

Category	: International Rice Research Conference
Select Theme	: Systems physiology
Keyword 1	: Drought tolerance
Endorsement email	:
Keyword 2	: Root biology
Keyword 3	: Phenomics
Title of Entry	: QTLs Identification of Agronomic Traits, Root Morphology and Architecture in KDML105-CSSLs under Flooded and Drought Conditions
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Rice is one of the stable food of world's population. Drought reduces rice yield and impairs rice quality. Improving root morphology and architecture for drought resistance in rice is important because root is a major organ for absorbing water and mineral. Deep rooting improves plant drought avoidance and maintains yield under water stress by increasing water capture from deep soil. This study aims to assess the effects from drought stress on agronomic and root traits and identify QTL controlling these traits under flooded and drought conditions. One hundred and thirty-five KDML105-CSS lines were screened for yield (YLD), 100 grain weight (100SW), flowering time (FT), plant height (PH), tiller number (TN), root angle (RA), root distribution (RD), lateral root density (LRD) and nodal root number per tiller (NRN/T). A RCB design with three replications was conducted at Rice Gene Discovery Unity in wet season of 2016 and intermittent drought was developed. FT, TN, 100SW and NRN/T were significantly reduced by 1.0, 7.7, 2.2 and 9.1%, respectively under drought while LRD was significantly increased by 70.6%. No significant differences were detected for YLD and PH. Moreover, CSSLs have more shallow roots (20-50o) than deep roots (50o-85o) but under stress, shallow and deep root distribution increased by 33 and 65%, respectively. Multivariate analysis shows that YLD under stress was positively correlated with NRN/T, PH and 100SW. QTL were analyzed by ICI mapping with LOD score of 2.5 using single marker analysis. Three QTL were identified for FT on chromosomes 4 and 6, three QTL for PH on chromosomes 1 and 4, four QTL for NRN/T on chromosome 4, one QTL each for shallow and deep root, both on chromosome 4 and one QTL

for LRD on chromosome 3 under flooded condition with total PVE of 18.8, 36.6, 28.4, 4.9, 4.5 and 2.7%, respectively. Five QTL were identified for FT on chromosome 4, six QTL for plant height on chromosome 1 and 3, one QTL for NRN/T on chromosome 4 and one QTL for LRD on chromosome 1 under drought condition with total PVE of 37.8, 42.3, 2.6 and 5.7%, respectively.

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