Identification of Sorghum stem-preferred genes and their cis-regulatory elements through de novo promoter analysis

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https://cabbi.bio/research/feedstocks-theme/

Project Goals: The goal of this study is to mine tissue-specific transcriptome data sets over development to identify stem preferred genes and their promoter elements that drive strong expression in a stem-specific manner. This study will be expanded by performing experiments to confirm applicability of promoters of these stem-preferred gene to drive strong expression of genes involved in oil biosynthesis for improvement of plant-derived fuel.

Plant-derived fuels present an exciting alternative to fossil fuels. However, a major roadblock to making biofuels a viable alternative is that the amount of energy invested given the amount of return is imbalanced. Increasing the total bio-product content per plant could help to balance the equation, especially when scaled up to the field level. Accumulation of oils or oil precursors in large grass stems is one promising strategy. By identifying stem-preferred genes and exploring their regulatory promoters, we may be able to synthetically drive the strong expression of genes involved in oil biosynthesis and transport in grass stems. Use of native tissue- and developmental stage-specific promoters for genetic engineering may also avoid known negative effects of constitutive promoter expression, such as dwarfing. We performed transcriptome analysis on RNA-seq data from sorghum samples taken from specific tissues over development to identify stem-preferred genes over time and space (McCormick et al, 2018). Using a stringent computational analysis, we identified 14 high confidence, stem-preferred genes, including lipase, a lipid transporter, xylem/phloem pattern formation related proteins, and several transcription factors (TFs). These genes had tissue-specific expression in stems at early developmental stages (juvenile, vegetative); however, during the later stages these genes were expressed at similar levels among stem, flag leaf, and reproductive tissues. Promoter analysis of the stem-preferred genes revealed an over-representation of cis-regulatory elements (CREs) for 14 TF families including MYB, bZIP, C2H2, Dof, and ERF. Subsequent co-expression analysis of the 14 stem-specific genes with all stem-expressed TFs (belonging to the discovered TF family CREs) revealed dynamic regulation of these genes by different TFs at different stages. We are poised to experimentally explore the regulatory role of the discovered TFs and promoter CREs in driving stem-specific gene expression in sorghum.

References

1. McCormick et al., (2018), The Sorghum bicolor reference genome: improved assembly, gene annotations, a transcriptome atlas, and signatures of genome organization. Plant J, 93: 338-354. doi:10.1111/tpj.13781