

## Research Article

## Unraveling the Mechanism of Resistance to Rice Bacterial Blight Pathogen (*Xanthomonas oryzae* pv. *oryzae*) in a Three BB Resistance Genes (*xa5*+ *xa13*+ *Xa21*) Pyramided Rice Variety, Improved Samba Mahsuri Through Metabolic Profiling

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### Abstract

The metabolic response of three gene pyramided (*xa5*+ *xa13*+ *Xa21*) bacterial blight resistant (Improved Samba Mahsuri) and susceptible (Samba Mahsuri) rice genotypes to *Xanthomonas oryzae* pv. *oryzae*, the causal agent of rice bacterial blight disease was assessed at 72 h after inoculation by using gas chromatography coupled to electron impact ionization-time of flight-mass spectrometry (GC/EI-TOF-MS). A total of 20 metabolites were found up regulated which were identified and annotated using the Golm Metabolome Database and Tag Finder software. Among them, six metabolites were unique to resistant cultivar Improved Samba Mahsuri and 14 metabolites were common to both the rice genotypes. Infection by *X. oryzae* pv. *oryzae* substantially alters the plant metabolic profile, including significant changes in sugars, amino acids and phenylpropanoids. Up-regulation of arginine, quinic acid, ornithine, putrescine, phenylalanine, and salicylic acid were detected in the resistant rice cultivar after inoculation. This investigation provides new insight into the biochemical mechanisms of resistance of three resistant gene pyramided rice cultivar, Improved Samba Mahsuri against *Xanthomonas oryzae* pv. *oryzae* at the metabolite level.

**Key words:** Bacterial blight, metabolomics, *Oryza sativa*, Rice, *Xanthomonas oryzae* pv. *oryzae*

**Citation:** Krishnan Sakthivel, Gautam RK, Srinivasan Madhavan, Kaari Manigundan, Singh Reena, Singh PK, Laha GS, Kumar Aundy and Rethinasamy Velazhahan. 2017. Unraveling the mechanism of resistance to rice bacterial blight pathogen (*Xanthomonas oryzae* pv. *oryzae*) in a three BB resistance genes (*xa5*+ *xa13*+ *Xa21*) pyramided rice variety, improved samba mahsuri through metabolic profiling *J Mycol Pl Pathol* 47 (3): 302-308.