

## RICE BLAST DISEASE AND DEVELOPMENT OF GENETIC RESISTANCE AGAINST IT

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**R**ice is the most important staple food in India covering a total area of 43.5 mha coupled with the total production of 159.2 MT (FAOSTAT 2013). Being a rich source of carbohydrate it is considered as the most important food grain. This crop is affected by various types of biotic and abiotic stresses which causes a substantial reduction in its yield every year. Rice blast is one of the most dangerous and dreadful diseases of rice worldwide. To control this important disease different types of management practices have been tried over time like fungicides, different agronomical practices, resistant cultivars and biotechnological approaches. Though many mechanisms are available to control or to reduce the severity of blast; host gene manipulation to impart resistance at the gene level and make the plant able to protect itself is a more effective and economic way to achieve a comparatively stable and durable performance to prevent pathogen attack (Hulbert et al., 2001). Here in this study, current advances on developing genetic resistance against rice blast have been discussed.

### Rice Blast

Rice is the most important staple food of India. It occupies 43.5 mha area coupled with the total production of 159.2 MT in India (FAOSTAT 2013). As an agricultural commodity, it is on the third position from the production point of view, however, it is the most important food grain since it contributes to more than one-fifth caloric intake of human worldwide. Across the world, it is cultivated in 162.3 mha of the area to give a production of 738.1 MT (2012). But this crop goes through various types of biotic and abiotic stresses which causes a substantial reduction in its yield every year.

Among the biotic stresses which affect the rice crop, rice blast is the most extreme contagious ailment, which restricts the production of rice. Yield loss has been recorded up to 157 million tons of rice for each annum around the world. The ‘Habitats for Disease Control

and Counteractive action' has distinguished and proclaimed rice blast to be a potential natural weapon. Rice blast disease is spreading over the world in such a quick pace that blast was first time reported in Asia just three centuries ago, but now, unfortunately, covers almost 85 nations. *Magnaporthe oryzae* is a filamentous ascomycete, the causative living organism for rice blast. This fungus produces lesions on leaves, nodes and different parts of panicles and grains at different developmental stages. Rice blast is of two types namely leaf blast and neck or panicle blast. Leaf blast affect plants at the seedling stage whereas panicle blast shows symptom after heading or panicle formation. As panicle blast directly target panicles, the economic part of rice, it leads to huge yield loss which has been recorded up to 70%.

The occurrence of the disease is higher when the temperature is low with high moisture in nature. Thus, Eastern India experiences frequent occurrence of the malady due to the great favorable climatic conditions for the development of the pathogen. The frequency of blast was accounted for to be high in the hilly areas like Uttaranchal, Himachal Pradesh and Jammu and Kashmir, where favorable condition prevails mainly during *Kharif* season.

### Genetics of Rice Blast

The gene for gene theory works for the blast disease. Rice blast resistance genes are of two types: qualitative or complete resistance and quantitative or partial or field resistance. Qualitative or true resistance is administered by major resistance genes, which may lead to the incompatible interaction against a specific race of pathogen. More than 100 blast R genes have been identified till now and they are also mapped on chromosomes of rice. Among them, thirteen genes i.e. *Pib*, *Pita*, *Pi9*, *Pi2*, *Pid2*, *Pi36*, *Pi37*, *Pikm*, *Pi5*, *Pit*, *Pid3*, *Pi21*, *Pi54* have been cloned and characterized.

Many times partial resistance is controlled by more than one gene each having minor contribution towards resistance development. These together are called quantitative trait loci (QTL). Though in any breeding programme, be it conventional or molecular, it is a bit difficult to derive QTL into other varieties, the most advantageous quality of QTL is that it renders durable resistance against pathogen and also active against a broad range of the pathogen. Till date, no such advancement has taken place to identify other QTL for panicle blast disease. QTLs discovered for panicle blast are 'qpbm11' (from Miyazakimochi) and 'pit' which are novel panicle blast resistant gene but are not well-characterized till date.

## Control measure against Blast

### Chemical control

There is an extensive variety of chemicals – fungicides which are in vogue to reasonably control the development of *M. oryzae*. The amount and time of application, their nature of the compound, stage in the life cycle of the pathogen are the determining factors for their efficacy. There are numerous fungicides and they are different in terms of their target stage of pathogen and in mechanism too. For instance, melanin biosynthetic inhibitors repress the development of the appressorium, while the choline biosynthesis fungicides influence the amalgamation of phosphatidylcholine-component of the fungal cell wall. Other than the fungicide alone, plant defence activators additionally being utilized against this malady. These chemicals will instigate the systemic acquired resistance and these chemicals give resistance not just to the parasitic pathogens but to other microscopic organisms and infections likewise. These chemicals are most certainly not a reasonable and financial burden to the poor ranchers. These are most certainly not eco-accommodating and they are dangerous to the earth and lead to the land, air and water contamination. Subsequently, these fungicides are not appropriate for long term use.

### Development of genetic resistance

#### Broad-spectrum resistance gene

Establishing wide range resistance is a broadly embraced methodology to prevent a large variety of pathogens and lessen the danger of breakdown of the resistance. This technique has been turned out to be prudent, naturally amicable and powerful to control the rice blast disease (Skamnioti and Gurr, 2009). For instance, the resistance gene *Pi2* has been proved to be effective against 455 diverse races of *M. oryzae*, which were gathered from various districts of Philippines and 13 essential rice developing territories in China. *Pi9* is another gene, which demonstrated resistance against 43 distinctive strains of *M. oryzae*, which were collected from 13 distinct nations. *Pi39(t)* also demonstrated resistance to an extensive variety of races, gathered from different Chinese regions.

#### Gene pyramiding

One of the best strategies to throw challenge against pathogen is stacking different resistance genes, which together can offer imperviousness to an extensive variety of pathogen races. The effect is equivalent to broad-spectrum resistance gene. This prevents rapid genetic

modification of pathogen to evolve as a virulent strain and to break resistance barrier of plants. When genes of complementary resistance spectra are stacked in a sole plant variety it strengthens the plant and will reduce the selection pressure on the pathogen. For instance, when *Pik* and *Piz* genes were combined gave a high level of resistance.

### Potential genes for conferring resistance against rice blast

#### R genes

Plants face many attacks from lots of pathogens every day but every time infections do not become successful because of the plant's innate immunity. Effector molecules secreted by pathogen induce an immune reaction in the plant (Effector Triggered Immunity or ETI). The receptor of effector molecules are encoded by R genes. R gene works in a dominant and race-specific manner. R genes, to mediate its effect on the pathogen, should recognize the specific Avr protein it is meant for.

This principle lies under Gene-for-Gene hypothesis given by Flor. When the product of plant dominant or semi-dominant R gene and that of specific dominant pathogen avirulence (*Avr*) gene interacts, race-specific pathogen recognition and downstream defense response take place. If pathogens mutate their *Avr* protein, it can escape recognition by the corresponding R gene of the host plant. However, in order to safeguard the plant from this virulent modifications, R genes also have been subjected to coevolution. Upon successful recognition of pathogen elicitor, plants can formulate different types of defense mechanism which are associated with hypersensitive response (HR), oxidative burst and superoxide production, calcium flux, cell wall reinforcement. The hypersensitive response involves the death of the host cell, may it be a single cell or a group of cells, followed by pathogen interaction. In the case of biotic stress or infection, it helps the plant to keep the pathogen confined in the location of infection by depriving the later of nutrition and thus a crucial component of disease resistance. Both compatible and incompatible plant-pathogen interactions lead to HR formation. It was recently established that HR is the consequence of two types of events: 1. Cell switch to a metabolic pathway which generates toxic compounds as by-product and 2. When pathogen Avr protein is sensitized, attacked cell go through an apoptotic response and cell death occurs.

### **Panicle blast 1 (*Pb1*) gene**

*Pb1* is panicle blast resistance gene rendering broad-spectrum protection. In one of the study, Miyazakimochi line has been found with different genetic source of defense against blast fungus. Till date, *Pb1* is the only gene isolated and conferring resistance against panicle blast identified in Modan, one indica cultivar from Japan. *Pb1* has been mapped on the middle part of the long arm of the chromosome. It shows considerable durability or ‘field resistant’. It produces CC-NBS-LRR protein but distinct from that of other R genes. The dissimilarities between the NBS domain of *Pb1* protein and that of R proteins increase towards N-terminus and decrease towards C-terminus of the NBS domain. The *Pb1* gene has been developed by duplication of a part of the genome and thereby achieving a new promoter region upstream of the gene. The transcript level of WRKY45 protein has been gradually enhanced up to adult stage even without pathogen inoculation. In *Pb1*-overexpressed lines, it was found that WRKY45 expression level is more than the normal one and the transcript level of WRKY transcription factor is dependent on that of *Pb1* gene because ubiquitin mediated degradation of WRKY45 is suppressed by *Pb1*. Nuclear localization of *Pb1* protein is shown to be crucial to provide resistance since rice transformants with over expressed *Pb1* fused to Nuclear Exclusion Sequence showed marked reduction in blast resistance. 1/20<sup>th</sup> part of total *Pb1* protein was detected in the nucleus and sub cellular distribution of *Pb1* protein remain same before and after the pathogen inoculation (Inoue et. al, 2013). *Pb1* is also partially dependent on the SA pathway as blast susceptible phenotype was observed in *Pb1*-ox/*NahG* lines where *NahG* is a SA degrading protein. Two conceivable systems can account for the incomplete SA reliance of *Pb1*-interceded blast resistance. One is that *Pb1* stimulate the SA pathway upstream of SA like other R proteins do, prompting WRKY45 activation through the SA pathway. Another is that lowering of basal SA levels which results in an abatement of basal WRKY45 protein level, which subsequently accelerates the decreased accumulation of WRKY45 protein in spite of the restraint of WRKY45 ubiquitination by *Pb1*. In the last-mentioned situation, initiation of *Pb1* by pathogen acknowledgement is definitely not essentially required in *Pb1*-dependent blast resistance on the grounds that incitement of WRKY45 through the SA pathway (or another pathway) and the resulting improvement of WRKY45 protein levels by nuclear-localized *Pb1* can represent the *Pb1*-dependent blast resistance.

## Conclusion

In the concluding note, it must be stated that though there is couple of ways to fight against the potential agricultural threat i.e. ‘rice blast’ the only effective and sustainable way is to develop genetic resistance in the existing germplasm. In the light of this fact, *Pbl* is the only gene found to show resistance against panicle blast of rice which in turn hold the prime importance to be introduced in breeding programs to incorporate broad-spectrum genetic resistance in existing germplasm of rice to protect the later from deadly panicle blast disease.

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