

Cell-type-specific Transcriptomics Uncovers Spatial Regulatory Networks in Bioenergy Sorghum Stems

Background/Objective

- Bioenergy sorghum is a low-input, drought-resilient, deep-rooting annual crop that has high biomass yield potential enabling the sustainable production of biofuels, biopower, and bioproducts. Stems accumulate high levels of sucrose that could be used to synthesize bioethanol and useful biopolymers if information about cell-type gene expression and regulation in stems was available to enable engineering.
- In a collaboration with the DOE Great Lakes Bioenergy Research Center (GLBRC) to help close the gap in our understanding of sorghum stem biology, we used laser capture microdissection (LCM) to isolate different cell types.

Approach

LCM was used to isolate and collect transcriptome profiles from five major cell types that are present in stems of the sweet sorghum Wray. Transcriptome analysis identified genes with cell-type-specific and cell-preferred expression patterns that reflect the distinct metabolic, transport, and regulatory functions of each cell type.

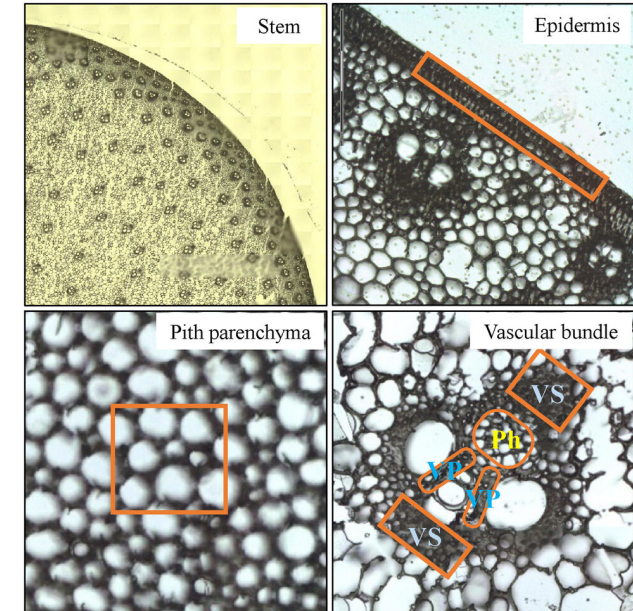
Results

Analysis of cell-type-specific gene regulatory networks (GRNs) revealed that unique transcription factor families contribute to distinct regulatory landscapes, where regulation is organized through various modes and identifiable network motifs. Cell-specific transcriptome data was combined with known secondary cell wall (SCW) networks to identify the GRNs that differentially activate SCW formation in vascular sclerenchyma and epidermal cells.

Significance/Impacts

The spatial transcriptomic dataset provides a valuable source of information about the function of different sorghum cell types and GRNs that will enable the engineering of bioenergy sorghum stems. To assist the community in using this dataset, we developed a web application to provide an interactive and faster way to explore gene-specific expression patterns (<https://mc-lab.shinyapps.io/lcm-dataset/>). To our knowledge, this is the first comprehensive spatial analysis of transcriptomes from sorghum stem cell types.

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Five stem cell types isolated using laser capture microdissection (LCM) have distinct transcriptomes.