UGC MAJOR RESEARCH PROJECT ON

DEVELOPMENT OF SUBMERGENCE TOLERANT RICE CULTIVARS THROUGH MARKER ASSISTED BACKCROSS BREEDING

(UGC F. No-41-1228/2012 (SR) dated 25.07.2012)

EXECUTIVE SUMMARY OF THE PROJECT

Submitted by

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UNIVERSITY GRANTS COMMISSION

NEW DELHI – 110 002

PROFORMA FOR FINAL REPORT OF THE WORK DONE ON THE PROJECT

1.	Title of the Project	**Development Of Submergence Tolerant Rice Cultivars Through Marker Assisted Backcross Breeding**
2.	Name of the Principal Investigator	**Dr. Y. ANBUSELVAM** **Professor and Principal Investigator,** **UGC Major Research Project** **Department of Genetics and Plant Breeding** **Faculty of Agriculture** **Annamalai University**
3.	Name of the University/College	**Dept. of Genetics and Plant Breeding** **Faculty of Agriculture** **Annamalai University**
4.	UGC Approval Letter No. and Date	**F. No-41-1228/2012 (SR) dated 25.07.2012**
5.	Date of Implementation	**August 2010**

6. OBJECTIVES OF THE STUDY

i) To develop a panel of tightly linked and flanking SSR markers for identification of QTLs for submergence tolerance.

ii) To develop a submergence tolerant version of widely grown locally adopted (high yielding) cultivar through a targeted marker assisted backcross approach for Sub 1 QTL.

7. ACHEIVEMENTS

i. The selected BC_2F_2 plants *viz.* 13-4-78 and 13-56-77 also had 15 Mb linkage drag ultimately, which was a fixed chromosomal segment of donor parent.

ii. The findings demonstrated the superiority of recombinant selection with respect to minimizing linkage drag.

iii. The major recommendation for MABC programs based on this study is for a range of advanced backcross lines should be evaluated together including the lines with the highest proportion of recipient parent genome and other lines with larger introgression segments or unlinked donor segments.

8. EXECUTIVE SUMMARY

Submergence can affect rice crop at any stage of growth. Most studies focus on submergence tolerance at vegetative stage only. Identification of the highly tolerant variety Swarna Sub 1, posses the sub 1 gene in chromosome, resulted in the development and release of submergence tolerant varieties introgressing the tolerant gene in otherwise agronomically superior varieties.

Despite this progress in breeding, adoption of these new varieties has been somewhat limited. Hence, identification of new donors through exploring new genetic resource is highly desirable.

The present study established the utilization of marker-assisted backcrossing technique for developing transgressive backcross recombinant line (BRL) having different phenotypes of flood tolerant donor with the recurrent parent genome. This type of variety was developed so that the new stress tolerant variety can be easily developed. If the newly developed stress tolerant variety is exactly similar to the original recipient variety, The BRLs were produced through self-pollination of BC_2F_1 plants which had five heterozygous loci in addition to the heterozygous target gene locus. The BC_2F_1 plants had around 15 Mb heterozygous chromosomal segments on the carrier chromosome 9. This large donor segment on the carrier chromosome was obtained due to not practising recombinant selection. In this study, we did not perform recombinant selection as used previously (Iftekharuddaula *et al,* 2011), but we used phenotypic selection instead in order to select plants that closely resembled the recipient parent, and obtained transgressive segregants for yield or other desirable traits.

Since the selected BC_2F_2 individuals in this study had a 15 Mb fixed donor chromosomal segment and the lines were produced by two backcrosses utilizing marker-assisted background selection, the newly developed lines were designated as BRLs.

The submergence tolerance of the newly developed BRLs was again found superior compared to the PILs. The submergence tolerance of 146-125-6, 145-125-46, 146-141-9,146-141-52 of ADT 36 × Swarna sub 1, 24-33-17,24-33-69,24-73-13,24-73-46 of ADT43 × Swarna sub 1 and 13-4-21,13-4-78,13-56-27 and 13-56-77 of Adhisaya Ponni × Swarna sub 1 had the highest survival rate and the highest grain yield under controlled submergence trial. The submergence tolerant lines were also tested in the flash flood affected field. The line from the cross Adhisaya Ponni × Swarna sub 1 *viz.,* 13-4-78 followed by 13-56-77 which produced the highest grain yield and significantly higher survival rate compared to the Swarna Sub 1. The higher submergence tolerance of 13-4-78 and 13-56-77 might be associated with some minor genes remaining in the 15 Mb donor segment on the carrier chromosome which again can be inherited from he donor parent Swarna Sub 1 or might be due to some positive interaction of *SUB1* QTL with the genes remaining in that region.

The introgression size in these two BRLs was 15 Mb on chromosome 9 including *SUB1* QTL from Swarna Sub 1. Due to not practising recombinant selection, the size of the donor introgression on the chromosome 9 was 15 Mb in the BRLs. The best plant of BC_1F_1 of Adhisaya Ponni × Swarna sub 1 (plant number 13) and the best plant of BC_2F_1 (plant number 13-4) had heterozygous chromosomal segment with a size 15 Mb on the carrier chromosome 9. The selected BC_2F_2 plants *viz.* 13-4-78 and 13-56-77 also had 15 Mb linkage drag ultimately, which was a fixed chromosomal segment of donor parent. With this context, Young and Tanksley (1989) pointed out that the donor genes on the carrier chromosome were the most difficult to eliminate, and could persist long after the donor genome content of non-carrier chromosomes had returned to approximately zero if no selection on markers was applied. The 15 Mb portion of donor genome can contain approximately 1500 genes. If the donor parent possesses many genes conferring undesirable agronomic traits in this region, this can reflect negatively on the agronomic performance of the selected plants. In general, this large introgression indicated considerable weakness of this approach with respect to minimizing linkage drag. Interestingly, as the donor parent was already a moderately improved genotype, this huge introgression did not reflect any negative effect on the phenotype of the BRL. In fact, there appeared a positive effect on yield in this study which was unexpected. Therefore, a major recommendation for MABC programs based on this study is for a range of advanced backcross lines should be evaluated together including the lines with the highest proportion of recipient parent genome and other lines with larger introgression segments or unlinked donor segments.