

Identifying Differential Expression and Conserved Alternative Splicing (AS) Events in Zea mays (Maize)

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Zea mays is a staple crop worldwide known for extensive genetic diversity, making it a worthy plant model to study. Alternative splicing (AS) is a post-transcriptional regulatory mechanism in many eukaryotes and can generate multiple transcript isoforms for a single gene through the splicing of mRNA. Studies show that AS contributes greatly to transcriptome diversity in humans and animals. Preliminary studies in Arabidopsis show that AS plays a significant role in a plant's response to stress and can be induced by various abiotic stress conditions, but little is known on how this regulatory process affects staple crops like maize. The purpose of my study was to (1) develop a maize-specific computational workflow to predict differential AS variants, where the events either negatively or positively affect the plant, and (2) to see if these AS events are conserved. To do this, public RNA-seq data was aligned to a reference genome. Stringtie was used to predict transcripts, these were quantified by expression, and filtered through custom-made Python scripts to identify the AS events most likely to encode for a functional protein. SUPPA2 detected differential splicing events across multiple conditions. Based on transcriptional-expression levels, Ballgown was used to determine differentially expressed genes. Evolutionary analysis was used to determine if a particular AS event was conserved between multiple maize inbreds and sorghum. This study will give scientists a better understanding of the complexity of AS events in maize and identify candidate genes that may be tolerant to various abiotic stressors. Since climate change is a serious agricultural issue affecting crop production, understanding how AS contributes to gene function could help foster resilient crop varieties.

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