

Category	: 8th Rice Genetics Symposium
Select Theme	: Genetics of Biotic interactions: Stress tolerance, Mitigation and Microbiome
Endorsement email	:
Genetics of Biotic interactions Stress tolerance Mitigation and Microbiome Keyword 1	: Diseases
Genetics of Biotic interactions Stress tolerance Mitigation and Microbiome Keyword 2	: blast blight
Genetics of Biotic interactions Stress tolerance Mitigation and Microbiome Keyword 3	: fungi
Title of Entry	: Pyramiding of Bacterial leaf blight resistance genes in high yielding rice variety HUR-105
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Select only one type of presentation	: 15 minute oral presentation

Abstract : The development of high yielding rice genotypes with durable resistance to bacterial leaf blight is suitable considering the extensive damage caused by the disease in most of the rice cultivated regions. The two resistance genes xa13 & Xa21 were transferred from IRBB55 pyramid line, using a marker-assisted backcross breeding strategy, into the background of susceptible, high yielding and scented grain popular rice variety HUR-105 a popular variety of Eastern Uttar Pradesh. Markers closely linked to the two genes were used to select plants possessing these resistance genes and markers polymorphic between donor and recurrent parent were used to select plants that have maximum contribution from the recurrent parent genome. The 15.22% SSR markers were identified to be polymorphic between HUR-105 and IRBB-55. The highest 28.57% polymorphism was observed for the chromosome number 3 while lowest 8.00% for chromosome number 9. Based on background selection the recovery percentage of recurrent parent genome content in the selected 23 BC2F1 plants having both the genes Xa21 and xa13 were ranged from 67.91% to 91.25%, which was more than expected per cent contribution of recurrent parent genome content (87.50%) in the BC2F1 generation as observed earlier. Under conditions of BLB infection, the two-gene pyramided lines exhibited a significant yield advantage over HUR-105. The gain in test weight and grain yield was increased up to 4.40% and 4.91%, respectively over susceptible parent HUR 105. The disease severity and area under disease progress curve in selected BC2F1 plants varied from 3.7% to 7.6% and from 39.55 to 102.90, respectively. These pyramided lines exhibited high level of durable resistance with high similarity in agro-morphologic traits and absence of antagonistic effects for yield and other characters. This work demonstrates the successful application of marker-assisted selection for targeted introgression of multiple resistance genes into a high yielding rice variety.

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