

[P4] Crop Genetics and Physiology

Thu. Sep 9, 2021 12:15 PM - 2:00 PM Room 4 (Poster) (Crop Genetics and Physiology)

1:15 PM - 2:00 PM

[P4-40] Genetic Analysis of Root Vascular Traits in a Population from Two *Temperate Japonica* Rice Ecotypes

*Nominated for Presentation Awards

○Ha-An Thi Nguyen¹, Akihiko Kamoshita¹, Poornima Ramalingam^{1,2}, Phoura Y¹ (1.Asian Research Center for Bioresources and Environmental Sciences, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan, 2.Department of Plant Biotechnology, Tamil Nadu Agricultural University, India)

The genetic basis for root vascular traits in rice, despite its direct impacts on root axial and radial hydraulic conductivity, has not been widely studied compared with deep rooting traits. We used five phenotyping datasets (i.e., from maturity stage grown in upland field in 2013, and from vegetative and maturity stages grown in upland and lowland fields in 2019) to quantify the genotypic variations and genomic regions of root vascular traits in a *temperate japonica* mapping population (from lowland Otomemochi and upland Yumenohatamochi). Yumenohatamochi had larger stele transversal area (STA) and total late metaxylem area (LMXA), as well as higher deep root ratio and total root length at deeper layers (>30 cm) than Otomemochi. Root vascular traits were significantly different among progenies in each dataset, and the sum square of each component of genotype-by-environment interactions was less than genotypic variation but their total sum was comparable. From the combined analysis of all five datasets, five out of 13 genomic regions related to root vascular traits were found collocated with deep rooting traits, although no root vascular traits were positively correlated with any of deep rooting traits. Two key genomic regions were (1) RM3703-RM6379 in Chromosome 2 for STA, collocated with a previously reported *qSTA-2* in an *indica* x *japonica* population, and (2) RM1388-RM5503 in Chromosome 4 for STA, LMXA and root transversal area collocated with deep rooting traits. This study is the first report of genomic regions of root vascular traits in a *temperate japonica* mapping population.