

## [P1] Field Crop Production

2021年9月9日(木) 12:15 ~ 14:00 Room 1 (Poster) (Field Crop Production)

13:15 ~ 14:00

### [P1-06] Identification of Quantitative Trait Loci Controlling Nitrogen Use Efficiency-Related Traits in Rice at the Seedling Stage under Salt Condition by Genome-Wide Association Study

\*Nominated for Presentation Awards

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**Background:** Rice cultivation is facing two severe environmental concerns, salt intrusion and overuse of nitrogen fertilizers. Hence, breeding new varieties aiming to improve nitrogen use efficiency (NUE), especially under salt conditions, is indispensable. However, genetic information related to NUE traits under salt conditions is limited.

**Methods:** A total of 2,391 rice accessions from the 3K Rice Genome Project were selected to evaluate dry weight under two N concentrations (0.36 mM N - LN and 2.86 mM N - SN) crossed with two NaCl concentrations (0 mM NaCl - ONa and 60 mM NaCl - 60Na) at the seedling stage. We carried out an association study for shoot dry weight (SDW), root dry weight (RDW), whole plant dry weight (PDW), the ratio of SDW and RDW (SRR), and relative PDWLN0Na-SN0Na, PDWSN60Na-SN0Na, PDWLN60Na-LN0Na, and PDWLN60Na-SN60Na. The GWAS was conducted with 235,210 SNPs and phenotypic data of 2,391 accessions.

**Results:** A total of 157 QTLs associated with eight tested traits under the four applied treatments were identified by GWAS. Among them, 39, 27, 30, and 31 QTLs were detected under 0SN, 0LN, 60SN, and 60LN treatment, respectively, whereas 12, 5, 4, and 9 QTLs related to the relative PDWLN0Na-SN0Na, PDWSN60Na-SN0Na, PDWLN60Na-LN0Na, and PDWLN60Na-SN60Na were identified. Few QTLs were detected in both treatments of low N and normal N levels or of non-saline and saline conditions. Many QTLs co-located with previously detected QTLs related traits. These results indicated that the false positive probability of the QTLs identified in this study could be very low.