

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

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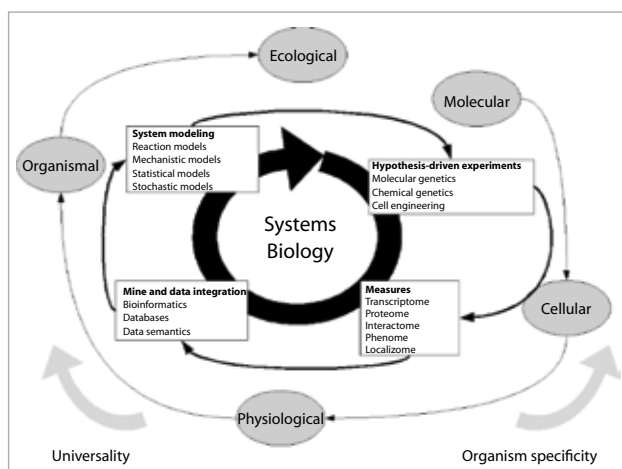


Figure 1. Systems biology overview

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 propose to develop a research approach which integrates molecular and systems biology to improve the knowledge about carbohydrates biosynthesis and sugar regulatory signaling in sugarcane. In this research project we will elaborate ways to apply analyses of regulatory network and dynamic metabolic models in molecular and genetic data of sugarcane related with sucrose biosynthesis, and define the diversification of glucose and sucrose-induced gene expression programs among angiosperms. 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. As an initial step towards an evaluation of the evolutionary conservation of sugar signaling in angiosperms, we are analyzing the short term (0h, 15 min, 2h and 4h) regulation of sugarcane, sorghum, rice and *Arabidopsis* signal transduction components by glucose, fructose, sucrose, trehalose and 3-oxy-methyl-D-glucose. In previous study, 58 genes were regulated by glucose including 44 up-regulated and 14 repressed genes. On the other hand, sucrose treatment resulted in 55 differentially regulated genes, 46 of which were induced while 9 were repressed as compared to the untreated sample. A sugarcane cDNA microarray previously described was used to assess the gene expression program of mature leaves. Three ESTs coding for 14-3-3 proteins were found to be more expressed in mature leaves from a low sugar content population. It was suggested that the members of this family affect carbohydrate metabolism by binding to SPS. This enzyme has several putative phosphorylation sites that regulate its activity by 14-3-3-dependent and -independent mechanisms. Phosphorylation by a kinase, such as SNF1, does not inactivate SPS, but tags the enzyme for 14-3-3 binding which completes the signal-induced transition towards inactivation. In line with these data, the up regulation of three ESTs coding for 14-3-3 proteins in low sugar mature leaves could reflect the inactivation state of SPS and consequently the low sugar content in these plants. Our finding may indicate that the decrease in the expression of these genes in the mature internodes may allow for sucrose accumulation. The knowledge that will be produced by this research will be useful to refine the current acknowledgment and to develop a global model of sucrose metabolism and allocation. Clarification of how the sink acts to regulate source activity in sugarcane will provide researchers with

additional potential targets for manipulation towards improving sucrose yield.

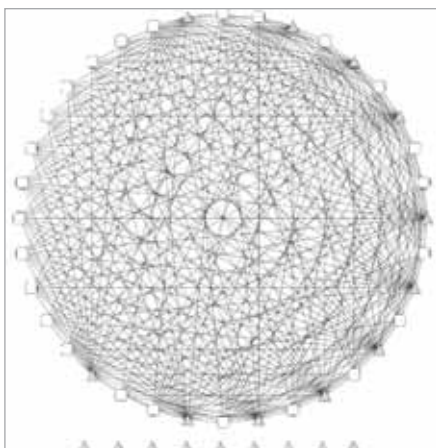


Figure 2. Regulatory network representation of genes coexpressed in sucrose biosynthesis process

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