

Category	: 8th Rice Genetics Symposium
Select Theme	: Genome biology: Structure, Function and Comparison
Endorsement email	:
Genome biology Structure Function and Comparison Keyword 1	: Genome evolution
Genome biology Structure Function and Comparison Keyword 2	: Annotation
Genome biology Structure Function and Comparison Keyword 3	: Comparative genomics
Title of Entry	: Diversity of rice blast resistant gene Pi-ta in Sri Lankan rice accessions
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Select only one type of presentation	: 15 minute oral presentation

**Abstract** : Rice blast is one of the most devastating fungal diseases, caused by the fungi, *Magnaporthe oryzae* and it is a scourge to farmers across the rice-growing areas of the world. The Pi-ta gene is reported to be effective to combat blast causing fungi that hold the corresponding avirulence gene, AVR-Pita1. The present study was conducted to identify the existence of Pi-ta gene in 47 Sri Lankan rice accessions. Pi-ta locus position 12g0281300 from the 47 rice accessions were retrieved from the Rice SNP-Seek Database. The coding sequence of the reference Pi-ta gene (Gen bank accession no AF207842.1) was obtained from variety IR64 which is considered as highly blast-resistant variety. To study the polymorphism, exon wise comparison was made with reference sequence using clustalW of Bioedit Version 7.2.5. Complete exons were analyzed by NCBI ORF finder tool to obtain open reading frames and amino acid sequences. Thereafter pairwise alignment of amino acid sequences was made and changes of amino acids were observed. Finally, 3D models were predicted for the proteins having mutations using Phyre2 server version 2.0. The results revealed that only 37 accessions showed 18 and 21 different SNP variations in exon 1 and exon 2, respectively. Although SNPs were noted, truncation of the protein have not been detected. Since all the accessions completed open reading frame, amino acid sequence comparison resulted in 16 polymorphism along the length. Matholuwa and Hoderawala were shown with the highest number of variation (11) while Podiheenati, Sayam and A69-1 depicted the next higher variation (10). Remarkably, single amino acid difference of alanine to serine at avr protein binding site was noticed in 918th position of amino acid sequences in all 37 accessions. The 3D structures clearly indicated that the nucleotide variations altered the structure of the protein. But 10 accessions namely, Alagusamba, Honderawala, Pachchaiperumal, Podiwee, Pokkali, Race perumal, Samba, Sithaiyan kottai samba, 3210 and BW 295-5 were identical to the reference sequence. These findings show that ten accessions which possess Pi-ta sequence as that of IR64 could be potential sources of Pi-ta allele with blast resistance, especially in breeding indica rice.

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