

ENERGETIC HOMEOSTASIS AND SUGAR SIGNALING: DIVERSIFICATION OF THE MOLECULAR MECHANISMS INVOLVED IN THE CONTROL OF THE ENERGETIC BALANCE IN ANGIOSPERMS

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To optimize their growth and development, plants, as sessile organisms, have developed a range of efficient mechanisms to sense and respond adequately to ever changing environmental conditions. The production of sugar through photosynthesis primarily relies on light accessibility.

These photosynthetic-derived sugars represent important signals, which, in combination with developmental and environmental cues, such as mineral nutrition, water availability or pathogens attacks, influence the use of energy resources to ensure survival and propagation. Interaction between developmental, hormonal and sugar regulatory signals is deeply involved in growth control and ultimately in biomass production. The molecular mechanisms responsible for the cross talk between these different signaling pathways and their diversification in plants still need to be further elucidated to better understand plant growth patterns and biomass production. Overall, the present proposal aims at unraveling new mechanistic aspects of sugar signal transduction in plants. More specifically, we intend to: 1) define the diversification of glucose and sucrose-induced gene expression programs among angiosperms (sugarcane, rice and Arabidopsis); 2) evaluate and describe glucose-mediated mRNA stability; 3) characterize the function of bZIP transcription factors mediating glucose-related processes; 4) provide new insight into mannose signaling. We anticipate that the data will improve our view of sugar signaling and energy homeostasis control in plants and the results will be integrated into databases that could feed projects related to biomass and bioenergy research.

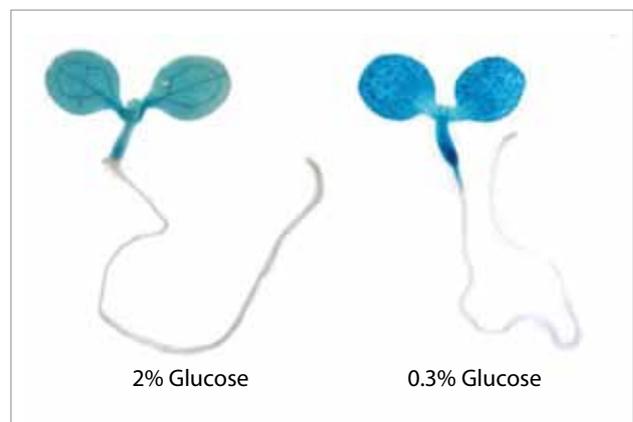


Figure 1. Transgenic *Arabidopsis thaliana* plants expressing *AtbZIP63* promoter: *gusA* fusion was generated and *GUS* expression in seedlings grown in 2% and 0.3% glucose show differential levels of *GUS* activity



Figure 2. *AtbZIP63* promote growth under short day photoperiod. Comparison of wild type (Ws) and *atbzip63-2* nul mutant growth under short day conditions showed that *AtbZIP63* is required for normal growth under these conditions. B) Growth under long days does not require *AtbZIP63*. C) Leaf expansion is altered between Ws and *atbzip63-2* under short days conditions

SUMMARY OF RESULTS TO DATE AND PERSPECTIVES

We found that the Transcriptional Regulatory Factor (TF) AtbZIP63 is a key regulatory node that integrates energetic status, abiotic and biotic signals to adjust growth and development in phase with the diurnal cycle (Figure 2). RNA profiles comparison between AtbZIP63 mutant and wild-type indicates that AtbZIP63 could regulate cell wall expansion and starch degradation which are two important facets of growth. We are in the process of unraveling new aspects of the regulatory networks in which AtbZIP63 is involved and are obtaining important clues about how AtbZIP63 mediates the communication between various environmental signals to adjust growth and development.

We obtained evidences that the control of AtbZIP63 expression is under a complex set of regulatory pathways including, transcriptional, mRNA decay control and protein degradation. The stress-related hormone Abscissic Acid (ABA) and Glucose interact to promote AtbZIP63 mRNA degradation. The underlying mechanisms are being investigated. This data prompted us to analyze at genomic scale the extent of mRNA decay regulation mediated by ABA and/or Glucose. We found that ABA possibly negatively feed-back regulates its own signaling pathway by promoting destabilization of mRNA of ABA receptors and ABA-activated TFs (Figure 3).

We obtained clear evidences for the existence of a mannose-specific signaling pathway and the details of the signaling process are being revealed. We identified a de novo originated Arabidopsis thaliana gene which is involved in the control of starch metabolism. This gene is prone to epigenetic switches that impact its expression in a manner independent of genetic variation. This gene represents a new tool to obtain new insights into the role of epigenetic variation in adaptation/evolution and how epialleles arise.

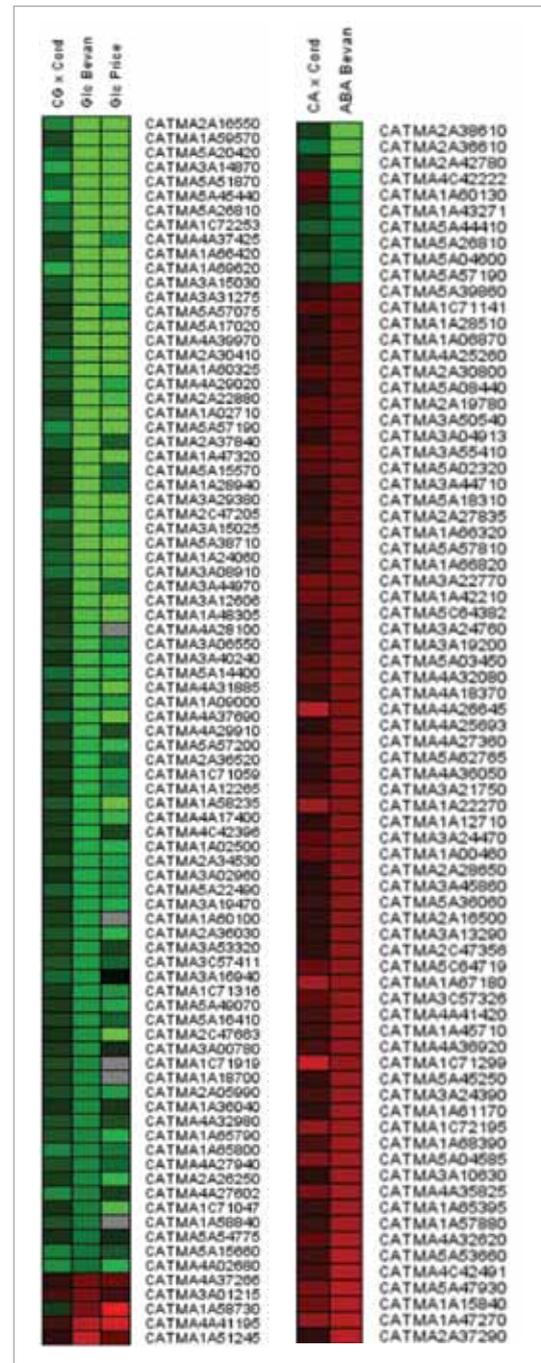


Figure 3. mRNA decay regulation by ABA or Glucose. Expression level heat map highlighting ABA-mediated degradation of mRNA and Glucose-mediated stabilization of mRNA

MAIN PUBLICATIONS

Matiolli CC, Tomaz JP, Duarte GT, Prado FM, Del Bem LE, Silveira AB, Gauer L, Corrêa LG, Drumond RD, Viana AJ, Di Mascio P, Meyer C, Vincenz M. 2011. The Arabidopsis bZIP gene AtbZIP63 is a sensitive integrator of transient abscisic acid and glucose signals. *Plant Physiol.* **157**: 692-705.

Del Bem LE, Vincenz M. (2010) Evolution of xyloglucan-related genes in green plants. *BMC Evolutionary Biology (Online)*. **10**: 341.

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