

Category	: International Rice Research Conference
Select Theme	: Genetic improvement
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Keyword 1	: Abiotic stress tolerance
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Title of Entry	: Mapping QTLs for Reproductive Stage Salinity Tolerance in Rice (<i>Oryza sativa</i> L.) using F2 Population of the Cross NSIC Rc222 x BRRI dhan47
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Salinity is the most common and extensive soil problem in coastal rice production environments. Tolerance at the reproductive stage is the most crucial as it determines grain yield. An F2 mapping population was developed from two rice genotypes contrasting in tolerance: NSIC Rc222 (sensitive) and BRRI dhan47 (tolerant). The performance of F2 population showed transgressive segregation in the yield components under salinity stress of 10 dS/m. Ninety-six single nucleotide polymorphism (SNP) markers polymorphic between the parents were used to construct a linkage map of 1306.2 cM (Kosambi), with an average of 13.6 cM. Eight QTLs with logarithm of odds (LOD) values ranging from 2.9 to 4.1 were identified on chromosomes 1, 2, 5 and 11, explaining 13.4 to 18.4 % of the phenotypic variation. Results of this study suggest that genomic region on chromosome 2 affects salinity tolerance at the reproductive stage through alterations in the number of filled spikelets, percent filled spikelet and yield. The study reports the construction of a genetic map for reproductive-stage salt tolerance in rice and demonstrates its utility for molecular mapping of QTLs controlling salinity tolerance-related traits, which will be useful in marker-assisted selection.

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