SUGARCANE ENERGETIC BALANCE: A SYSTEMS APPROACH TOWARDS UNDERSTANDING REGULATION OF SUCROSE METABOLISM AND SUGAR SIGNALING

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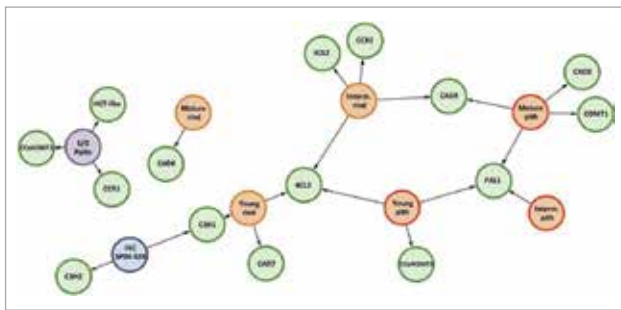FAPESP Process 2008/58031-0 | Term: Aug 2009 to Oct 2013 | Young Investigator

Figure 1. Bayesian network based on the relationships between gene expression, lignin composition, and lignin content data from internodes at three developmental stages and different tissue types of high- and low-lignin content sugarcane genotypes (Bottcher A. et al. 2013)
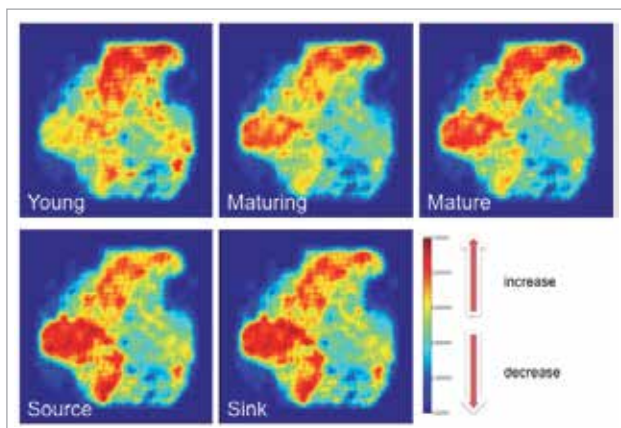

Figure 2. Gene regulatory network of source-sink relationship for sugarcane and its transcriptional activity

Our laboratory has dedicated in developing Systems Biology approach for understanding molecular and physiological aspect of plants species. Sugarcane research has identified and characterized a suite of proteins involved in carbon biosynthesis and sugar sensing. However, current results towards understanding sucrose biosynthesis and accumulation have fallen short of expectations. The molecular mechanisms responsible for the cross talk between these different regulatory and signaling pathways and their diversification in plants still need to be further elucidated to better understand plant growth patterns and biomass production. We are only beginning to produce the detailed gene expression data needed for understanding the network of interactions at a molecular level. To address the rate of gene discovery, high-throughput approaches have being developed for biological experimentation and relevant biological questions regarding gene, protein interactions or networks of biological process can now be addressed. Here, we developed a research approach that integrates molecular and systems biology to improve the knowledge about carbohydrates biosynthesis and sugar regulatory signaling in sugarcane. In this research project we elaborated ways to apply analyses of regulatory network and dynamic metabolic models in molecular and genetic data of sugarcane related with sucrose biosynthesis. We expected that the models captures the regulation of many sugarcane genetic components and anticipate that the data will improve our view of sugar signaling in plants. Simulations of our models will provide an efficient tool for the identification of candidate to genetic manipulations that have the best chance to promote increase in sucrose content and for the prioritization of future analyzes.

SUMMARY OF RESULTS
TO DATE AND PERSPECTIVES

A long-term goal of sugarcane growth modeling is to be able to do analysis based on gene expression data organized into genetic and metabolic pathways that are modeled for interactions. In this study we developed ways to apply analyses of gene regulatory network in molecular, physiological and genetic data of two contrasting sugarcane genotypes submitted to changes in the sink:source ratio. The lowest sucrose content genotype shows the highest levels of chlorophylls and a highest efficiency in the photosystem II, mainly in the middle of the day. This genotype also shows high levels of sucrose in leaves but do not accumulate high levels of sucrose in the stems. The de novo transcriptome analyses results in a total of 191,871 transcripts, where the most of transcripts have at least one hit with viridiplantae known proteins, which almost half of the transcripts are related to sorghum. Alignment against Sorghum genome showed that ~13.3% of transcripts could be ncRNAs. With the comparison of gene networks against different plant species was possible to reduce measurement noise and to reinforce the common signal present in the networks. Using the differential expressed genes identified in the source-sink experiments we can detect more than 50% genes inside regulatory complex conserved across sugarcane and rice. We also detected several gene clusters, including many hubs, which incorporate different regulatory genes (ncRNAs, siRNAs, and miRNAs). In source-sink experiment was possible to detect that 1% of transcripts change its expression to response to the sink manipulation and 5% of transcripts show differential expression between the contrasting sugarcane genotypes. The sugarcane source-sink gene regulatory network shows a strong negative correlation between photosynthetically genes and genes involved in the cell wall metabolism. This study brings new knowledge on the diversification of the regulatory network that controls sucrose metabolism and source-sink balance in sugarcane. The results should contribute to improve our ability to manipulate the biomass production through classical breeding or biotechnological approaches.

MAIN PUBLICATIONS

Vicentini R, Bottcher A, Brito MS, Santos AB, Creste S, Landell MGA, Cesarino I, Mazzafera P. 2015. Large-scale transcriptome analysis of two sugarcane genotypes contrasting for lignin content. *Plos One.* **10**: e0134909.

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