ABSTRACT

Rice is one of the most important staple food crops of the world. Ninety percent of the world rice is grown in Asia where it supplies 35-60% of the total food calorie intake at any given day (Khush 1997). Drought is a major constraint limiting rice production in the rainfed agro-ecosystems. The present study was done with the main objectives: (i) to develop the BC$_2$F$_1$ introgression lines in background of Swarna; (ii) to evaluate the drought related morphological and molecular traits; (iii) to identify the possible linkage drag in the introgression lines; and (iv) to identify the best introgression lines suitable for rainfed areas.

Three different F$_{3:4}$ mapping populations were developed with drought tolerant variety Nagina 22 (N22) as donor and high yielding mega varieties, Swarna, IR64 and MTU1010 as recipient, which drought susceptible parents.

The three populations were screened for yield under drought in the Dry season (DS) 2009 and DS 2010 at main experiment station, IRRI under lowland drought stress as well as well irrigated condition. Traits observed were grain yield, plant height, biomass, harvest index and days to 50% flowering.

Genotyping of the populations was done using whole genome scan and selective genotyping of bulked segregant analysis approach. N22 x MTU1010 population was screened by using 125 polymorphic SSR markers evenly spread throughout the rice genome at 10-25 cM (according to the Cornell IR64 x Azucaena SSR map). N22 x Swarna and N22 x IR64 populations were genotyped using bulked-segregant analysis approach in which DNA of 5% high and 5% low yielding tail lines
were bulked and analyzed with 140 polymorphic SSR markers evenly distributed throughout rice genome.

A major QTL for yield under drought, $qDTY_{1.1}$ was identified on rice chromosome 1 in all the three populations showing additive effect up to 38% in the N22 x Swarna population. This QTL showed consistent effect in all the three populations in the dry seasons of both 2009 and 2010. Other QTLs identified for yield under drought were $qDTY_{10.1}$ in N22 x MTU1010, $qDTY_{3.2}$ in N22 x Swarna and $qDTY_{2.2}$ in N22 x IR64 populations. The QTLs $qDTY_{1.1}$ and $qDTY_{10.1}$ showed consistent effect across the years, while $qDTY_{1.1}$ was consistent across the genetic backgrounds also.

These QTLs could be efficiently used for marker assisted back cross breeding, marker assisted selection or QTL pyramiding in a way to breed drought stress tolerant rice varieties. Fine mapping and candidate gene isolation could also be done for better understanding of the molecular aspects of drought tolerance in rice.