

Category	: International Rice Research Conference
Select Theme	: Systems physiology
Keyword 1	: Root biology
Endorsement email	:
Keyword 2	: Drought tolerance
Keyword 3	: Phenomics
Title of Entry	: Quantitative trait loci analysis of root anatomical traits in KDML105-CSSLs under well-watered and drought conditions
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Drought is a major constraint to rice production in rainfed areas across Asia. Rice varieties with improved growth and yield under drought are urgently needed. During the past decade, many researchers reported that variation of root anatomical traits are associated with adaptation under drought. Molecular marker-assisted breeding has been proposed as an important tool to develop improved varieties of crop plants. In this study, we studied the drought effect and identified DNA markers associated with root anatomical traits including root cross sectional area, aerenchyma area, and percentage of aerenchyma area in cortical area, xylem area, average xylem area and number by using SNP marker. The 135 Chromosome Segment Substitution lines (CSSLs) were used as a mapping population and were grown in the field under well-watered and drought conditions in Ubon Ratchathani province, Thailand, during in 2016. A large phenotypic and genotypic variations were observed for all the traits. Drought caused a significant reduction in plant height and leaf dry weight by 6.51% and 16.63%, respectively. Xylem area and average xylem area increased under drought by 27.63% and 25.05, % while aerenchyma area and % aerenchyma area in cortical area were decreased in response to drought by 5.21% and 4.86%. Correlation analysis revealed that majority of root anatomical traits were positively correlated among one another. In drought, xylem area was correlated with plant height ($r= 0.18$, $p<0.05$) while root cross sectional area and aerenchyma had significant positive correlation with leaf dry weight ($r=0.21$, $p<0.05$). QTL analysis were performed by ICI mapping using simple marker analysis with LOD score of 2.5. A total of 5 QTL were identified. Three QTL were detected for

xylem number on chromosome 3 and 4 and two QTL were detected for xylem area on chromosome 2 and 4 under well-watered condition with total PVE of 19.42% and 13.08%. In drought, SNP markers for xylem area were identified on chromosome 4 with total PVE of 9.966% but not significant. Identification of QTL for root anatomical traits may be useful for breeding programs for optimization of the root function in specific environments.

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