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Dynamics of host pathogen interaction in plants

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Till now approximately 102 blast R genes and 500 blast resistance QTLs have been mapped in rice, while only 38 among them have been characterized and cloned (Devana et al., 2022). Disease resistance (R) genes like Pi9, Pita, Pi21, Pi54 are playing important role for broad spectrum blast resistance in rice. Development of near isogenic lines (NILs) using these broad-spectrum genes and understanding their signaling networks is essential to cope up with highly evolving Magnaporthe oryzae strains for longer duration. The genomic plasticity of this pathogen helps it to adapt according to the host. In order to counter the adaptability potential of the pathogen we made extensive effort to understand the mechanism of resistance. Monogenic or near-isogenic lines (NILs) that differ in a single rice-blast resistance gene are useful as differential varieties in pathogenicity tests and as genetic resources in rice breeding programs. However, because the development and phenotyping process is time-consuming and laborious, such lines exist only for a few genes. In this study novel monogenic lines containing Pi9 and Pi54 in the background of Pusa Basmati1 (PB1), a variety released in 1989 as the first high-yielding, semi-dwarf, photoperiod-insensitive, and superior quality scented rice line were used. However, transcriptome profiling studies of rice NILs upon M. oryzae infection are few in number (Sharma et al., 2016). This is the first study in which transcriptional level changes in PB1 and its three NILs carrying Pi1, Pi9, and Pi54 genes upon M. oryzae infection are compared. In this study NILs carrying Pi9 and Pi54 blast resistance gene respectively (in the background of Pusa basmati 1) serves an excellent biological material for understanding the molecular basis of rice-Magnaporthe interactions (Jain et al 2017; Jain et al 2019).

Biography

PhD in Bioinformatics with 3+ years of post-doctoral experience. I am having 14 years' experience on next generation sequencing data analysis (hybrid genome assembly, whole genome sequencing (seq), exome seq, RNA seq, small RNAseq, single cell RNA-Seq, Bisulphite seq, Chip-Seq, ATAC-Seq) of different platforms and interpretation using different omic pipelines. Experience in shell scripting, R, Perl and Python in linux environment use fast high-performance compute (HPC). Experience in next generation sequencing library preparation, array based and florescent dye-based SNP genotyping sample preparation. Worked on animal, human (type 2 diabetes and cancer) and plant genomics data applying statistical methods. Persistent learner with exceptional understanding of genomics and transcriptomics.

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