

Category	: International Rice Research Conference
Select Theme	: Genetic improvement
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Keyword 1	: Breeding Strategy
Keyword 2	: Abiotic stress tolerance
Keyword 3	: Marker-assisted selection
Title of Entry	: Mapping and comparative assessment of root QTLs using bi-parental Sri Lankan rice (<i>Oryza sativa</i>) population under non-stress and salinity stress conditions
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Development of rice root genetic architecture is important to have higher yield potential and greater yield stability under abiotic stress conditions. Root related traits exhibit polygenic inheritance and therefore the dissection of the genetic determinants of the root architectural traits could be achieved by mapping of Quantitative trait loci (QTLs) using molecular markers. Accordingly, present study was focused on mapping of root related QTLs in rice using the Recombinant Inbred Line population (RIL) derived from At354 and Bg352 under normal growth condition. At354 has less extensive, thin root structure while Bg352 has comparatively larger extensive, dense root structure. Comparative assessment of root QTLs identified under non-stress condition was made based on the root QTLs identified in our previous study under salinity stress condition using the same mapping population. Four root traits, namely, root volume (RV), top root girth (TRG), root dry weight (RDW) and root length (RL) were assessed in 91 RILs grown in hydroponics (56 days) under non-stress condition. Mapping population was genotyped in our previous study using the Illumina Infinium rice 6K SNP chip containing 5274 SNP loci covering all 12 rice chromosomes. Accordingly, QTL mapping was conducted using the densely saturated molecular maps resulted from 1135 polymorphic SNP markers, spanning 1460.81 cM of the rice genome with an average interval of 1.29 cM between marker loci. Gaps of the molecular maps were

saturated with few SSR markers. Results revealed eight QTLs associated with TRG and RDW explaining 8.3%-14.8% of phenotypic variation under non-stress condition. Identified root QTLs were located within the narrow flanking SNP marker intervals of chromosome 2,4,5,7,8 and 10. According to the comparative assessment of root QTLs, six root QTLs were co-localized within the same flanking regions of the root QTLs identified under salinity stress, indicating their contribution under both stress and non-stress environment. These QTL regions would be promising genomic regions which would facilitate future breeding approaches of rice root system development adaptive to different environmental conditions. A SSR marker, RM24894 closely associated with the QTLs, qNTRG10 and qNRDW10, was also identified as a user friendly marker to be used in marker assisted breeding.

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