Chapter - 5

Summary and Conclusion
Soil salinity is a major deterrent to higher rice productivity in the world including India. Therefore there is a constant need to look for and utilize rice genetic resources which can withstand the adverse effects of such unfavourable environments. The present investigation was carried out to screen and evaluate rice genotypes introgressed with SALTON QTL for salt tolerance and diversified genotypes including check varieties developed and maintained at International Rice Research Institute (IRRI), Philippines. The evaluation of the novel rice material for salt tolerance upto reproductive stage was carried out in artificially created microplots or lysimeters at Central Soil Salinity Research Institute (CSSRI), Karnal, India during two consecutive years of kharif 2009 and 2010. Nursery of the plant material was raised in a normal field. The seedlings were transplanted during both years in thrice replicated randomized complete block design in the normal soil (no stress, pH 8.2, ECe 0.7 dS/m), moderate sodic (pH 9.5) and high saline (ECIw 10dS/m) microplots. During both years, weather parameters during crop cycle were recorded by the meteorological section of CSSRI, Karnal. The observations were recorded on five randomly selected plants of each genotype in each replication for nine traits viz. plant height (cm), total tillers/plant, productive tillers/plant, panicle length (cm), 1000 grain weight (g), spikelet fertility (%), biological yield (t/ha), grain yield (t/ha) and harvest index (%). For molecular screening of the diverse salt tolerant rice germplasm/land races, rice genotypes leaves were sampled and the DNA was extracted using CTAB method and the seven SALTON QTL linked SSR markers were used for the screening of salt tolerant rice genotypes for the presence/absence of markers linked with SALTON QTL region.

The observations on important growth characters, yield attributes, yield and quality characters were recorded across 3 environments in both the years and thus the data collected so far, averaged and tabulated for statistical analysis for individual years. Further, homogeneity of the data for both the years was tested and if the data was found homogenous the pooling was performed. The data were analysed to assess genetic variability, heritability broad sense (h²b), expected genetic advance, the degree of inter character association and their direct and indirect effects on grain yield under salt stress environments in rice genotypes. The major findings of the study are summarized below:
1) Significant differences among SALTOL QTL introgressed genotypes were observed for all the characters in different environments. Mean squares due to genotypes were highly significant for all nine characters (plant height, total tillers, productive tillers, panicle length, biomass, grain yield, 1000 grain weight, spikelet fertility and harvest index) indicating that the genotypes were sufficiently different from each other for the traits studied in the non stress and two salt stress environments.

2) The phenotypic coefficients of variability (PCV) were in general higher than genotypic coefficients of variability (GCV). As seen, highest coefficient of variation (CV) was observed under saline stress for spikelet fertility and grain yield, followed by biological yield in moderate sodic stress, and harvest index under saline stress. Heritability was recorded as the highest for total tillers followed by grain yield, plant height and spikelet fertility in moderate sodic stress. The high heritability along with high genetic advance were registered for grain yield, spikelet fertility, harvest index, panicle length, biological yield in both moderate sodic and saline stress environments.

3) Character associations revealed close relationship among growth attributes and yield contributing traits. Harvest index, biological yield and spikelet fertility per plant showed positive and significant association with grain yield per plant in moderate sodic and saline environment. Harvest index was found to be positively and significantly associated with spikelet fertility in saline environment.

4) Path coefficient analysis revealed that biological yield per plant exerted high order direct effect and also had positive association with grain yield per plant followed by harvest index in normal and moderate sodic environment while harvest index exhibited high positive direct effect on grain yield in saline stress environment. The characters showing relatively higher indirect effects on grain yield were plant height, total tillers, productive tillers, panicle length, biological yield, 1000 grain weight, spikelet fertility across all environments.

5) Inorganic analysis for Na$^+$ and K$^+$ content in leaves and stem of rice genotypes showed that genotypes have accumulated the high concentration of Na$^+$ and
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lower concentration of K\(^+\) in saline soil environment while in normal and moderate sodic environment low concentration of Na\(^+\) was found than K\(^+\). The Na\(^+\)/K\(^+\) ratio got increased from normal condition to high salinity level both in leaves and stem.

6) It has been found that the genotype IR 84645-305-6-1-B, performed highest grain yield in normal, moderate sodic and high saline environments followed by IR 84645-275-3-2-B, IR 84649-95-1-1-B, IR 84649-275-4-1-B, IR 84649-129-5-1-B, IR 84649-320-3-1-B, IR 84649-292-3-1-B while IR 84649-320-21-1-B and IR 84649-33-24-1-B genotypes have showed high grain yield in high saline stress environment among all the 18 SALTOL introgressed rice genotypes. Among all SALTOL introgressed rice genotypes, IR 84645-305-6-1-B consistently topped across three environments. However compared to conventionally bred salt tolerant check varieties, none of the QTL materials could outperform best checks in normal (CSR 36), and sodic & salinity stresses (CSR 23), though IR 84649-275-3-2B could attain parity with best check in sodic soil.

7) The stress intensity under salinity stress was almost three times more than that of sodicity stress. High saline stress susceptibility index (SSI) was significantly and negatively correlated with plant height, panicle length, grain yield, spikelet fertility and harvest index in high saline stress condition. The high saline stress tolerance index (STI) was significantly and positively correlated with plant height, total tillers, productive tillers, biomass, grain yield and harvest index in all three environments studied. Salinity yield performance was found directly correlated with stress tolerance indices for both sodicity and salinity. Stress tolerance indices (STI) for sodicity stress was positively correlated with that of salinity stress. It is useful finding to conclude that superiority of germplasm under sodicity stress is most likely sustainable under salinity stress also, plausibly due to presence of common genetic and physiological mechanisms underlying tolerance to both types of salt stresses.

8) The seven SALTOL linked SSR markers on chromosome 1 were used to compare haplotypes for the screening and discrimination of salinity tolerant rice genotypes. Among sixty three rice genotypes forty two haplotypes were
identified. Sixteen haplotypes possess thirty seven genotypes with different combinations of Pokkali’s alleles, while twenty six genotypes have different marker alleles in reference to Pokkali. The genotypes Pokkali, FL 478, IR 65209-3B-6-3-1, IR 65847-3B-9-2, BR28, BR11, IR 59418-7B-13-1, IR 63291-B-3R-B-8-3, IR 64196-3B-14-3, IR 64419-3B-4-3, IR 64197-3B-12-3, IR 64426-4B-17-2 and IR 58443-6B-10-3 were found to be highly tolerant to salinity stress and found that all genotypes had the Pokkali allele for RM 3412 marker and some of salt-tolerant genotypes had the Pokkali marker allele for AP 3206. All the seven markers were able to discriminate the salt tolerant genotypes with respect to SALTOL genomic region. The crosses have been made between high yielding and popular rice varieties i.e. PR114, PR115, NDR 359 and Pusa44 with FL478 (carrying SALTOL QTL) for transfer of SALTOL QTL in these mega varieties for long term impact.

The overall results revealed parameters of genetic variability, correlation and path analysis and agronomic performance of the novel lines which are the product of DNA marker assisted breeding. A new spectrum of molecular diversity was also revealed among diverse salt tolerant rice genotypes by employing DNA markers which are associated with SALTOL genomic region on chromosome 1 in rice. It is indicated that that the new SALTOL rice material could have better adaptability and advantage under moderate salinity situations of coastal areas rather than higher inland salinity stress conditions. It is also opined that through development of NILs (near isogenic lines), it would be worthwhile to simultaneously evaluate SALTOL introgressed genotypes along with non-QTL (control) parent to quantify the beneficial effect for the QTL impact across genetic backgrounds and locations.