

Category	: International Rice Research Conference
Select Theme	: Genetic improvement
Endorsement email	:
Keyword 1	: Biotic stress tolerance
Keyword 2	: Marker-assisted selection
Keyword 3	: Breeding Strategy
Title of Entry	: Marker assisted backcross breeding for improvement of BPT5204 (Samba Mahsuri) a mega rice variety of India, for blast and sheath blight disease resistance.
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Select only one type of presentation	: 15 minute oral presentation

Abstract : Blast disease caused by *Magnaporthe oryzae* and sheath blight due to *Rhizoctonia solani* are the two major constraints for rice production. Rice variety BPT5204 is extremely popular among the farmers and consumers of India because of its high yield, medium-slenderness, fine-grain type and excellent cooking and eating quality. Despite its popularity, BPT5204 is highly susceptible to many diseases such as blast and sheath blight. Hence, effort was initiated at University of Agriculture Sciences, Dharwad, Karnataka, India to improve BPT5204 for blast and sheath blight resistance by applying Marker Assisted Backcross Breeding Approach. In this study, broad-spectrum blast resistance genes Pi2 and Pi5 were introgressed independently into BPT5204 by applying marker-assisted backcross breeding approach. Tightly linked markers AP5930 for Pi2 and 40N23r for Pi5 gene were used in foreground selection. Background selection helped to identify the lines with maximum recovery of recurrent parent genome (RPG) Homozygous introgression lines in BC3F4 generation carrying Pi2 and Pi5 gene were field evaluated for blast resistance, yield per se and yield-related traits. Improved lines with improvement for blast resistance were on par with original BPT5204 for grain yield and grain features. The lines showed resistance to leaf and neck blast in multi location field evaluation in India. To incorporate sheath blight (ShB) resistance, major QTL qSBR11-1 was transferred from Tetep into improved BPT5204 with Pi2 gene. Genotyping of backcross population (BC1F2) aided in identification of plants introgressed with sheath blight QTL, qSBR11-1 and blast resistance genes in different combination. Plants pyramided with Pi1 + Pi2 + Pi54 and qSBR11-1 are identified and similarly plants having two Pi genes and QTL and one Pi gene and QTL are also identified.

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