



PE0858 Characterization of Alternative Splicing Patterns Modulated by Biotrophic Smut Pathogen in Sugarcane

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Body

Alternative splicing (AS) is a key posttranscriptional process in eukaryotes that promotes transcriptome and proteome diversity during growth, development, and response to stress. Genome-wide studies of AS in sugarcane (*Saccharum* spp.) are lacking, mainly due to absence of a high-quality sequenced reference genome, its complex genome architecture and polyploidy. Here, we attempted to analyze sugarcane isoform-level transcriptome and AS landscapes, modulated during infection with smut fungus (*Sporisorium scitamineum*), using a hybrid approach using *Sorghum bicolor* reference-based and Trinity *de novo* mapping tools. Approximately 16,039 and 15,379 transcripts were detected (≥ 2 FPKM) at 5 and 200 days after infection (DAI), respectively. A conservative estimate of isoform-level expressions suggests that approximately 5,000 (14%) of sugarcane genes are alternatively spliced. Differential expression analysis of the miss-spliced genes in healthy and smut-infected sugarcane revealed ~896 AS events modulated at the different stages of infection. Gene family and gene-ontology based functional enrichment analysis of the differentially-spliced genes revealed overrepresented functional categories such as cell-wall, defense, and redox homeostasis pathways. Together, our study provided the first glimpse and insights into the AS landscapes of sugarcane altered during smut disease interactions.