Breeding for drought tolerance: accomplishments and future strategies

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Drought regularly affects 23 million ha of rainfed rice in South and Southeast Asia and is also widespread in rainfed environments in Sub Saharan Africa. The problem is particularly severe in Eastern India, with more than 10 million ha of drought-prone fields. Drought tolerant cultivars are therefore an important breeding goal. Over the last few years, IRRI has improved drought phenotyping methodologies and standardized screening protocols. State-of-the-art drought-breeding methods are currently being used to transfer the drought tolerance of donors into elite lines through pedigree breeding and through back cross breeding for improving the drought tolerance of currently grown mega varieties. Multi-location evaluation of breeding lines in the IRRI-India drought network have identified several lines like ARB 3,ARB 4, ARB 6, ARB 8, IR74371-70-1-1, IR 55419-04, CBO-15-24, and Swarna/IR42253-54/116, which have a yield potential as high as that of the mega varieties grown in these regions, but maintain yields of 1.5-2.5 t/ha under severe drought. In such MTU1010, Swarna, Sambha Mahsuri often completely failed to set grains. IRRI and collaborators have recently reported the existence of major QTLs for yield under drought and demonstrated that, in many populations, a relatively few genes often often explain much of the variation in yield under stress. A major QTL for upland drought tolerance has been identified on chromosome 12 between SSR markers RM28048-RM511 explaining up to 50% of the genetic variance in the lines derived from the cross Vandana/Way Rarem. The effect of this QTL has been tested in a range of environments. Sets of lines with and without this QTL were compared at some of the network sites during 2006 season. Under severe drought stress, selected lines with QTL yielded at least three times higher than the lines without QTL with no yield difference between these lines under non-stress situation. This QTL is currently being fine mapped for use in marker assisted breeding. Its effect across different genetic backgrounds is also being tested. The hypothesis that small numbers of loci can have a large effect on variation of yield under stress is supported by recent observations at IRRI that BC_3-derivatives of IR64 introgressed with small segments (less than 10% of the genome) Aday Selection have substantially higher yield under drought stress than the recurrent parent. Identification of additional major QTLs for grain yield under stress and validation of their effect across genetic backgrounds and environments are underway. IRRI has also initiated efforts to develop near-isogenic lines for the identified QTLs for drought tolerance and to investigate their physiological effects. NILs differing for yield under drought in field conditions have been identified in IR77298 cross. Genotyping using whole genome arrays revealed differences at six regions. Efforts are underway to identify/characterize the gene(s) responsible. The physiological mechanisms by which RM511 QTL confers drought tolerance are being investigated. Lines with QTL showed higher number of spikelets, spikelet fertility and 100 filled grain weight, associated with an improved plant waster status, and higher rate of C^{13} discrimination in the grain under stress. It is hypothesized that a more prolific and/or deeper root system may be the possible cause

of the increased water uptake in the lines with QTL. Research is now under way to test this hypothesis. Overall, the use of molecular breeding technologies is expected to strengthen and speed up conventional breeding efforts to develop drought tolerant rice cultivars.