CHAPTER 6

Summary

Rice is one of the most important food crops at the world level with nearly 2.5 billion people using it as a staple food. It provides 21 percent world’s calorific energy and 15 percent of dietary protein requirement.

Rainfed rice occupies approximately 45 percent of world’s total rice growing area but its contribution is only 25 percent to total rice production. Drought is the primary cause of poor yield in rainfed rice. Development of high yielding well adapted rice varieties is the prime requirement to increase food production and sustain livelihoods.

The genetic improvement for adaption to drought is addressed through the conventional approach by selecting for yield under drought stress and stability. Due to the inherent variation in field and unpredictability of drought occurrence, such programs are slow in attaining progress. Drought tolerance on the other hand comprise a more complex phenomena of interaction of various traits, which are polygenic in nature called as quantitative traits.

QTL mapping provides some insight into understanding the complexity expected to be encountered in drought tolerant quantitative traits. Within these quantitative trait QTLs, actually thousands of genes individually called as candidate genes are associated which are interacting with each other to express that trait. Interaction of these various candidate genes and their expression is greatly influenced by environmental condition. Thus, mapping of candidate genes under water stress environmental condition for quantitative traits associated with drought tolerance opens an opportunity to understand expression of that trait so that in future
incorporation of favorable alleles of only targeted genes can serve to improve cultivar performance under water stress condition.

To map candidate genes associated with water stress the Masuri-Moroberekan recombinant inbred lines population was screened under low moisture regime and then the QTLs for drought related traits were identified. Based on physical position of QTLs, the candidate genes associated were mapped using bioinformatics tools.

The results obtained on all such aspects during present investigation are summarized below:

- Field evaluation revealed highly significant difference among the genotypes for traits indicating presence of wide range of variability in mapping population.
- High phenotypic coefficient of variance was observed for number of tillers, flag leaf length, leaf rolling, leaf drying, grain yield and moderate phenotypic coefficient of variance could be noticed for plant height, spikelet fertility and test weight.
- Genotypic coefficient of variance was moderate for plant height, number of tillers, flag leaf length, spikelet fertility, test weight, while high genotypic coefficient of variance was observed for leaf rolling, leaf drying and grain yield.
- While moderate heritability could be noticed for plant height and number of tillers, all other traits showed high level of heritability. These results revealed that there is less difference in genotypic coefficient of variance and phenotypic coefficient of variance indicating that variation is governed by genetic architecture of genotype.
- Correlation studies revealed that grain yield was positively associated with plant height, number of tillers, spikelet fertility,
flag leaf length. While it was negatively associated with leaf rolling and leaf drying.

- Number of superior performing lines over tolerant check ARB 6 were observed. These lines were 39, 89, 269, 272, 62, 115, 21, 144, 268 and 156. All these entries showed medium height, small number of tillers, spikelet fertility more than 80%, low leaf drying and leaf rolling sores besides medium flag leaf length.

- QTL mapping revealed 18 QTLs for eight traits on all chromosomes except on chromosome 11.

- For plant height, three highly significant QTLs could be identified, qPHT3-1 and qPHT8-2 showed more than 15% phenotypic variation. Within these QTLs candidate genes like Beta-glucosidase, Amygdalin hydrolase isoform AH I precursor, Glycoside hydrolase, Phosphoglucomutase, Glucosamine-fructose-6-phosphate aminotransferase, ETHYLENE-INSENSITIVE3-like 3, Oxalate oxidase 1, Luminal binding protein 2 precursor (BiP2), various transcription factors and transporter proteins were identified.

- Two significant QTLs from chromosome 9 were identified for number of tiller trait. Within these QTL regions, 63 unique candidate genes have been identified, out of which some important candidate genes comprised Glycoside hydrolase, Beta-primeverosidase, UDP-Glucose 4-epimerase, EGF-like calcium-binding domain containing protein, Beta-1,3-glucanase homologue, CMCase cellulase has endo-1,4-beta-D-glucanase , Endo-beta-1,4-glucanase, Beta-galactosidase, Heat shock protein 82, Serine/threonine-protein kinase , Pirin proteins, Auxin responsive SAUR protein family proteins, Hd1-like protein, Phosphofructokinase family protein and various transcription factor protein.
One strong QTL with phenotypic variation of 22.62% was identified for flag leaf length on chromosome 2 at RM 213. Within this QTL, candidate genes like Aux/IAA Protein Family proteins playing novel role in auxin signaling and ERECTA-like kinase 1 involved in protein phosphorylation could be identified.

For spikelet fertility two highly significant QTLs have been identified. They were namely qFER1-1 and qFER6-2 representing 23.64% and 25.66% of phenotypic variation respectively. Among these two QTLs, 39 unique candidate genes were identified out of which some important candidate genes were RF2, GA 3beta-hydroxylase NBS-LRR disease resistance protein homologue, Leucine-rich repeat, GTP-binding protein and Cytokinin dehydrogenase 1.

For leaf rolling three QTLs were identified on chromosome 4, 5 and 7 one on each. Within these QTLs, some important transcription factors like Snapdragon myb protein 305 homolog, Myb protein, WD40-like domain containing protein, Zn-finger, CCHC type domain containing protein have been noted. Auxin responsive factor 10, Defence responsive genes like Leucine-rich repeat, NBS-LRR protein, Heat shock protein DnaJ, N-terminal domain containing protein Ethylene responsive element binding proteins (EREBPs) and various Protein kinase were also identified.

Leaf drying QTLs were identified on chromosome number 1 and 2 as qDRY1-1 and qDRY2-2, respectively. Both these QTLs showed more than 10% variation in phenotype. For leaf drying also various transcription factors like Myb, DNA-binding domain containing protein, WD40 repeat protein, Zn-finger, MYND type domain containing protein, Histone-fold domain containing protein, WRKY transcription factor 67, MCB2 protein, DNL zinc finger domain containing protein, Zn-finger, LSD1 type domain
containing protein were identified along with various protein kinase.

- Only one minor QTL was indentified for test weight on chromosome 12 having positional candidate genes like seed maturation protein domain containing protein, Sucrose transporter gene, Ethylene-responsive methionine synthase and Auxin responsive SAUR protein family protein.

- Under grain yield QTLs, various candidate genes like Globulin 2 a seed storage protein, Glutathione S-transferase family proteins, Fructosyltransferase, Glycoside hydrolase, Beta-D-glucan exohydrolase, isoenzyme ExoII, Endo-1,4-beta-glucanase, Beta-glucanase, Glutamate dehydrogenase, Glycosyl transferase, Glucose-6-phosphate, Rf1, Cytochrome P450, gibberellin regulated family protein, AUX/IAA protein family protein, Heat shock protein Hsp20 and Amino acid/polyamine transporter II family protein have been co-localized.

The future scope of these findings can be indicated as:

- For improving existing cultivar or hybrids for drought tolerance through incorporating alleles of targeted genes by marker assisted breeding program,
- To understand upstream and downstream regulation of various genes associated with drought tolerance,
- To establish complex network of various genes associated with drought tolerance, And
- To develop tolerant cultivars through transgenic breeding program.