Marker assisted introgression of BB and blast resistant genes in mega rice variety MTU1010

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MTU1010 (Cotyledona sannulau) is one of the popular rice varieties released by Andhra Pradesh Rice Research Institute (APRRI), Maruteru. It is a short duration, high yielding; long slender rice variety occupied maximum area in India particularly during Rabi season. It is susceptible to bacterial blight (BB) disease, which is endemic to many rice growing areas in India and is also susceptible to blast disease. The present investigation was attempted to introgress BB and blast resistance genes into MTU 1010 using marker assisted backcross breeding method. Improved Samba Mahsuri (ISM) or B95-1 was used as a donor for bacterial blight resistance genes, xa13 and Xa21, while NLR 145 (Swarnamukhi) was used as donor for blast resistance Pi-kh (renamed as Pi54) gene. Donor parents were validated for the target genes by using xa13-promo (functional marker) for xa13 gene, pTA248 (STS marker) for Xa21 gene and RM206 (SSR marker), Pi54 MAS (functional marker) for Pi54 gene and found that the resistant alleles were present in accordance with earlier reports. Recurrent parent and donor parents showed polymorphism for the selected target genes. Parental polymorphic study was carried out between two donors and recurrent parent (MTU 1010) with 617 SSR markers. Out of 617, 82 markers showed polymorphism between MTU 1010 and ISM, while 83 are polymorphic between MTU 1010 and NLR145. Fifty six markers in common showed polymorphism between recurrent parent and both the donor parents.

Two crosses viz., MTU 1010 x ISM and MTU 1010 x NLR 145 were made during Rabi 2009-10 and confirmed hybrid plants were used for producing BC1F2 generation. At each backcross generation foreground as well as background analysis was carried out to identify target genes in hetrozygous condition with maximum recurrent parent genome. Inter cross was made between two BC1F2's of MTU 1010 x ISM (female) and MTU 1010 x NLR 145 (male) to obtain ICF1. Out of 320 ICF1 plants, four plants having required three gene combination, viz., xa13, Xa21 and Pi54 in heterozygous condition. These four ICF1 plants were analysed to screen the recovery percent of recurrent parent genome by using parental polymorphic markers. ICF1-16th plant with recurrent parent genome (90.75%) was selected and selfed to produce ICF2 seed. A total of 880 F2 plants were screened and 11 triple gene homozygous plants identified. Phenotyping for BB was carried out at 55 days old seedling stage with DRR isolate. As compared to MTU 1010, BB gene introgressed plants (lines having xa13 and Xa21) exhibited very small lesion lengths indicating a very high level of resistance. In addition, the lines containing either Xa21 alone or xa13 alone also exhibited limited lesion lengths. The 'triple positive' ICF2 plants (possessing xa13, Xa21 and Pi54) in homozygous condition were screened with parental polymorphic SSR markers for selecting those 'positive' plants which possess maximum recovery of recurrent parent genome. Highest value recorded in ICF2-16-59th (92%) plant. Donor parent introgression was analysed using Graphical genotypes, in all individuals 1.0Mb region around the xa13 gene 3.5 Mb region around the Xa21 and Pi54 gene was introgressed from the donor parents.

All the ICF2, pyramided lines selected through marker assisted selection, which are having xa13xa13Pi54Pi54, Xa21xa21Pi54Pi54 and triple positive xa13xa13Xa21xa21Pi54Pi54 in homozygous condition were selfed and ICF2 lines were screened for blast resistance at Agriculture Research Station, Nellore and APPRI, Maruteru which are hotspots for blast disease. The donor parent NLR145, which possessed Pi54 gene showed high level of resistance for rice blast with ‘3’ disease score and the MTU 1010 showed a disease score ‘7’ and all introgressed lines showed score between ‘1 and 3’ (highly resistant). The three gene and two gene lines which showed resistance to BB and blast (14 lines) were analysed for agro-morphological characters along with parent MTU 1010 was planted in RBD design. Replication data subjected to statistical analysis by using window stat software for obtaining the CV, CD and ANOVA. ICF2-16-59 line showed statistically on par with respect to yield and yield related characters when compared with MTU 1010 besides showing resistance to both BB and blast. ICF2-16-235 line showed significant superiority to MTU 1010. These lines can be further backcrossed with MTU 1010 and the material will be evaluated to select individuals with more than 95% recurrent parent genome.

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