AgriCos e-Newsletter
ISSN: 2582-7049
Volume : 01 Issue : 04 August 2020 Article No: 39

Submergence Tolerance in Rice Cultivars

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SUMMARY

The submergence of rice cultivars due to frequent flooding is causing yield reductions in most rice-growing areas. With the identification of submergence tolerance gene, SUB1, derived from FR13A which is tolerant and survive up to two weeks of complete submergence enabled the use of marker-assisted backcrossing (MABC) to introduce the gene into popular rice cultivars with submergence intolerant. Under the deep-water condition, expression of SNORKEL genes was also identified with the accumulation of ethylene then triggered internode elongation to avoid anoxia through gibberellic acid biosynthesis. Several mega varieties have been improved and shown a significant increase in yield with the introgression of desired traits. .

INTRODUCTION

Rice (*Oryza sativa*) is one of the main staple foods in major parts of the world. Due to the increase in population, the production of high-yielding rice varieties is a prerequisite to meet the growing demand. Submergence tolerance in rice cultivars is important for maintaining the stable yields in low land regions where flooding is a common phenomenon mainly in the south and south-east Asia. Flooding of rice fields leads to a restriction in the diffusion of oxygen and carbon dioxide; and a decrease in the pH of the soil, which further leads to nutrient deprivation (Fukao et al., 2006). One of the most important solutions is to develop high-yielding rice varieties that are tolerant in submerged conditions (Septiningsih et al. 2009). Several studies reported that submergence tolerance in rice genotypes is contributed by a major quantitative trait locus (QTL) located on chromosome no.9 which is derived from FR13A, the most submergence-tolerant variety found in east India. It is determined by the SUB1A gene of the SUBMERGENCE1 (SUB1) QTL, which is an ethylene-responsive factor (ERF) that controls survival and retrieval of the plants after the submergence up to two weeks (Xu et al., 2006; Singh and Sinha 2016, Arya and Shylaraj 2018). This is one of the strategies rice plants use to adapt during submergence situations through conserving the entire energy by stunting growth and stand for a few weeks. Another strategy is the accumulation of ethylene that triggers the expression of SNORKEL genes (SNORKEL1, SK1 and, SNORKEL2, SK2) which contributes to internode elongation to avoid anoxia via the biosynthesis of gibberellic acid (GA) (Hattori et al., 2009).

Expression of Genes in Submerged Condition

The Sub1 region contains a cluster of three Sub1 genes i.e. Sub1A, Sub1B, and Sub1C encoding proteins with the DNA binding domain common to the ethylene response factors/ethylene-responsive element binding proteins/Apetela2-like proteins. Genotypic variation at this complex locus led to the distinction in submergence tolerance, besides Sub1B is common in all the rice genotypes irrespective of the submergence tolerance (Xu et al., 2006). Submergence-intolerance *japonica* rice lacks Sub1A and possesses Sub1B and Sub1C whereas a tolerant line containing the Sub1 locus from the *indica* FR13A encodes the ERF gene Sub1A. The level of transcript accumulation showed that the ERF domain genes Sub1A and Sub1C differentially regulated by submergence, ethylene, and GA (Fukao et al., 2012). In a recent study, Singh and Sinha (2016) reported the physical interaction of Sub1A1 with mitogen-activated protein kinase (MAPK), MPK3 in a tolerant-allele-specific manner. Though FR13A is considered as the most submergence tolerant variety, the yield is low due to the elongation of internode and lodging during floods. Therefore, the production of submergence tolerant varieties with high yield is the best solution to address the challenges at the time of the flash flood (Arya and Shylaraj 2018). Several other studies described the expression of SK genes under deepwater conditions. Hattori et al. (2009) demonstrated that the SK genes were significantly expressed in deepwater rice C9285 when treated under deepwater conditions by elongating the internodes, whereas showed low expression under dry conditions. Moreover, SK2 showed more internode elongation up to seven internodes as compared to the elongation regulated by SK1 gene (Hattori et al., 2009).

Development of Submergence Tolerant Mega Varieties

Several works have been done to incorporate submergence tolerant genes into different varieties of rice to strengthen the tolerance conferred by Sub1 genes while maintaining the desired agronomic qualities. In 2003, the International Rice Research Institute (IRRI) initiated a program for introducing the Sub1 QTL to popular meg-varieties through marker-assisted backcrossing (MABC). The main objective is to transfer only a small part of chromosome 9 harboring the Sub1A gene while at the same time recovering all the genetic traits of the varieties used as recurrent parents (Ismail et al., 2013). Introgression of Sub1 gene has been shown significant result on different varieties such as Swarna, IR64, BR11, PSB Rc18, and Ciherang, etc. (Xu *et al*., 2006; Neeraja et al., 2007; Septiningsih *et al*., 2009; Toledo *et al*., 2015). Moreover, additional traits can be introduced which could lead to beneficial characteristics, for example, anaerobic germination (AG) tolerance QTL, *AG1* has been transferred to Ciherang-Sub1 via MABC and showed significantly increased AG tolerance as well as submergence tolerance (Toledo *et al*., 2015).

CONCLUSION

The identification of the Sub1 region has helped in developing new rice cultivars capable of tolerating submergence stress during floods. Moreover, the expression of SK genes triggered internode elongation to escape stagnant partial flooding. However, there is a need to identify the underlying mechanisms of the pathways conferred by the Sub1 and SK genes that would ease to produce more cultivars with desired traits through transgenic approaches. Additionally, it may be possible to discover more genes that have better tolerance ability in order to improve yield stability in rainfed areas. Advances in breeding techniques are crucial for the improvement of popular varieties in submergence tolerance and also for combination with other traits that are important to tolerate different abiotic and biotic stresses.

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