Stem Parenchyma Cell-specific Gene Characterization in Energycane

Jiang Wang¹ (jwang846@illinois.edu), Ya Chi Yu¹, and Li-Qing Chen¹

¹University of Illinois at Urbana-Champaign, Urbana, IL

https://rogue.illinois.edu/

Project Goals:

Renewable Oil Generated with Ultra-productive Energycanes—or ROGUE—is engineering the two most productive American crops—energycane and Miscanthus—to produce a sustainable supply of biodiesel, biojet fuel, and bioproducts. This work investigates mature stem parenchyma cell-specific genes with the aim to increase oil production in the stem.

Abstract

Triacylglycerols (TAG) are major components of plant oil. Engineering energycane to produce an abundance of TAG for further conversion into biodiesel, biojet fuel, and bioproducts, is an essential goal of ROGUE. Constitutively engineering TAG biosynthesis throughout the plant may produce pleiotropic effects, therefore manipulations should be restricted in a specific tissue or cell type, such as mature stem parenchyma cells, where tremendously stored photoassimilates are available for efficient TAG conversion. However, the information of mature stem parenchyma cell-specific or preferential genes still lacks up to now. Several stem highly expressed candidates were selected from the published sugarcane RNA-seq dataset. The real-time PCR analysis was conducted to confirm the candidate gene expression levels across various tissues at two developmental stages (immature and mature) in energycane. Spatial expressions of candidate genes in the stem were examined using optimized RNA in situ hybridization. Two candidate genes, namely SPCG1 (Stem Parenchyma Cell-specific Gene 1), and SPCG2, were strongly expressed in the mature stem of energycane. Additionally, abundant SPCG2 RNA transcripts were found in the pith parenchyma cells of the mature stem using two different gene-specific RNA probes. Further validating the promoter activities of SPCG1 and SPCG2 in energycane is needed for potential applications of engineering energycane.

References

1. Zhang, J., Zhang, X., Tang, H. et al. Allele-defined genome of the autopolyploid sugarcane Saccharum spontaneum L.. Nat Genet 50, 1565–1573 (2018). https://doi.org/10.1038/s41588-018-0237-2

This material is based upon work supported by the U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research (Award Number DE-SC-0018254).