**Genome-wide identification of genotype-specific RNA splicing as the basis of differential response to salt stress in rice**

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Pre-mRNA splicing is an essential step for the regulation of gene expression. To specifically capture the splicing variants in plants for genome-wide association studies (GWAS), we have 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 method 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 variants for shoot growth under salt stress conditions. Phenotypic validation for *OsRAD23* in response to salt stress will be presented.