

Investigation of seedling-stage salinity tolerance QTLs using near isogenic lines derived from Pokkali.

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Abstract

The major quantitative trait locus (QTL), *Saltol*, for seedling-stage salinity tolerance and low Na⁺/K⁺ ratio has been previously identified on rice chromosome 1 using recombinant inbred lines (RILs) from the cross of tolerant rice landrace 'Pokkali' and sensitive 'IR29'. A backcross mapping population (BC₃F₃, BC₃F₄ and BC₃F₅ near isogenic lines) derived from a cross of the same parent lines Pokkali and IR29 has been used for the fine mapping of *Saltol* (continuation of the previous work) and for the investigation of additional QTLs. Salinity tolerance is a multi-trait system. For durable tolerance to salinity, it is necessary to find out other QTLs for salinity tolerance and introgress to farmer popular mega varieties along with the *Saltol*. This mapping population consisted of a different combination of genotypes i.e. tolerant genotypes (with SES 3-5) with and without the *Saltol* locus, sensitive genotypes (with SES 6-9) with and without the *Saltol* locus. All of these genotypes were subjected to salinity tolerance screening (in hydroponics) and many of those were genotyped with markers at the *Saltol* locus as well as throughout the 12 chromosomes. The polymorphic marker data was analyzed by QGene mapping software. The results showed 4 QTLs at markers RM26063, RM3867, RM20224 and RM222 on chromosome 11, 3, 6 and 10, respectively, having LOD > 5. The next plan would be the characterization of the QTL with highest LOD score 6.25 and coefficient of determination (R²) of 15%. Major QTLs will be targeted for fine mapping by saturating identified region with more polymorphic markers. Identification of markers flanking the additional QTLs will be important for introgression of multiple QTLs in farmer popular varieties.

