Title: Genome-wide identification of genotype-specific RNA splicing for salt stress response in rice

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Pre-mRNA splicing is an essential step for the regulation of gene expression. In order to specifically capture splicing variants in plants for genome-wide association studies (GWAS), we developed a software tool to quantify and visualize Variations of Splicing in Population (VaSP). VaSP can quantify splicing variants from short-read RNA-seq datasets and discover genotype-specific splicing (GSS) events, which can be used to prioritize causal pre-mRNA splicing events in GWAS. We applied our methods to an RNA-seq dataset from a rice diversity panel exposed to optimal and saline growing conditions. Significant GSS events were used as markers for a GWAS with the shoot Na+ accumulation, which identified six GSS events in five genes significantly associated with the shoot Na+ content. Two of these genes, *OsNUC1* and *OsRAD23* emerged as top candidate genes with splice variants that exhibited significant divergence between the variations for shoot growth under salt stress conditions. To investigate the role of *OsRAD23*, two sets of mutant lines targeting different domains within *OsRAD23* were generated using CRISPR-Cas9 systems. An automated high-throughput imaging was conducted to capture phenotypic differences in wild-type and mutants, with daily imaging for over 2 weeks. Mutant lines exhibited increased shoot growth both under optimal and salt stress conditions. This finding improves our understanding of rice plant mechanisms under salinity stress.