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Category	: International Rice Research Conference
Select Theme	: Systems physiology
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Endorsement email	
Keyword 2	: Root biology
Keyword 3	: Drought tolerance
Title of Entry	: ROOT TRAITS PHENOTYPING OF RICE GERMPLASM GROWN UNDER MOISTURE STRESS
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Select only one type of presentation	: 15 minute oral presentation				
Abstract	: Rice (Oryza sativa L.) crop is sensitive to water stress, particularly at seedling and reproductive stages resulting in significant yield loss. Aside from growth phenology, secondary traits such as root traits have a pivotal role in reducing risk of yield loss through absorption of water from deep soil layer. In this context, phenotyping of root traits is a desirable approach for identifying genotypes with promising root traits. A set of 190 drought tolerant germplasm lines identified previously from large scale field screening were exposed to PEG-6000 (10%) mediated moisture stress to study their different root traits in hydroponic condition. Observations of different shoot and root traits were taken when maximum number of seedlings started showing leaf rolling, a symptom of moisture stress. Agglomerative hierarchical clustering analysis of genotypes was				

performed based on seven traits to analyze the extent of similarity and differences among the genotypes. Under control condition 20 best genotypes observed to have higher values for more than one root trait which indicates that their tolerance to vegetative stage drought may be based on different root traits. Under stressed condition, genotypes were divided into two groups and in one group, 41 genotypes form a single cluster having high values for six traits, viz., maximum root length (MRL), root dry weight (RDW), shoot dry weight (SDW), root to shoot dry weight (RDW/SDW) ratio, shoot length (SL), maximum root length/shoot length (MRL/SL) ratio and low value for specific root length (SRL), among which again eight genotypes SGM 82, EC 306563, EC 291159, AC 26671, IC516583, IC516168, EC 268909 and IC516122 were found to be most promising having highest values for MRL, RDW, SDW, moderate for SL, RDW/SDW and MRL/SL and lowest for SRL. Two genotypes, N-22 and Dubraj diverged from the other group had a separate but very small cluster having higher values for four traits, MRL/SL, RDW/SDW, RDW, SL and moderate value for MRL. So the commonly observed major traits MRL, RDW, RDW/SDW and MRL/SL and SL can be considered as important root traits for water and nutrient use efficiency and can be further exploited in crop improvement programme. Read Less»

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