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

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M TU 1010 (*Cottondora sannalu*) 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 NLR145. Fifty six markers in common showed polymorphism between MTU 1010 and NLR145. Fifty six markers in common showed polymorphism between recurrent parent.

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 BC₁F₁ generation. At each backcross generation foreground as well as background analysis was carried out to identify the plant carrying target genes in heterozygous condition with maximum recurrent parent genome. Inter cross was made between two BC₂F₁s 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. ICF₂-16th 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' ICF₂plants (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 ICF₃ 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. ICF₃-16-59 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. ICF₃-16-235 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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