Austin Journal of Plant Biology

Open Access

Austin Publishing Group

Editorial

Understanding Disease Resistance Signaling in Rice against various Pests and Pathogens

Rawat N*

Gulf Coast Research and Education Center, University of Florida, USA

***Corresponding author:** Nidhi Rawat, Gulf Coast Research and Education Center, University of Florida, 14625 Co Rd 672, Wimauma, FL 33598, USA

Received: May 04, 2016; **Accepted:** May 05, 2016; **Published:** May 06, 2016

Editorial

Rice is one of the major food crop for half of the world's population. The production of rice is influenced by various biotic and abiotic factors. Although over 100 species of insects have been reported as pests of rice, major pests that are of economic importance are the stem borers (*Chilosuppressalis*), the Brown Plant Hopper, (BPH) (*NilaparvatalugensStal*), Asian rice gall midge (*Orseoliaoryzae*) and rice bugs [1-3]. Rice blast (*Magnaportheoryzae*), bacterial blight (*Xanthomonasoryzaepv oryzae*), are the most destructive fungal and bacterial diseases of rice [4,5]. A crucial step in plant defense is the timely perception of the stress in order to respond in a rapid and efficient manner. Present study reviews rice defense signaling pathway in disease resistance against blast, bacterial blight, BPH and Asian rice gall midge.

Molecular responses of plants are associated with the feeding way and tissue damage amount caused by different plant-pathogens/herbivore interaction [2]. Plants induce a multilayered immune system after recognition of non-self-molecules such as microbial-associated molecular patterns (PAMPs) from pathogenic organism and cease the growing pathogen by two effective ways of plant innate immunity which is called PAMP-Triggered Immunity (PTI) and Effector-Triggered Immunity (ETI).These PAMPs which include bacterial flagellin, Lipopolysaccharides (LPSs), Elongation Factor Tu (EF-Tu) and fungal chitin are perceived in plants *via* membrane-bound receptor known as Pattern Recognition Receptors (PRRs), which eventually results in activation of PTI [6-7]. PRRs typically consist of an extracellular Leucine-Rich Repeat (LRR) domain and an intracellular Receptor Like Kinases (RLKs) domain [8]. *Xa21*, a rice resistance (R) gene that confers resistance to diverse *X. oryzae pv. Oryzae* strains was considered a pattern recognition receptor [9]. In most cases, PTI is adequate to suppress disease development *via* hindering pathogen establishment. However virulent pathogens, escape PTI-based surveillance by transporting small effector proteins in the plant cells, which in turn cause effector triggered plant susceptibility. Second level of innate immunity which is known as Effector-Triggered Immunity (ETI) has been observed in plants. ETI, also known as R-gene-mediated resistance, or specific resistance, represents a more amplified form of resistance [10]. ETI is initiated through plant cultivar-specific recognition of microbial effectors. Specific recognition is generally mediated *via* resistance (R) gene products carrying Leucine-Rich Repeats (LRRs), and is typically distinguished from PTI by elicitation of Hypersensitive Response (HR)-associated localized program cell death.

Majority of R genes cloned so far belong to the Nucleotide-Binding Site Leucine-Rich Repeat (NBS-LRR) or LRR Kinase super-families [7]. NBS-LRR gene family organized in large clusters of orthologous genes and comprised about 1500 genes in rice [11]. Examples of known NBS-LRR R genes include the *Xanthomonas* resistance gene *Xa1* in rice [12]. For example, most (22 out of 23) cloned functional blast resistant R genes and one cloned gene (*Xa1*) against bacterial blight in rice represents NBS-LRR domains [12-14]. The *Bph14* gene against brown-plant hopper also encodes CC–NB–LRRprotein of the NB–LRR family [2]. Most of the R genes mapped against gall midge resistance in rice are also from NBS-LRR gene family [15-17]. Even though the recognition mechanisms and outcomes of PTI and ETI are different, the intermediate signaling pathways overlap [10]. After recognition, plant's constitutive basal defense mechanisms [12] initiates a diverse set of downstream signaling events, leading to an activation of complex signaling cascades such as rapid microbursts of Reactive Oxygen Species (ROS), callose deposition to strengthen the cell wall, ion channels and MAP kinase cascades, phytohormones like Salicylic Acid (SA), Jasmonic Acid (JA), Ethylene (ET) and transcriptional induction of defense related genes [18,19].

ROS

A virulent pathogen, successfully recognized by the action of disease resistance (R) gene products in plant, elicit a biphasic ROS accumulation that act as direct reactive substrates to kill pathogens, and to strengthen plant cell walls by *via* cross-linking of glycoproteins to obstruct further extension of the pathogen [20]. ROS commonly triggers and precedes programmed cell death and also functions as signal molecules for production of Pathogenesis-Related (PR) protein. In rice, OsRac1 GTPase complex, which is essential for PTI, participate in direct regulation of NADPH oxidase which in turn controls ROS production [21]. Enzymes generating ROS during the defense response include NADPH oxidase, peroxidase, oxalate oxidase and amine oxidase. The increase of Ca2+ concentration is an important factor in the development of Reactive Oxygen Intermediate (ROI) mediated cell death [22]. Ca2+ is a well-known secondary signal in numerous signaling pathways among eukaryotes. ROS induction has been implicated in rice against bacterial blight [23], blast [24] and gall midge resistance [25]. In rice-BHP interaction, Ca2+influx is triggered by insect feeding as one of the earliest cellular event [26].

Mitogen-Activated Protein Kinase (MAPK) Cascades

MAP kinase signaling has been reported to be involved in both PTI and ETI plant defense pathways [27]. MAPK pathways are activated by pathogen attack and mediated by SA which subsequently result in

Citation: Rawat N. Understanding Disease Resistance Signaling in Rice against various Pests and Pathogens. Austin J Plant Biol. 2016; 2(1): 1011.

pathogenies-related protein expression. Seventeen MAPK genes have been identified in the rice genome, however the role of these *OsMPKs* in rice defense responses yet to be deciphered [28]. The *OsMAPKs* negatively regulates rice resistance to both the pathogens (blast and bacterial blight) [29]. *BWMK1*, the first cloned MAPK gene in rice interacts with AP2/EREBP family of Transcription Factor (TF) and phosphorylates ERFs *Pti4* and *OsEREBP*, pivotal step in regulating resistance to blast and bacterial blight disease [30]. Expression levels of four MAPK genes (*OsMPK5/12/13/17*) were found to be induced by Blast and BPH [31].

Hormone signaling

Plant hormones are typically divided in two groups; one groups is for growth hormones such as auxin, Gibberellic Acids (GAs), Brassinosteroids (BRs) and Abscisic Acid (ABA) and, the other group is for defense related hormones such as SA, JA and ET those are associated with the regulation of diverse array of biotic stress responses [32]. However in past few decades, the role of growth hormones in plant defense have been widely studied which regulate plant defense, either by themselves or in combination with the defense hormones [33]. Biotic stress responses are preferentially mediated by antagonism of SA and JA/ET pathways. SA pathway is mostly connected with responses to biotrophic pathogens, while JA and ET pathways generally act synergistically and are linked to defenses against necrotrophic pathogens and herbivorous insects.

Downstream of SA biosynthesis, the SA pathway in rice shares a typical redox protein, NPR1 (NON-EXPRESSOR OF PR1) [34]. NPR1 exists as dimeric inactive protein which gets activated by SA-pathway. Salicylic acid reduces the intermolecular disulphide bonds and releases monomeric NPR1, which is translocated to the nucleus from cytosol where it interacts with TGA TF to activate defense-related gene expression [34,35]. Jasmonic Acid (JA) and its derivatives such as Methyl Jasmonate (MeJA) are known as lipid-derived hormones that play multiple and important regulatory role which comprise the regulation of developmental and defense processes in plants [36]. The only jasmonate receptor identified to date is COI1 protein, an F-box protein, which binds to JAZ proteins, a negative regulator of JA-responsive genes, finally leading to ubiquitin-dependent degradation [37]. Other JA responsive genes include leucine aminopeptidase and Allene Oxidecyclase (AOC) those are crucial in the proper functioning of JA signaling. It has been reported that the JA signaling pathway negatively regulates rice resistance to BPH, while the transcription levels of genes that are known to function in the SA pathway are activated in the *Bph14*-mediated insect resistance following BPH feeding [38]. Rice-gall midge interaction showed up-regulation of SA pathway in HR+ and not in HR- mediated defense [39-41].

Transcription Factors (TFs)

Changes in gene expression and the reprogramming of the molecular defense machinery is regulated by the action of TFs. Among many different type of TFs available in plants, the most common TFs involved in plant defense mainly belong to six groups; WRKY,AP2/ERF, MYB, BZIP, MYC and NAC [42]. Among the WRKY TFs, *OsWRKY45* is known as second master regulator of SA pathway which functions parallel to NPR1 to mediate resistance to blast and bacterial blight diseases of rice [43]. *OsWRKY45* seems to be activated at least in part by an SA-dependent phosphorylation cascade controlled by the *OsMPK4* and *OsMPK6*. *OsWRKY70* induction increases plant susceptibility in rice against BPH feeding [44]. *OsWRKY62* is a negative regulator of both types of plant immunity (PTI and ETI). AP2/ERF TFs constitutes ~163 members in rice and ~ 140 members in Arabidopsis [45]. *OsEREBP1* was reported to be induced in rice and bacterial pathogen, *Xanthomonas, oryzaepv, oryzae* (Xoo) interaction [29]. MYB15 and WRKY40 TFs may play important roles in the transcriptional regulation of carbohydrate metabolism in citrus–HLB interactions [46,47]. A number of NAC proteins such as OsNAC4 have been reported inducing HR and cell death by activating PR genes. NAC TFs (ONAC122 and ONAC131) in rice increased susceptibility to blast disease [48]. BZIP transcription factors are characterized by their basic leucine Zipper (bZIP) domain which is involved in DNA binding. Rice rTGA2.1 interacts with *OsNPR1* which has a negative impact on SAR by altering accumulation of PR genes in response to bacterial blight disease [49]. In contrast, *OsbZIP1* may play a positive role in the SA-dependent signal transduction after Blast infection [50]. BPH feeding could suppress *OsbZIP60* expression levels by introducing effector proteins which suggest that the BPH may protect itself that suppress stress responses and enhance susceptibility [31].

The present study summaries and presents an informal description of complex and comprehensive molecular mechanism of rice defense against several pests and pathogens. Plant defense and pathogen counter defense mechanisms evolved as a part of co-evolutionary race between plants and their natural enemies. In the past decades significant progress was made in elucidating the molecular mechanism and cross talk has been recognized between hormone-regulated and defense-signaling pathways. Future studies will be focusing more to understand the specific responses against different combinations of stress that could be controlled by different signaling pathways and may elucidate additional candidate disease resistance genes/pathways for crop protection and breeding programs.

References

1. Pathak MD, Khan ZR. Insect pests of rice. Int Rice Res Inst. 1994.
2. Du B, Zhang W, Liu B, Hu J, Wei Z, Shi Z, et al. Identification and characterization of Bph14, a gene conferring resistance to brown plant hopper in rice. Proc Natl Acad Sci USA. 2009; 106: 22163-22168.
3. Bentur JS, Rawat N, Divya D, Sinha DK, Agarwal R, Atray I, et al. Rice-gall midge interactions: Battle for survival. J Insect Physiol. 2016; 84: 40-49.
4. Dean RA, Talbot NJ, Ebbole DJ, Farman ML, Mitchell TK, Orbach MJ, et al. The genome sequence of the rice blast fungus Magnaporthe grisea. Nature. 2005; 434: 980-986.
5. Mansfield J, Genin S, Magori S, Citovsky V, Sriariyanum M, Ronald P, et al. Top 10 plant pathogenic bacteria in molecular plant pathology. Mol Plant Pathol. 2012; 13: 614-629.
6. Jones JD, Dangl JL. The plant immune system. Nature. 2006; 444: 323-329.
7. Schwessinger B, Ronald PC. Plant innate immunity: perception of conserved microbial signatures. Annu Rev Plant Biol. 2012; 63: 451-482.
8. Zipfel C. Pattern-recognition receptors in plant innate immunity. Curr Opin Immunol. 2008; 20: 10-16.
9. Liu W, Liu J, Triplett L, Leach JE, Wang GL. Novel insights into rice innate immunity against bacterial and fungal pathogens. Annu Rev Phytopathol. 2014; 52: 213-241.
10. Thomma BP, Nurnberger T, Joosten MH. Of PAMPs and effectors: the blurred PTI-ETI dichotomy. Plant Cell. 2011; 23: 4-15.
11. Young ND. The genetic architecture of resistance. Curr Opin Plant Biol. 2000;

3: 285-290.

12. Okuyama Y, Kanzaki H, Abe A, Yoshida K, Tamiru M, Saitoh H, et al. A multifaceted genomics approach allows the isolation of the rice Pia-blast resistance gene consisting of two adjacent NBS-LRR protein genes. The Plant J. 2011; 66: 467-479.

13. Liu J, Wang X, Mitchell T, Hu Y, Liu X, Dai L, et al. Recent progress and understanding of the molecular mechanisms of the rice-Magnaporthe oryzae interaction. Mol Plant Pathol. 2010; 11: 419-427.

14. Yoshimura S, Yamanouchi U, Katayose Y, Toki S, Wang ZX, Kono I, et al. Expression of Xa1, a bacterial blight-resistance gene in rice, is induced by bacterial inoculation. Proc Natl Acad Sci USA. 1998; 95: 1663-1668.

15. Rawat N. Identification and characterization of differentially expressed genes in rice involved in rice gall midge interactions (Doctoral dissertation, Dissertation, Osmania University). 2012.

16. Sama VS, Rawat N, Sundaram RM, Himabindu K, Naik BS, Viraktamath BC, et al. A putative candidate for the recessive gall midge resistance gene gm3 in rice identified and validated. Theor Appl Genet. 2014; 127: 113-124.

17. Yasala AK, Rawat N, Sama VA, Himabindu K, Sundaram RM, Bentur JS. In silico analysis for gene content in rice genomic regions mapped for the gall midge resistance genes. Plant Omics. 2012; 5: 405.

18. Qiu D, Xiao J, Ding X, Xiong M, Cai M, Cao Y, et al. OsWRKY13 mediates rice disease resistance by regulating defense-related genes in salicylate- and jasmonate-dependent signaling. Mol Plant Microbe Interact. 2007; 20: 492-499.

19. Baker B, Zambryski P, Staskawicz B, Dinesh-Kumar SP. Signaling in plant-microbe interactions. Science. 1997; 276: 726-733.

20. Mittler R, Vanderauwera S, Gollery M, Van Breusegem F. Reactive oxygen gene network of plants. Trends Plant Sci. 2004; 9: 490-498.

21. Wong HL, Sakamoto T, Kawasaki T, Umemura K, Shimamoto K. Down-regulation of metallothionein, a reactive oxygen scavenger, by the small GTPase OsRac1 in rice. Plant Physiol. 2004; 135: 1447-1456.

22. Alvarez ME, Pennell RI, Meijer PJ, Ishikawa A, Dixon RA, Lamb C. Reactive oxygen intermediates mediate a systemic signal network in the establishment of plant immunity. Cell. 1998; 92: 773-784.

23. Yin Z, Chen J, Zeng L, Goh M, Leung H, Khush GS, Characterizing rice lesion mimic mutants and identifying a mutant with broad-spectrum resistance to rice blast and bacterial blight. Mol Plant Microbe Interact. 2000; 13: 869-876.

24. Huang K, Czymmek KJ, Caplan JL, Sweigard JA, Donofrio NM. HYR1-mediated detoxification of reactive oxygen species is required for full virulence in the rice blast fungus. PLoS Pathog. 2011; 7: e1001335.

25. Rawat N, Himabindu K, Neeraja CN, Nair S, Bentur JS. Suppressive subtraction hybridization reveals that rice gall midge attack elicits plant-pathogen-like responses in rice. Plant Physiol Biochem. 2013; 63: 122-130.

26. Cheng X, Zhu L, He G. Towards understanding of molecular interactions between rice and the brown plant hopper. Mol Plant. 2013; 6: 621-634.

27. Meng X, Zhang S. MAPK cascades in plant disease resistance signaling. Annu Rev Phytopathol. 2013; 51: 245-266.

28. Hamel LP, Nicole MC, Sritubtim S, Morency MJ, Ellis M, Ehlting J, et al. Ancient signals: comparative genomics of plant MAPK and MAPKK gene families. Trends Plant Sci. 2006; 11: 192-198.

29. Seo YS, Chern M, Bartley LE, Han M, Jung KH, Lee I, et al. Towards establishment of a rice stress response interactome. PLoS Genet. 2011; 7: e1002020.

30. Cheong YH, Moon BC, Kim JK, Kim CY, Kim MC, Kim IH, et al. BWMK1, a rice mitogen-activated protein kinase, locates in the nucleus and mediates pathogenesis-related gene expression by activation of a transcription factor. Plant Physiol. 2003; 132, 1961-1972.

31. Hu J, Zhou J, Peng X, Xu H, Liu C, Du B, et al. The Bphi008a gene interacts with the ethylene pathway and transcriptionally regulates MAPK genes in the response of rice to brown plant hopper feeding. Plant Physiol. 2011; 156: 856-872.

32. Pieterse CM, Leon-Reyes A, Van der Ent S, Van Wees SC. Networking by small-molecule hormones in plant immunity. Nat Chem Biol. 2009; 5: 308-316.

33. Torres-Vera R, García JM, Pozo MJ, Lopez-Raez JA. Do strigolactones contribute to plant defence? Mol Plant Pathol. 2014; 15: 211-216.

34. Tada Y, Spoel SH, Pajerowska-Mukhtar K, Mou Z, Song J, Wang C, et al. Plant immunity requires conformational charges of NPR1 *via* S-nitrosylation and thioredoxins. Science. 2008; 321: 952-956.

35. Gatz C. From pioneers to team players: TGA transcription factors provide a molecular link between different stress pathways. Mol Plant Microbe Interact. 2013; 26: 151-159.

36. Wasternack C. Jasmonates: an update on biosynthesis, signal transduction and action in plant stress response, growth and development. Ann Bot. 2007; 100: 681-697.

37. Thines B, Katsir L, Melotto M, Niu Y, Mandaokar A, Liu G, et al. JAZ repressor proteins are targets of the SCF (COI1) complex during jasmonate signalling. Nature. 2007; 448: 661-665.

38. Lu J, Ju H, Zhou G, Zhu C, Erb M, Wang X, et al. An EAR-motif-containing ERF transcription factor affects herbivore-induced signaling, defense and resistance in rice. Plant J. 2011; 68: 583-596.

39. Rawat N, Sinha DK, Rajenderakumar P, Shrivastava P, Neeraja CN, et al. Role of pathogenesis-related genes in rice-gall midge interactions. Curr Sci. 2010; 99:1361-1368.

40. Rawat N, Neeraja CN, Nair S, Bentur JS. Differential gene expression in gall midge susceptible rice genotypes revealed by Suppressive Subtraction Hybridization (SSH) cDNA libraries and microarray analysis. Rice. 2012; 5: 1-5.

41. Rawat N, Chiruvuri Naga N, Raman Meenakshi S, Nair S, Bentur JS. A novel mechanism of gall midge resistance in the rice variety Kavya revealed by microarray analysis. Funct Integr Genomics. 2012; 12: 249-264.

42. Century K, Reuber TL, Ratcliffe OJ. Regulating the regulators: the future prospects for transcription-factor-based agricultural biotechnology products. Plant Physiol. 2008; 147: 20-29.

43. Shimono M, Koga H, Akagi AY, Hayashi N, Goto S, Sawada M, et al. Rice WRKY45 plays important roles in fungal and bacterial disease resistance. Mol Plant Pathol. 2012; 13: 83-94.

44. Wang Y, Guo H, Li H, Zhang H, Miao X. Identification of transcription factors potential related to brown plant hopper resistance in rice *via* microarray expression profiling. BMC Genomics. 2012; 13: 1.

45. Nakano T, Suzuki K, Fujimura T, Shinshi H. Genome-wide analysis of the ERF gene family in Arabidopsis and rice. Plant Physiol. 2006; 140: 411-432.

46. Rawat N, Kiran SP, Du D, Gmitter FG, Deng Z. Comprehensive meta-analysis, co-expression, and miRNA nested network analysis identifies gene candidates in citrus against Huanglongbing disease. BMC Plant Biol. 2015; 15: 1.

47. Du D, Rawat N, Deng Z, Gmitter FG. Construction of citrus gene co expression networks from microarray data using random matrix theory. Hortic Res. 2015; 2: 15026.

48. Sun L, Zhang H, Li D, Huang L, Hong Y, Ding XS, et al. Functions of rice NAC transcriptional factors, ONAC122 and ONAC131, in defense responses against Magnaporthe grisea. Plant Mol Biol. 2013; 81: 41-56.

49. Fitzgerald HA, Canlas PE, Chern MS, Ronald PC. Alteration of TGA factor activity in rice results in enhanced tolerance to Xanthomonas oryzae PV. Oryzae. Plant J. 2005; 43: 335-347.

50. Meng XB, Zhao WS, Lin RM, Wang M, Peng YL. Identification of a novel rice bZIP-type transcription factor gene, OsbZIP1, involved in response to infection of Magnaporthe grisea. Plant Mol Biol Rep. 2005; 23: 301-302.