



Genome-Wide Alternative Splicing Landscapes Modulated by Biotrophic Sugarcane Smut Pathogen

Authors

Renesh Bedre (/pag_2020/speaker/7736f20fa028c8d30dbcb3c7396f6871)

Sonia Irigoyen (/pag_2020/speaker/7736f20fa028c8d30dbcb3c7396f3f79)

Patricia D C Schaker (/pag_2020/speaker/7736f20fa028c8d30dbcb3c7396f6318)

Claudia B. Monteiro-Vitorello (/pag_2020/speaker/7736f20fa028c8d30dbcb3c7396f4da7)

Jorge A Da Silva (/pag_2020/speaker/7736f20fa028c8d30dbcb3c7396f5843)

Kranthi K. Mandadi (/pag_2020/speaker/7736f20fa028c8d30dbcb3c7396f4fa2)

Body

Alternative splicing (AS) of pre-mRNA generates transcriptome and proteome diversity during growth, development, and stress responses in eukaryotes. In sugarcane (*Saccharum* spp.), genome-scale studies of AS are lacking, mainly due to the absence of a high-quality sequenced reference genome, sugarcane's large, complex genome, and aneuploidy and polyploidy of sugarcane cultivars. To identify AS landscape in sugarcane, we performed the isoform-level transcriptome (Illumina RNA-seq) analysis in sugarcane during infection with the smut fungus (*Sporisorium scitamineum*) using a hybrid approach by integrating *Sorghum bicolor* reference based and Trinity de novo mapping tools. Differential expression analysis detected 16,039 and 15,379 transcripts (≥ 2 FPKM) at 5 and 200 days after infection, respectively. Overall, isoform level expression analysis suggested that approximately 5,000 (14%) sugarcane genes undergo AS and differential transcript analysis identified 896 AS events modulated at different stages of smut infection. Analysis of AS landscape revealed that alternative donor (AD) was predominant event followed by intron retention (IR) among the four major AS events. Gene family and gene ontology functional enrichment analysis of the differentially spliced genes revealed overrepresentation of functional categories related to the cell wall, defense, and redox homeostasis pathways. AS generated transcripts that have shown protein-level changes by gain and loss of functional domains. To our knowledge so far, this is the first study of AS in sugarcane and, demonstrates novel insight and bioinformatics approach to explore the AS landscape of sugarcane during smut disease interactions.

Sessions



W1022 Genome-Wide Alternative Splicing Landscapes Modulated by Biotrophic Sugarcane Smut Pathogen

Sunday, Jan 12 10:35 AM

Royal Palm Salon 1-2

(/pag_2020/event/fdc7c9bd19fb3b7d56b32e042b643ee7)