

## Exploration of Blast Resistant Genes and their Allelic Determinant in Sri Lankan Rice Varieties using their Domain Structures for Utilization in Breeding

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### ABSTRACT

Numerous rice blast resistance (R) genes have been identified, and a comprehensive understanding of their underlying mechanisms was deemed essential. Therefore, three major genes (*Pb1*, *Pi21*, and *Pita*) associated with rice blast (BL) were studied using genome sequences of 32 Sri Lankan rice varieties. The domain structure of each gene, *Pb1*, *Pi21*, and *Pita* of each variety was comprehensively analyzed in comparison to the three resistant varieties, *Modan*, *Owarihatamochi*, and *Tetep*. Results revealed that *Alagusamba* and *Mudaligawee* could be possessed relatively a stronger resistance compared to other varieties, due to the presence of complete pathogen recognition LRR domain which is necessary for triggering innate immunity. The resistant allele of the *Pb1* gene is reported to contain two deletions with 21 bp and 48 bp giving rise to a low amount of proline amino acids, but such lengthy deletions could not be found in any of the Sri Lankan varieties. Few Sri Lankan varieties contained alanine at the 918<sup>th</sup> amino acid position which is considered as a feature of a resistant allele of the *Pita* gene. The results of the characterization of 32 Sri Lankan rice varieties regarding three blast-resistant genes would be useful for breeding rice for blast resistance.

**KEYWORDS:** Amino acid polymorphism, Blast, LRR domains, *Magnaporthe oryzae*, Molecular breeding

### INTRODUCTION

According to the Department of Agriculture (DOA) Sri Lanka, rice blast (BL) disease which is caused by the fungal pathogen *Magnaporthe oryzae* is able to cause a significant yield loss of about 60%. The northern province of Sri Lanka, renowned for its substantial role in rice production within the country, experienced a severe outbreak of blast during the *Maha* season of 2016/2017, resulting in significant economic losses during the period spanning from 2013 to 2016 the development and adoption of resistant cultivars (Terensan *et al.*, 2022).

Among the cloned and well-characterized rice blast resistance (R) genes, the majority are nucleotide-binding site (NBS) and leucine-rich repeat (LRR) proteins, which are defined by their NBS and LRR domains. Of the three major domains, the coiled-coil (CC) domain is involved in protein-protein interactions or localization within the cell. The NBS domain is associated with signal transduction, and the LRR domain is crucial for pathogen recognition. Specifically, the LRR domain (leucine-rich repeat) plays a pivotal role in identifying pathogen-specific effectors. Notably, LRR domains are highly variable and are subject to diversifying selection (Devi *et al.*, 2016).

Therefore, identifying the diversity of major domains in Sri Lankan germplasm is crucial, as it will provide insights into the molecular mechanisms that confer resistance to rice blast disease. This knowledge is essential for developing more effective strategies to enhance resistance in rice varieties. Given the limited studies on domain diversity in Sri Lankan germplasm, this research aimed to address this gap by examining the different mutations in Sri Lankan rice accessions based on the domain structure of resistance genes.

The NRC-16-16 project has revealed the whole genome sequences of At 354 and Bg 352 Sri Lankan rice varieties by next-generation sequencing using Illumina HiSeq 2500 100PE platform and mapped to Nipponbare and R498 genomes (Abhayawickrama *et al.*, 2020). This study used these two rice varieties, At 354 and Bg 352 together with 30 Sri Lankan rice accessions reported in the International Rice Research Institute (IRRI), Philippines to find out the rice blast-resistant gene diversity in comparison with wild varieties reported to have R genes as reference varieties so that the information could be used in breeding programmes.