

## [P3] Abiotic Stress for Crop Production

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

1:15 PM - 2:00 PM

### [P3-18] Mapping of Salinity Tolerance in Rice Through Genome-Wide Association Study (GWAS) at Seedling and Reproductive Stages

\*Nominated for Presentation Awards

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Rice genotypes may have different stress tolerance levels depending on the growth stage of the crop. Studies are needed to investigate whether traits contributing seedling stage tolerance can also contribute to reproductive stage tolerance. In this study, 299 lines from the previously genotyped rice diversity panel 1 (RDP1) were used to assess morphological and physiological traits, and map loci controlling salinity tolerance in rice for both seedling and reproductive stages through genome-wide association studies (GWAS). The salinity stress treatment was 12 dS m<sup>-1</sup> in the seedling stage and 10 dS m<sup>-1</sup> in the reproductive stage. The filtered, 4.8 M SNP dataset from 3KRG Release 1.0 and phenotypic data were analyzed using a linear mixed-model by the R package of GAPIT. The threshold was  $1.11 \times 10^{-8}$  at level of 1% after Bonferroni multiple test correction. GWAS identified highly significant peaks for salinity tolerance at seedling stage on chromosome 5 (SES score); and chromosome 10 (root length, shoot Na<sup>+</sup>:K<sup>+</sup> ratio and vigor) and no significant peaks at the reproductive stage. One variety, Dhala Shaitta, showed salinity tolerance at both seedling and reproductive stages. SES score was strongly correlated with shoot Na<sup>+</sup>:K<sup>+</sup> ratio at seedling stage, and grain yield was highly correlated with leaf chlorophyll a+b content at reproductive stage. Further genetic and physiological studies are needed to divulge the underlying mechanisms and genes involved in seedling and reproductive stage salinity tolerance.