ABSTRACT

Rice, a cereal though grown under testing conditions in several parts of the world, remains as a major food crop for nearly half of the world’s population. The rice crop is constantly exposed to a wide range of environmental stresses such as drought, salinity, heat/cold and submergence, that seriously affect productivity and cause significant yield losses. One of ways to minimize the yield losses is the enhancement of host plant tolerance to these major abiotic stresses. As the tolerance traits in crops are controlled by many genes/quantitative trait loci (QTLs), their identification and functional analysis of them is an essential prerequisite. Studies on morphological and physiological traits of the crop under stress can lead to identification of genotypes having tolerance to abiotic stresses and molecular analysis can reveal the gene/QTL involved.

The main objective of the present study was to identify new genes/alleles associated with tolerance to drought in rice. Detailed investigations were conducted on the thirty eight rice accessions that were identified from the field screening study of 758 rice accessions against drought. Three sets of experiments were conducted to phenotype the 38 genotypes (along with five controls) for identification of drought tolerant genotypes. The experiments include: i. Drought phenotyping based on morphological traits by applying stress (5, 7, 9 d) on five weeks old plants under pot conditions ii. Drought phenotyping based root growth parameters by applying stress (15 d) at the vegetative stage on 45 days old plants using the longitudinal vessels (PVC pipes) and iii. Drought phenotyping using germination parameters under osmotic stress, created by PEG 6000, under laboratory conditions. In the fourth experiment, the same set of 38 genotypes along with controls was subjected to salinity stress under hydroponic conditions. The results indicate not only variation for morphological and physiological traits and also showed significant variability in their tolerance level to stress conditions.

Molecular profiling was performed on 43 genotypes (including controls) through PCR assays using 33 markers linked to QTLs that are associated with drought tolerance trait and six gene based STS markers. Of the thirty three, twelve markers were observed to polymorphic and are closely associated to drought stress tolerance traits while the remaining were observed to be monomorphic and their PIC values are in the range of 0.129 (RM250) to 0.493 (RM545) with an average of 0.37, a higher value observed than in earlier reports.
Based on the information available with the public data bases and literature, gene specific primers were designed to amplify DNA sequences of candidate six selected putative candidate gene or regulatory sequences associated with both drought and salinity tolerance in rice. The alignment of the amplified sequence of the target loci/genes in the selected fourteen rice accessions indicated the presence of InDels at different positions of the candidate genes/regulatory sequences. The pooled data from phenotypic, physiological and molecular information on sequence alignment, and sequence similarity analysis of the selected 14 rice genotypes (reference genome is Nippon bare) clearly detected allelic variations between tolerant and susceptible genotypes. Among the six genes examined, allelic variation was observed in the conserved regions of exons of the key candidate genes OsCDPK7, OsERF3, OsGRF8 and OsDREB1 while variation in the intron regions was observed in OsRacB and OsCam genes.

In summary, the morphological, physiological and molecular characterization of thirty eight promising genotypes has led to the identification of genotypes with high level of tolerance to both drought and salinity and the sequence variations observed in different genes could account for tolerance and susceptibility. In the study, four rice accessions i.e. BAM47, BAM859, BAM971 and BAM4060 which were identified as highly tolerant to both drought and salinity were found to have similar allelic pattern and sequence similarity with known tolerant controls i.e. N22 and CR-143-2-2. The four markers i.e. RM 256, RM314, RM289 and RM545 that could clearly demarcate the tolerance and susceptibility to drought can be employed in marker assisted selection programs for efficient and precise transfer of tolerance trait to drought stress in to elite genotypes of choice.