

**MARKER-AIDED QTL BREEDING FOR ENHANCEMENT OF  
SUBMERGENCE STRESS TOLERANCE IN RICE**

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**R**ice (*Oryza sativa* L.) is one of the principal cereal crops growing throughout the world. The global population is expected to reach nearly nine billion by 2050, and therefore about 160 million tons of rice is thought to be produced annually to meet out nutrition as well as food security of this growing population. The changing nature of the climate in this scenario is becoming a serious threat upon sustainable agricultural productivity and creates high yield gap. Although rice (Self-pollinated annual;  $2n = 24$ ) is known as a water-loving cereal and can tolerate prolonged submergence up to 8-9 days, severe floods in the major rice growing continents in India damage approximately 12-14 Mha (30%) of rice growing areas leading to loss of average productivity ranges from 0.5-0.8 t ha<sup>-1</sup> (Muthu et al.2020).

Majority of the rice varieties are susceptible to submergence. Genetic improvement for submergence tolerance through conventional breeding approaches has limited success report due to the complex nature of trait and barriers associated with phenotyping of the trait. Recent advancement in genetics and genotyping techniques facilitates the identification of major quantitative trait loci (QTLs) associated with submergence tolerance *Sub1*. Three related ethylene response factor (ERF) like genes have been identified from FR13A on the short arm of chromosome 9, i.e. *Sub1A*, *Sub1B* and *Sub1C* (Xu and Mackill 1996). Of them, *Sub1A* and *Sub1C* are generally up-regulated by submergence and ethylene. Deployment of the target QTLs through molecular techniques has opened the way for the development of submergence-tolerant popular rice varieties like Swarna and CO 43 by marker-assisted back cross-breeding (MABB).

## Marker Assisted Backcross Breeding (MABB)

In the present era of scientific development, use of molecular markers in crop improvement programs speed-up the genotyping process as well as precise introgression of novel genes from potential landraces to commercial cultivars by shortening the breeding cycle (Oladosu *et al.*2020). MABB for submergence tolerance is generally based upon three tiers, namely foreground, recombinant and background selection. Foreground selection deals with the selection of the desirable genes, closely linked with *Sub1*, whereas, recombinant selection involves the use of closely associated flanking markers to reduce the donor genomic region carrying the *Sub1*. Background selection describes the utility of molecular markers in accelerating the recovery of the recurrent parent genome (Oladosu *et al.*2020). Successful introgression of the *Sub1* region of FR13A through marker-assisted backcrossing has been well-documented for the betterment of submergence tolerance in mega-varieties.

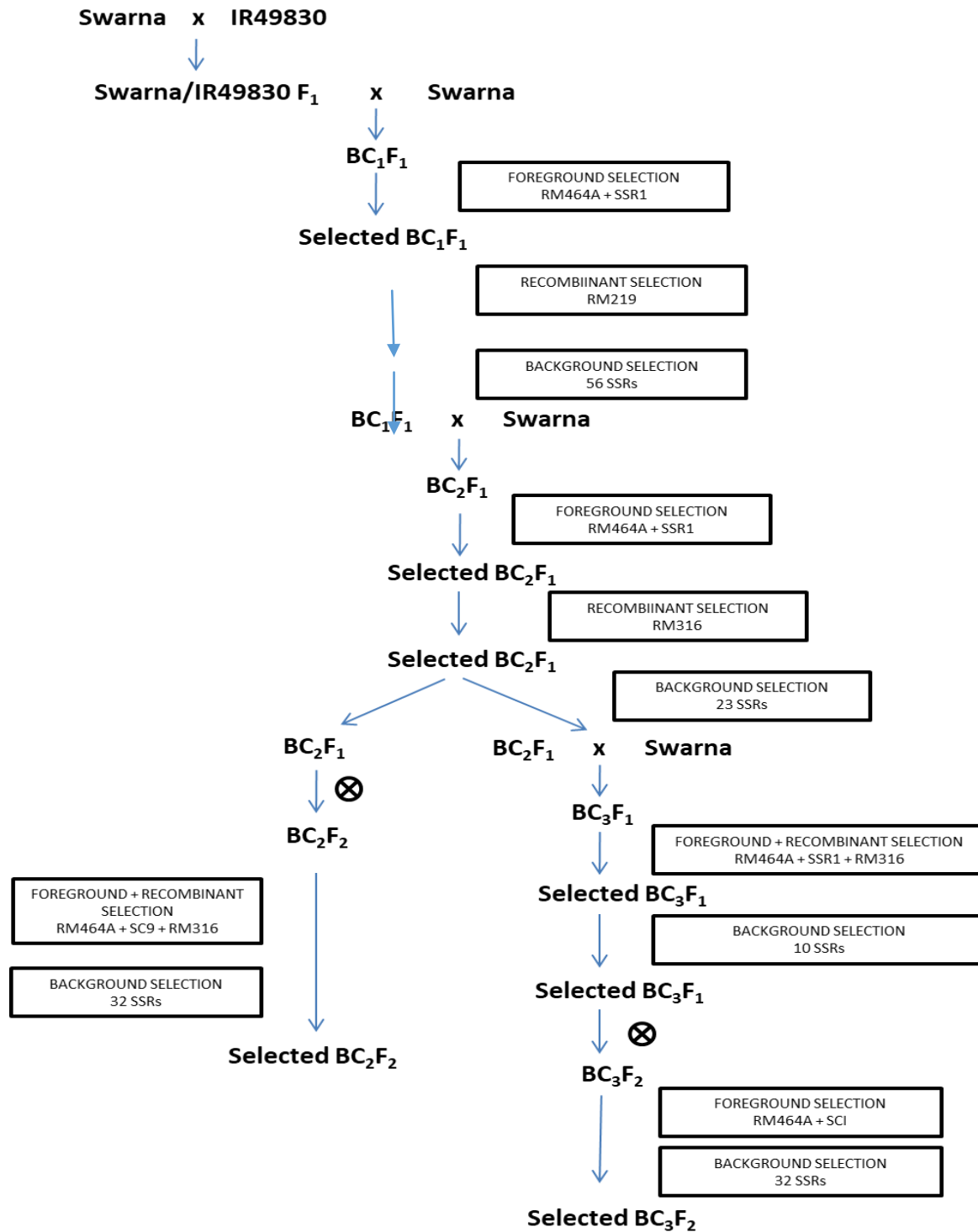
## QTL *Sub1*: from landrace to improved cultivar

The FR13A lowland rice variety is much popular among the common landraces tolerant to flesh flooding; but its direct utilization as donor parent is quite limited due to many poor agronomic traits (i.e. short thick grains, long awn, photo-sensitivity and low productivity). It is important to cross landraces (donor parent) with elite cultivars for development of submergence tolerant varieties. The molecular basis of submergence tolerance in rice imparts keen attention to the breeders in introgression of *Sub1* QTL from landrace to improved cultivars for reducing yield losses under submerged milieu (Oladosu *et al.*2020). The gene *Sub1* has been found responsible for the complete submergence tolerance up to 10-18 days. Marker-assisted backcrossing is mostly preferable in introgression of genomic region carrying *Sub1* into high-yielding varieties, such as BR 11, CR1009, Thadokkam 1 (TDK1), IR64, CO 43, Samba Mahsuri and Swarna (Septiningsih *et al.*2009).

## General workflow for QTL *Sub1* introgression in Swarna through MABB

Development of improved cultivars showing submergence tolerance involves several steps. First of all, F<sub>1</sub> generation is raised by crossing Swarna (recurrent parent) with IR49830-7 (donor parent derived line of FR13A) followed by repeated backcrossing with Swarna to obtain a large BC<sub>1</sub>F<sub>1</sub> population. From the BC<sub>1</sub>F<sub>1</sub> generation, individual plants exhibiting heterozygosity at *Sub1* locus to reduce population size for further screening (foreground

selection). Now from the individual plants having heterozygosity for *Sub1*, selection of lines having homozygosity for the recipient allele at another marker locus distally flanking the *Sub1* locus by RM219 marker (recombinant selection).



**Figure 1** Development of the submergence-tolerant Swarna-Sub1 through MABB

Source: Neeraja *et al.* 2007

Individuals with very few numbers of markers in the recombinants from the donor genome have critically opted (background selection). In the second backcross generation, the same strategy is followed for isolation of individual plants with desirable allele combination at target loci. Recombinants of *Sub1* and the nearest proximal marker locus (RM316) with suitable genomic composition at the non-target loci are crossed with recipient parent to develop the next generation in figure 1 (Neeraja *et al.* 2007).

The ultimately developed BC<sub>2</sub>F<sub>2</sub> generation having submergence tolerance with Swarna type alleles and the isolated BC<sub>3</sub>F<sub>3</sub> recombinants show homozygosity for all Swarna type alleles.

## Conclusion

The survival mechanism of rice under submerged conditions consists of internal aeration and growth controls (escape strategy). Identification of *Sub1* gene and successful introgression into mega-varieties through MABB has encouraged rapid development and release of new versions of submergence tolerance, maintaining all the desirable traits of the recurrent parent. But the effectiveness of marker-assisted backcrossing depend on the availability of closely linked markers and flanking markers for the target locus, population size, number of backcrosses and position of the markers for background selection. There is a scope to increase rice yield in marginal growing regions, by generating new genotypes with new QTLs for complete submergence tolerance and other environmental stresses altogether.

## References

Muthu V, Abbai R, Nallathambi J, Rahman H, Ramasamy S, Kambale R, Thulasinathan T, Ayyenar B and Muthurajan R. (2020). Pyramiding QTLs controlling tolerance against drought, salinity, and submergence in rice through marker assisted breeding. *PLoS ONE* 15: e0227421.

Neeraja CN, Rodriguez RM, Pamplona A, Heuer S, Collard BCY, Septiningsih EM, Vergara G, Sanchez D, Xu K, Ismail AM and Mackill DJ. (2007). A marker assisted backcrossing approach for development submergence-tolerant rice cultivars. *Theoretical and Applied Genetics* 115: 767-776.

Oladosu Y, Raffi MY, Arolu F, Chukwa SC, Muhammad I, Kareem I, Salisu MA and Arolu IW. (2020). Submergence tolerance in rice: review of mechanism, breeding and future prospects. *Sustainability* 12: 1632-1648.

Septiningsih EM, Pamplona AM, Sanchez DL, Neeraja CN, Vergara GV, Heuer S, Ismail AM and Mackill DJ. (2009). Development of submergence tolerant rice cultivars: The Sub1 locus and beyond. *Annals of Botany* 103: 151-160.

Xu K and Mackill DJ. (1996). A major locus for submergence tolerance mapped on rice chromosome 9. *Molecular Breeding* 2:219-224.