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602-P: Genome-wide characterization of alternative splicing patterns in sugarcane modulated during infection with smut pathogen, *Sporisorium scitamineum*

Monday, August 7, 2017

04:00 PM - 05:00 PM

📍 *Henry B. Gonzalez Convention Center - Exhibit Hall 1*

In eukaryotes, alternative splicing (AS) is a key posttranscriptional process 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 sequenced reference genome and its complex ploidy. Here, we analyzed sugarcane isoform-level transcriptome and AS landscapes, modulated during infection with smut fungus (*Sporisorium scitamineum*), using a combination of *Sorghum bicolor* reference-based and Trinity *de novo* mapping tools. Approximately 15,514 and 14,934 transcripts were detected (≥ 2 FPKM) at 5 and 200 days after infection (DAI), respectively. Approximately 5000 (14%) of the genes were found to be alternatively spliced. Among them, ~415 (8%), ~235 (5%), ~435 (9%), and ~215 (4%) were intron retention, exon skipping, alternate acceptor and alternate donor type of splicing events, respectively. Differential splicing analysis of healthy and smut-infected sugarcane revealed ~14 and ~506 AS events modulated at 5 and 200 DAI, respectively. Gene-ontology and enrichment analysis revealed overrepresented functional categories such as cell-wall modification, defense signaling and oxidative stress among the differentially spliced genes. Together, our study provided new insights and bioinformatics tools to understand sugarcane AS landscapes altered during biotic stress.

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