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## FINAL PROGRAM & ABSTRACT BOOK

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## HAPLOTYPE DIVERSITY IN THE 'SALTOL' REGION AND ITS ASSOCIATION WITH SEEDLING STAGE SALT TOLERANCE IN DIVERSE RICE GERMPLASM

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**Introduction:** Rice is sensitive to salinity at early seedling and flowering stages. A major QTL for seedling stage salt tolerance *Saltol* has been reported on chromosome 1. The present study was carried out with the objective of characterising the haplotypes diversity in the *Saltol* region and its association with seedling stage salinity tolerance in 23 diverse germplasm including land races, wild germplasm and improved varieties.

**Methods:** A set 20 polymorphic microsatellite markers associated with *Saltol* was used haplotype analysis. Phenotyping was carried out for seedling stage salt stress response using a visual score scale of 1 to 9 by exposing them to NaCl concentration of  $12 \text{ dS.m}^{-1}$  under controlled environmental conditions.

**Results :** Seedling stage salt response of the genotypes varied significantly. Allelic diversity within the *Saltol* markers showed variation ranging from 2 to 6 alleles. The genotypes from *Kaipad* region of Kerala, possessed similar haplotypes in *Saltol* and showed salinity tolerance similar to Pokkali. The salt tolerant wild rice genotypes, W19 and W20, were found to possess altogether different haplotypes and may be novel sources for salt tolerance.

**Discussion and conclusion:** Overall, 23 rice genotypes were found to possess 14 different haplotypes based critical markers linked to *Saltol* QTL located on chromosome 1 using Pokkali as the reference cultivar. The haplotypes possessing both of RM8094 and RM3412 markers could discriminate the salt tolerant genotypes from the susceptible genotypes and hence could be useful for marker-assisted selection of *Saltol* QTL.