

Sugarcane transcriptomics: Sugar signaling

Ribeiro C.^{1*}, Labate C.A.¹

¹ Laboratório Max Feffer de Genética de Plantas, Departamento de Genética e Melhoramento de Plantas, Escola Superior de Agricultura Luiz de Queiroz, Universidade de São Paulo, Piracicaba-SP, Brasil.

*E-mail: ribeiro-camila@hotmail.com

Keywords: sugarcane, sugar signaling, sugar accumulation, source-sink relationship.

Sugarcane (*Saccharum spp.*), for its ability to accumulate sucrose in high concentrations has been the focus in diverse biochemical and physiological studies. The relationship between leaf photosynthesis and sugar accumulation in the sink organ, the culm, is still not fully understood. In previous studies it has been observed that the photosynthesis declines during culm maturation in commercial cultivars. Sugarcane leaves appears to possess the capacity to increase the supply of sugars to the culm under increased demand conditions. In higher plants, sugar has an important role controlling the growth and development, however, the signaling networks and its molecular and metabolic components are still not fully understood. To understand the mechanisms related to sugar accumulation and the metabolic sugar signaling networks, we developed an exogenous signaling assay, coupled with HPLC analysis for sugar quantification. For the signaling assay, sugarcane 1+ leaves from the variety SP 80-3280 were treated with solutions of equal osmolarity, 50 µM of the following sugars: sucrose, glucose, fructose, mannose, 3-O-metilglucose, mannitol and water, as experimental control for 3 hours under high light, to represent and simulate a natural photosynthetic system.

Genes related to the metabolism of sugar accumulation and signaling in sugarcane were selected, based in previous studies (McCormick et al., 2008). Specific primers were designed using the SUCEST catalogue for the qPCR experiment. For the gene expression analysis, it was considered the relationship between the genes selected and the treatments applied. The results obtained from these experiments have showed the effects and influences of sugars as metabolic signaling effectors in those different genes. This is the first step for a complete study of the system biology from this signal transduction pathway.

Financing Support: FAPESP Proc. 2008/56100-5 and 2010/03207-7

This document was created with Win2PDF available at <http://www.win2pdf.com>.
The unregistered version of Win2PDF is for evaluation or non-commercial use only.
This page will not be added after purchasing Win2PDF.