



Category: Plant Genomics

## Marker Assisted Introgression of drought tolerance QTLs into popular high yielding varieties of rice

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### Abstract

Rice is the major staple cereal of India cultivated in about 44 million hectares area. In recent years, the increased occurrence and severity of drought stress has led to a yield decline in rice. This calls for development of varieties with higher yield potential combining drought tolerance. Even though many QTLs have been identified for various drought-related traits in rice; there are only few efforts to introgress them to develop improved breeding lines. Hence, the present research work aimed to transfer three QTL regions viz. *qDTY1.1*, *qDTY2.2* and *qDTY4.1* from Drt1IR-64 through marker-assisted breeding with the strategy of improving the grain yield of popular high yielding varieties of rice (MTU1010 and NLR34449) under reproductive stage drought stress. The parents (Drt1IR64, MTU1010 and NLR34449) were screened with flanking markers of the targeted QTLs. Among all, RM551 (*qDTY4.1*) showed clear polymorphism between drought tolerant (DrtIR64) and susceptible lines (MTU1010 and NLR34449). The flanking markers of *qDTY2.2* (RM555, RM279 and RM492) showed polymorphism of DrtIR64 with MTU1010 and NLR34449. Using these polymorphic markers as foreground markers, the BC<sub>1</sub>F<sub>1</sub> plants obtained from MTU1010/DrtIR64 (Donor for *qDTY1.1*, *qDTY2.2* and *qDTY4.1*) and NLR34449/DrtIR64 were confirmed for the presence of the targeted genes. Later, the confirmed BC<sub>1</sub>F<sub>1</sub> plants of two crosses will be backcrossed with recipient parents. Screening of the parents is being carried out at molecular level employing SSR markers that spanned the total genome, for identification of polymorphic markers. These will be used as background markers to test the recovery of recurrent genome content in the BC<sub>2</sub>F<sub>2</sub> progeny.

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