different diseases including sheath blight (*R. solani*). Only four genotypes viz. IET-16958, IET-14277, IET-17159 and IET-17048 were found to be moderately resistant to sheath blight [41]. Similarly, Biswas [15] screened, 161 germplasms in Kharif (wet) season, 1999 against sheath blight disease (*R. solani*) under artificial inoculated conditions. However, no genotype recorded resistant reaction; six expressed moderate reaction and the others (155) observed with susceptible reactions. Mew et al. [83] have evaluated in excess of 30,000 rice germplasm accessions at IRRI. In spite this, no effective source of resistance to the sheath blight pathogen has been identified. Further, the screening of various germplasms for sheath blight resistance were exhaustively done by various researchers and no complete donor level resistance has been found [78, 141, 159, 35].

Large variations in the level of resistance to the sheath blight pathogen under field condition was demonstrated by many researchers. Interestingly, [118] tested 60 wild *Oryza* spp. germplasms from 15 species in laboratory, greenhouse and field conditions. The researchers found seven accessions (IRGC100898, IRGC104705, IRGC104443, IRGC100223, IRGC100943, IRGC105306 and IRGC105979) from five *Oryza* spp viz. *O. meridionalis*, *O. barthii*, *O. nivara*, *O. officinalis*, and *O. sativa* as moderately resistant to sheath blight disease. Likewise, Mohanta et al. [88] screened a total of 28 bred restored lines and 4 standard controls against sheath blight (*R. solani*), during the 't. aman' and 'boro' seasons under natural field conditions and found none to be susceptible. Similarly, a total of 35 inbred and 13 hybrid varieties were tested by Latif et al. [76] and found moderate susceptibility to sheath blight disease. Also, Rush et al. [127] used the conventional breeding techniques such as, modified recurrent selection and backcross breeding methods over 25 years and registered 25 germplasms as resistant and moderately resistant for sheath blight with disease rating ranged from 3.3 to 5.2%.

Persaud [113], also tested 39 rice genotypes against sheath blight disease under natural field conditions and found two genotypes (R-1249-1440-3-1 and R-1240-927-3-1056-1) as immune and one (Shyamala) as resistant. In a separate research by Persaud [113], 38 rice germplasms were evaluated against sheath blight disease under artificial inoculated conditions for identification of slow blighting disease developing ability. He observed lowest percent disease severity (5.65%) with intermediate between resistant and susceptible disease reaction in Rasi germplasm. Also, reported the lowest AUDPC expressed by germplasm VL-30029 (478.31) and highest by germplasm R 1831-RF-16 (847.14). Similarly, the mean apparent infection rate at the exponential growth ranged from 0.0285 (RP 4353-MS-28-13-3-1-1-3) to 0.1982 (Rasi). Genotypes SJR 38 and RP 4353-MS-28-13-3-1-1-3 expressed a continuous decrease in rate of development. This indicates that the host resistance may have been involved in the reduction of the rate of disease development. Dey et al. [25] screened 1013 germplasm from different background during 2012-2014 and found seven genotypes *viz.* 10-3 (Introgression line), SM 801 (N 22 mutant), Wazuhophek, Ngnololasha, Phougak (land races from north east) and Gumdhan and RP 2068-18-3-5 (gall midge biotype differential) as moderately resistant to sheath blight. Also recently, fourteen genotypes found to express highly resistant to resistant reaction to sheath blight disease from 5 experiment carried out under artificial inoculated and natural field conditions in Guyana [172].

The challenges in development of commercial resistant varieties still exists due to non-availability of appropriate resistant sources. The *R. solani* pathogen is known to have a broad host range and resistance appear to be quantitative in nature controlled by polygenes [159]. Many other researchers have also utilized various advanced molecular techniques to study the whole genome of the rice to identify non-synonymous single nucleotide polymorphism (nsSNPs) and candidate genes for resistance to sheath blight [138]. These researchers identified two accessions of *O. nivara* with a resistant *nsSNP* alleles. Similarly, Liu et al. [78] confirmed quantitative trait loci (QTLs) of 216 recombinant inbred lines and found major ShB-QTL *qShB9-2* based on the field data.

The pathogen variability was viewed as the principal explanation for the instability of resistance in the field [108, 72]. However, breakdown of resistance can be attributed to extreme heterogeneity and variability of virulence in the pathogen, inappropriate use of resistance genes, inadequate resistance testing and evaluation method, or a combination of these features [168]. The pathogen's remarkable ability to overcome plant defenses within a short period has made the breeding for resistance against sheath blight a constant and ongoing challenge.

3.4. Understanding the Genotype by Environment Interactions Analysis by AMMI Model

Multi-environment testing (MET) trials were used by plant breeders in various parts of the world to understand the performance of new genotypes being breed and developed for

adoption to a particular environmental condition, effects of various abiotic and biotic stresses, meteorological components and cultivating practice. Environmental variables such as soil conditions, field management or weather factors influenced the expression of genes for the rice blast disease [164]. In order to have clear understanding on the interaction of genotypes by environment (GxE), many researchers have developed new and innovative analytical tools [21]. One such analytical tool developed was the Additive Main effects and Multiplicative Interaction (AMMI) model and the genotype main effects and genotype x environment interaction effects (GGE) model for understanding the interaction of the Genotype by Environment [38, 39, 91].

The AMMI model analysis first accounts for the main effects and then applies the principal-component analysis to account for the interaction effects [38]. Many researchers have successfully demonstrated the potential utility of the AMMI models to understand G x E and to identify resistant genotypes across varying environments [1, 91, 11, 17]. Yang et al. [164] studied the G x E interaction in *Japonica* high quality rice varieties for blast reaction patterns. The researchers reported that resistant was dominated by genotypes main effect and with a small influence for G X E interaction effect. Also, several researchers have demonstrated the interaction of genotypes can be suitably predicted by the two PCAs' [37, 163, 97, 91]. The AMMI model analysis also identified the best and average environment, the winning genotypes within the various mega-environments and stable performance of the genotypes [162]. Also recent studies in Guyana revealed that AMMI analysis of variance (ANOVA) found resistance was dominated by the genotype main effect. Further found that screening at Onverwagt Back, autumn 2016 (E7) and Black Bush Polder, spring 2015 (E5) to be the most representative environment Likewise, E4 (Canje, autumn 2015) observed closer to the ideal test environment[^], thus suggested as an ideal environment for blast resistant screening [174].

3.5. Proteomic Analysis Between Highly Resistant and Susceptible Genotypes

Proteomic analysis is a great means to study alterations in protein expression in response to a number of abiotic stresses and biotic [157]. As per Nature [96] website "Proteomics refers to the systematic identification and quantification of the complete complement of proteins (the proteome) of a biological system (cell, tissue, organ, biological fluid, or organism) at a specific point in time. Mass spectrometry is the technique most often used for proteomic analysis," [96].

When the rice plant challenged by the infection of various pathogenic microorganism, it react differently by triggering of an array of defense responses, often referred to as the 'basal resistance' [16, 19]. The pathogens can bypass this first line of defense by giving off effector molecules. These effectors molecules are often recognized by the resistance proteins that coded for major R-genes thereby providing effector-triggered plant immunity (ETI) [60, 55]. The similar defense response of plant response was explained by Boller

and He [16]; Flor [34] when they demonstrated the 'gene-for-gene' concept. The present understanding of differential response of the host to infection provide a great scope for the proteomic analysis. It also offers a new innovative technique that allow the complex cellular process occurring within rice plant genome to be widely investigated.

Over the years, extensive researches have been done on proteomic studies to investigate the alteration of protein expression levels in various plant species exposed to various biotic stresses. Ventelon-Debout et al. [151], Shi et al. [136], Xu et al. [158] and Huang et al. [51] studied the differential expression of proteins on viral infection; Campo et al. [18], Ryu et al. [128], and Li et al. [77] demonstrated proteomics approach against fungal infection, and Jorin et al. [61], Cheng, McConkey, and Glick. [20], and Xiang et al. [156] studied it on bacterial infection.

Plants have several lines of defense mechanisms [55]. Many of the major R genes code for different classes and sub-classes of proteins [22]. These plant proteins belong to nucleotide-binding site-leucine-rich repeat (NBS-LRR) family have been used for pathogen detection [26]. In the rice genome greater than 500 NBS-LRR genes have been identified [90], and in the *Arabidopsis* genome close to 150 NBS-LRR [165]. These NBS-LRR found in plants form the largest class of R proteins and extensively used in a number of crop breeding for integrating R genes against various diseases. Yang et al. [165] demonstrated that the genomes of maize, sorghum, and *Brachypodium* NBS-LRR genes transformed into rice, confer resistance to 12 diverse strains of *M. oryzae*. Ryu et al. [128] studied the difference in protein expression levels between a resistant line, RIL260 rice strain carrying the *Pi5*-mediated disease resistance gene to *M. oryzae*, and susceptible mutants M5465 and M7023. Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) analysis was utilized. In this study, eight proteins were differently expressed between the resistant and susceptible plants. Also recently, Two-Dimensional Difference Gel Electrophoresis (2D-DIGE) plus Matrix-assisted laser desorption/ionization time-of-flight-mass spectroscopy (MALDI-TOF MS) and TOF/TOF tandem MS/MS was used to study differentially regulated proteins between a highly resistant (HR) genotype, FL 127 and a highly susceptible (HS) genotype, Rustic against blast pathogen in rice. Seventy eight protein spots were observed in 2D-gel analysis of HR and HS genotypes with a protein expression ratio of twenty protein spots predominant in differential expression against blast pathogen. These proteins found reported with functions either directly or indirectly related to plant defense and stress response, transcription and photosynthesis [173]. Therefore, it is suggested that proteomic analysis is useful method for identifying novel proteins associated in resistant genotypes.

3.6. Botanicals in Plants Disease Management

The use of plant extracts for the management of diseases in various crop has been studied by many researchers over the years [155, 40, 47, 62, 24, 87, 121, 94]. In rice, the use of

plant products for the management of various pathogenic microorganisms has also being explored for the control of some of the most destructive diseases [98]. Harish et al. [47] investigated the efficacy of fifty plant extracts against rice brown spot disease (*Bipolaris oryzae* (*Cochliobolus miyabeanus*)). Under *in vitro*, 2 leaf extracts (*Nerium oleander* and *Pithecolobium dulce*) showed higher percent inhibition to mycelial growth (75.1, 77.4%) and spore germination (80.0, 80.3%) of *B. oryzae*. In glasshouse and field trial, *N. oleander* showed 52 and 53% reduction in the disease incidence and increase in yield by 15%. Rani and Singh [122] demonstrated that seed extracts of *Aloe vera* and *Cassia occidentalis* at 100% concentration significantly reduced *X. oryzae*. Kagale et al. [62] found a high reduction in the sheath blight disease incidence under *in vitro* and field condition when plant extracts of *Ipomoea carnea* and *Zizyphus jujube* were applied. Venkateswarlu et al. [150] tested 15 plant extracts against stem rot of paddy (*Sclerotium oryzae*). Of these, 2% extracts of *Andrographis paniculata*, *Calotropis procera* and *Eucalyptus globules* significantly reduced the incidence of stem rot. Ghangaonkar [40] revealed that *Annona squamosa* significantly retarded the growth of *Botrytis cinera* by 41% followed by *Rhizopus arrhizus* (29%), *R. solani* (28%) and *Aspergillus niger* (11%).

The extracts of *Acorus calamus* at 20% inhibited 80% of mycelial growth of *Drechslera oryzae* and reduced 45.29% of brown spot disease compared to control [24]. Similar results were reported by Khoa et al. [69]. These researchers found that foliar spraying and seed soaking of extracts of either fresh or dried leaves of *Chromolaena odorata* caused a 68% reduction in sheath blight disease under controlled and semi-field conditions; 57% decreased in brown spot disease (*B. oryzae*) by using seed treatment, 45% reduction in blast (*P. oryzae*) disease by using foliar spray and a 50% decrease in bacterial blight (*X. oryzae* pv. *oryzae*) by using both seed treatment and foliar sprays. Islam and Monjil [53] tested 6 plant extracts against sheath blight and found Biskatali (*Polygonum hydropiper*) at 1:10 ratio of application significantly reduced the sheath blight disease. Likewise, Yadav and Thrimurthy [160] also reported the complete inhibition of mycelial growth of *Sarocladium oryzae* by leaf extracts of *Mentha viridis* (*M. spicata*).

Many success with the use of the various plant extracts for the management of rice disease have been reported by several researches. Handique and Singh [46] reported similar finding, where Lemongrass oil has showed antimicrobial activity against *R. solani*, *Sclerotium rolfii*, and *Sclerotinia sclerotiorum*. More specifically, the lemongrass oil showed 67% and 100% reduction in the growth of *R. solani* at 100 and 1000 ppm respectively. Leaf extracts of Madar plants reported for its high inhibition against several fungal pathogens, *Microsporum boudardii*, *A. flavus*, *A. niger* and *Candida albicans* compared to the control [109, 166]. Also, the extracts of *C. arabica* exhibit significant inhibitory effect against *P. oryzae* [65]. Recently the extracts of lemon grass and thick leaf thyme at 15% found to give effective control of sheath blight disease under Guyana agriculture conditions [171].

In addition, several researchers [106, 166] studied the presence of phytochemicals compounds in plant extracts. Also, many researchers (Venkateswarlu *et al.* [150]; Gurja *et al.* [44]; Al-Snafi [8]; Parihar and Balekar [109]; Yogi, Gupta and Mishra [166] reported that plant extracts possess phytochemical compounds with antimicrobial, insecticidal and medicinal properties. For instant, Venkateswarlu *et al.* [150] reported the presence of the phytochemical Steroid, Tannin, Flavonoid, Alkaloid, and Saponin in bale extracts. Gurja *et al.* [44] also found the bale extracts contain phytochemical class terpenoid, which is known for its mechanism of membrane disruption in microorganisms. Likewise, four unique chemical compounds *viz.*, Cordiaquinones A, B, J and K were reported in Black sage root for its antifungal activities against *Candida albicans*, *Cladosporium cucumerinum* and larvicidal properties against larvae of *Aedes aegypti* mosquito [52]. Similarly, Al-Snafi [8] and Parihar and Balekar [109] conducted a review and found a wide range of pharmacological activities such as acaricidal, antimicrobial, insecticidal, larvicidal, anticancer and anti-inflammatory activities of Madar plant.

Also, the authors found phytochemicals such as voruscharine, steroids calotropagenin, calotoxin, calotropin, calotropagenin and, di and triterpenes such as flavonoids, stigmasterol, polyphenolic compounds, β -sitosterol, and also various newer reported hydrocarbons and proteins.

Abu-seif *et al.* [8] and Handique and Singh [46] found traces of phytochemicals flavonoids, terpenoids and phenolic compounds in the lemon grass. Equally, essential oils of *Thymus vulgaris* showed effective control of *R. solani* [68, 12, 167]. The characterization of *T. vulgaris* plants demonstrated the presence of antifungal compounds *viz.*, carvacrol, thymol, p-cymene, γ -terpinene, 1, 8-cineole, geranial and β -caryophyllene [12, 167, 49]. These researchers suggested that the compounds found in the plant extracts are responsible for the antimicrobial activities. The hexane crude extract of *Alpinia galangal*, *Curcuma longa* and *Zingiber officinale* methanol crude extract showed strong (52.9%, 49.1% and 43.5%, respectively) inhibitory against *Pyricularia oryzae* *in vitro* and also reported that antifungal activities may be due to the presence of some chemical compounds such as alkaloids, saponins, tannins, phenols, glycosides, flavonoids and terpenes recorded from the phytochemical test [102].

3.7. Biological Control Agents in Disease Management

The use of biocontrol agents have received greater attention in the management of plant diseases over the years. It has been successfully use for the management of many plant diseases. The reports by several researchers [140, 29, 57, 63, 129, 6, 130, 95, 143] confirmed the successful evaluation and identification of bioagents for the control of plant diseases [65]. In addition, the growth promotion, antagonism and induction of defense enzymes were also reported as the mechanism in the biological control of rice diseases [131, 47] [132, 66, 82]. Suryadi *et al.* [142] reported that A6 consortium (consisted of *Pseudomonas aeruginosa*

C32b, *Bacillus firmus* E65, *Bacillus cereus* II. 14) and A2 (*Bacillus firmus* E65) significantly inhibited the mycelial growth of *P. oryzae*. Likewise, Singh *et al.* [139] conducted a field trial in Uttaranchal, India, to compare relative efficacy of commercial formulations and potential isolates of *Pseudomonas fluorescens* against sheath blight of rice. The foliar application of the different strains of *Fluorescent pseudomonads* reduced the severity of the sheath blight disease. A rice rhizosphere isolate, *Pfr 1* showed higher reduction in the sheath blight disease incidence and higher grain yield.

Alike was reported by Kazempour [67], and Neha, Balabaskar and Naveenkumar [99] where *P. fluorescens* exhibited high antagonistic activity against *R. solani* *in vitro*, green house and field conditions. Nirmalkar, Said and Kaushik [101] also evaluated bioagents against *P. oryzae*. The researchers found that *P. fluorocens* expressed control of leaf blast, while in case of neck blast *T. harzianum* gave better control. Another researcher evaluated 11 *P. fluorescens* strains and reported 4 strains *viz.* Pf1, Pf2, Pf9 and Pf11 demonstrated higher inhibition of mycelial growth, sclerotial lysis and germination of *R. solani* under laboratory condition. In addition, these 4 strains showed significantly higher control of sheath blight disease under greenhouse conditions [73]. Also, Ali and Nadarajah [7] evaluated several strains of *Trichoderma* and *Bacillus* and found *Trichoderma* T2 in combination with *B. subtilis* UKM1 gave the highest inhibition of mycelial growth of *P. oryzae* and control of the blast disease under field conditions. Further research recently found three strains of bioagents *viz.* *Bacillus subtilis* 5, *B. cereus* 3S5, and *Pseudomonas fluorecens* 10S2. to be highly effective under *in vitro* and greater than 31% reduction in disease severity than the control under field experiment [153]. Also similarly reports from research work indicated that *B. cereus* OG2L at 2 g/L demonstrated significant reduction in the sheath blight disease severity incidence [171].

Many other researchers [6, 57, 130] also reported similar success with the use of bioagents in the control of various rice diseases, as well as reported positive influence in terms of growth parameters and increase in yield. In addition, bioagents has been found to induce systemic resistance in plants against various pathogens. For instant, Smith and Metraux [140] reported the induction of systemic resistance in rice against *P. oryzae* when *P. syringae* pv. *syringae* was applied. Similarly, Nagendran *et al.* [95] found the application of endophytic bacterial isolate *B. subtilis* (FZB 24) on rice plants resulted in a higher induction of defense related enzymes *viz.*, phenylalanine ammonia lyase, peroxidase, and polyphenol oxidase, as well as resulted in increased accumulation of phenol compounds compared to control. Also, *B. subtilis* (FZB 24), treated rice plots revealed lower level of bacterial leaf blight (2.80%) and higher straw and grain yield as compared to untreated control. Of more recent, Amruta *et al.* [9] evaluated 60 strains of bioagents against *M. oryzae*. The researchers recorded the highest percent inhibition of *M. oryzae* and reduction in blast disease by *Bacillus amyloliquefaciens* treatment as compared to

control. Also, Prasanna Kumar et al. [119] reported that *B. subtilis* UASP17 was effective in controlling blast, sheath blight and bacterial leaf blight diseases of rice. The *B. subtilis* UASP17 treated plots also recorded an increase in yield compared to untreated control.

3.8. New Generation Fungicides

The use of agrochemicals has been one of the most widely used methods for the management of plant diseases over many years. In the past, there has been the highly dependent on old, highly toxic and hazardous fungicides [5, 143]. Thus, the continuous use of fungicide molecules with same mode of action could lead to problems such as development of resistance in pathogens. Also, the over use of highly toxic chemicals resulted in pesticide residues and negative impact to the environment [35, 10]. Over the years, several researchers have successfully evaluated new available fungicides for the efficacy against a number of plant diseases [122]. In case of rice diseases, Bhattacharya and Roy [13] screened several chemicals against *R. solani* and reported Calcium nitrate, Sodium selenite, Ferric chloride Lithium sulphate, Sodium fluorine and Zinc β -sulphate, were highly efficient in decreasing both lesion number and lesion length of sheath blight disease in laboratory and field experiments. Also, Kandhari and Gupta [64] conducted an experiment to test the efficacy of two new fungicides GFT-10 (S-methyls, s-diphenyl phosphorothioate) and Folicur (tebuconazole) against sheath blight disease in rice (*cv.* Pusa Basmati-1) under greenhouse conditions. The researchers reported that both fungicides applied as foliar spray significantly reduced the incidence of sheath blight disease compared to the untreated control. Similarly, Thapak et al. [145] investigated the efficacy of fungicides on rice *cv.* Kranti against sheath rot caused by *Sarocladium oryzae* and found that all the formulations (Antracol-Propineb; Tilt-Propiconazole; Bavistin-Carbendazim) tested were effective against the disease. Likewise, Venkateswarlu and Chauhan [149] evaluated the efficacy of 12 fungicides against sheath rot disease *in vitro* and *in vivo*. Under *in vitro* condition, Benomyl, Carbendazim and Copper oxychloride expressed high inhibition of the pathogen; while under *in vivo* conditions, Mancozeb, Carbendazim and Propiconazole showed significantly higher percent reduction in sheath rot disease incidence. Also the fungicide treated plots showed higher 1000 grain weight, grain and straw yield as compared to untreated control. In more recent study by Gupta et al. [43], seven different fungicides were tested against the brown spot disease in rice. The researchers found propiconazole at 250 ppm was effective with a 97% inhibition of the brown spot pathogen *in vitro*. Under field conditions, seven fungicides were evaluated on 3 rice varieties (Jaya, Basmati-370 and PC-19) at 0.1% concentration. The application of propiconazole significantly reduced the brown spot disease incidence by 73, 69 and 70% for the 3 varieties respectively and increased the grain yield by 1.9, 1.2 and 2.1 t/ha compared to their respective controls. Later in 2014, Kumar and Veerabhadraswamy [74] tested various combination of fungicides against blast disease and reported

combination fungicides, RIL-068/F1 48 WG (Kresoxim methyl 40% + Hexaconazole 8% WG), Dhanucop Team (Tricyclazole 75% WP) and Conika 50% WP (Kasugamycin 5% + Copper Oxychloride 45% WP) were effective against blast pathogen. The reason for the combination fungicides to be more effective against the pathogen is attributed to the display of different mode of action. Also, Jagadeeshwar et al. [56] evaluated five new generation fungicides against the blast pathogen and found that application of Metaminostrobin 20 SC (at 0.5, 1.5 and 2.0 ml/L) was effective in control of blast besides registering superior grain yield in rice. More recently, Hegde [48] evaluated a new molecule against blast and sheath blight diseases over a two year period. The results indicated that Tebuconazole at 0.2% has significantly reduced the incidence of sheath blight (10.24%) and blast (17.72%), and increased the grain yield compared to untreated control. Likewise, Pramesh et al. [117] screened 8 new generation fungicides against blast and sheath blight disease during 2014 and 2015. The researchers reported the combination fungicide Nativio 75 WG (Trifloxystrobin 25% + Tebuconazole 50%) was most effective with the least percent disease severity and recorded significant increase in the grain yield as compared to the other treatment and control. Also, Mushineni et al. [92] evaluated 7 new generation fungicides against *R. solani*. In this research, Azoxystrobin 23% SC followed by the Tebuconazole 50% + Trifloxystrobin 25%WG gave higher disease reduction (69.27 and 68.00%) and grain yields (6.9t/ha and 6.67t/ha) respectively, as compared to the other treatments and untreated control. Likewise, new generation fungicides *viz.*, Antracol 70WP at 2.5 g/L, Nativio 0.5 g/L and Serenade 1.5 ml/L recorded low percent disease severity compared to untreated in greenhouse and field trials [171].

4. Conclusion

The goal is to move away from the heavy reliance on use of old and harmful pesticides, overuse, frequent outbreaks, high environmental pollution and reduction of pesticides residues in grains. Some of the measures require to be adopted in order to mitigate the imminent danger posed by blast and sheath blight disease in particular is the development and use of highly stable blast resistant cultivars, identify cultivars that are resistant to sheath blight or showing slow blighting effect, evaluation of widely available plant extracts and biocontrol agents, as well as to evaluate the new generation type of fungicides that are more friendly to the ecosystem and environment. Also, the study of the differential protein expression of highly blast resistant and susceptible genotypes open a pathway for further detail DNA and molecular approach for breeding of blast resistant cultivars. These are some of the areas that should be explored and utilized for the effective and sustainable management of the blast and sheath blight disease. The utilization of these approaches provide a gate way for the significant reduction of some of the major problems, such as overuse, outbreaks, residues and environmental pollutions, that presently challenge the rice industry globally.

Authors' Contribution

First author Rajendra Persaud did the review, wrote and edited the manuscript and the other author assist with reading and checking of the manuscript.

Conflict of Interest

The authors declare that there is no potential conflict of interest with this review.

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