Poster Session | Abiotic Stress for Crop Production | P3: Poster Session

[P3] Abiotic Stress for Crop Production

Thu. Sep 9, 2021 12:15 PM - 2:00 PM Room 3 (Poster) (Abiotic Stress for Crop Production)

12:15 PM - 1:00 PM

[P3-41]Genetic Analysis of Drought Response Index in a *Temperate Japonica* Rice Mapping Population

*Nominated for Presentation Awards

OPoornima Ramalingam^{1,2}, Ha-An Thi Nguyen¹, Kamoshita Akihiko¹ (1.Department of Plant Biotechnology, Tamil Nadu Agricultural University, India, 2.Asian Research Center for Bio-Resources and Environmental Sciences, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan, 3.Asian Research Center for Bio-Resources and Environmental Sciences, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan)

Drought response index (DRI), a unique indicator of drought tolerance, was evaluated in a temperate japonica mapping population (97 recombinant inbred lines (RILs) from Otomemochi (OTM) and Yumenohatamochi (YHM)) in 2011 and 2012 under temperate monsoon climate conditions with the different extent of drought intensity during reproductive stage to flowering (i.e., July to August). Relationships between grain dry weight under drought with either 50% flowering date or grain dry weight under control (i.e., as regarded as potential yield) were not strong. DRI in the prolonged intense drought in 2011 (ranging from -6.4 to 15.9) was positively correlated with grain dry weight deriving from panicles that emerged after rewatering. Three genomic regions were identified as QTLs for DRI with phenotypic variation explained ranging from 10.3 % to 26.3% (1) RM3703-RM6911 on chromosome 2 detected in the severer drought year 2011, also in the combined analysis of the 2 years, with its positive allelic contribution from YHM, was co-located with QTLs for drought recovery ability after rewatering and for harvest index. (2) RM3703-RM6379 on chromosome 2 detected in the combined analysis was located relatively close to the first region but with its allelic contribution coming from OTM. (3) RM8102-RM7023 on chromosome 6 detected only in 2012 was co-located with grain dry weight under drought as well as root dry weight under control, with their allelic contribution all from OTM. Relative contribution of QTL x E was larger than main effect QTLs indicating the importance of defining the target environment for drought tolerance.