

Category	: International Rice Research Conference
Select Theme	: Genetic improvement
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Keyword 1	: Marker-assisted selection
Keyword 2	: Breeding Strategy
Keyword 3	: Selection accuracy
Title of Entry	: Polymorphic Survey in Donors for Bacterial Leaf Blight, Blast, Brown Plant Hopper and Recurrent Parent 'Krishna Hamsa' for Background Selection
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: The productivity of rice is affected by a number of biotic stresses and it is necessary that the rice varieties should possess resistance/tolerance to major biotic stresses. Conventional backcrossing can take up to five generations to recover the recurrent parent with the desired trait(s). Marker Assisted Backcrossing programs (MAB) help to reduce the number of backcross generations and greatly decrease the time for recovery of the recurrent parent. By using marker assisted backcrossing, not only genes of interest can be tracked, but also the contribution of the recurrent parent genome can be monitored during the process. For effective use of MAB, identification of polymorphic markers for background selection is important. Three donors, IRBB60 (Bacterial Leaf Blight-xa13+Xa21), IR64 NIL and Tetep (with Pi54 and Pi 9 respectively for Blast) and, DSB-2 (Bph20 and Bph21) were used. Seven hundred and eighty nine (789) SSR markers, spanning the entire rice genome on twelve rice chromosomes were used to assess the polymorphism between Krishna Hamsa and donor parents. Out of 789 markers, 50 markers were polymorphic with IRBB60, where most of them were found to be located on chromosome 2 and 4. Out of 62 polymorphic markers with IR64 NIL, chromosome 1 had the maximum. Among 71 polymorphic markers with Tetep, maximum polymorphic markers were positioned on chromosome 2 and 6. Out of 54 polymorphic markers with DSB-2, maximum were sited on chromosome 1. As the basic aim is to develop breeding lines quite similar to elite cultivar 'Krishna Hamsa' with resistance gene introgressions, donors with maximum morphological similarity (grain type, flowering duration, plant height etc) with the recurrent parent were chosen. Close proximity but with trait of interest of the donors to recurrent parent enables attaining recurrent parent phenotype at the earliest. Though we screened copious

markers, the polymorphism obtained was limited, which fulfilled our objective of selection of donors. These polymorphic markers will be valuable in mining the genome in advanced generations for speedy and reliable recovery of recurrent genome.

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