



Editorial Note on Rice Blast Disease

Feroz Khan*

National Institute of Agrobiological Sciences, Irvine, USA

Malady Rice (*Oryza sativa* L.) is one in every of the foremost vital staple foods that feed quite 1/2 the world's population, with Asia and continent because the largest overwhelming regions. Blast malady caused by *Magnaporthe oryzae* (Hebert) Barr is one in every of the foremost damaging diseases of rice. This malady was initially referred to as rice fever malady in China as early as 1637. Blast is arguably the foremost devastating plant malady of rice. Systematic studies of this malady have created important progress and known several genes.

Broad-spectrum resistance is very most popular in agricultural observe. Here, we have a tendency to focus our discussion on resistance (R) and defense-regulator (DR) genes that confer broad-spectrum resistance to *Magnaporthe oryzae*, especially those doubtless in inflicting no important yield penalties. Cross talks of defense sign mediate by these genes area unit which will permit the host to integrate totally different anti-fungal factors against *M. oryzae* infection. However, the activity pattern of this plant life breaks up the resistance barriers within the resistant or tolerant rice varieties.

These host-pathogen barriers are going to be presumably countered in future analysis by comparative genetics information from ordered sequence information of rice and *M. oryzae* for sturdy resistance and new molecular breeding approaches, transgenic and genetics approaches (i.e. miRNA and CRISPR editing) for the management of blast malady in rice. Extensive analysis of rice germplasm with physiological races within the past century reveals that complete genetic resistance (vertical resistance) is bestowed by major blast R genes named as PIR genes or Pi-genes [1].

These genes area unit typically specific in preventing infections by strains of *M. oryzae* that contain the corresponding avirulence genes; whereas, incomplete resistance (slow-blasting elements or horizontal resistance, field resistance, or dilatory resistance) is usually conditioned by quite one factor on totally different body regions. These genes

area unit remarked as quantitative resistant loci (QTLs). Resistant germplasm carrying each major and minor R genes and area unit extraordinarily vital genetic resources that rice breeders will use to boost blast resistance in elite rice varieties [2].

Blast malady could be a moving target wherever the plant life will

*Corresponding author: Feroz Khan, National Institute of Agrobiological Sciences, Irvine, USA; Email: ferozkhan@gmail.com

Received March 06, 2021; Accepted March 17, 2021; Published March 24, 2021

Citation: Khan F (2021) Editorial Note on Rice Blast Disease. J Rice Res 9: 243.

Copyright: © 2021 Khan F. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.