Metabolic and Transcriptional Changes During Induced Senescence in Maize

Rajandeep Sekhon[1]* (rsekhon@glbrc.wisc.edu), Kevin Childs[2], Nicholas Santoro[2], Cliff Foster[2], Robin Buell[2], Natalia de Leon[1], **Shawn Kaeppler**[1]

1 DOE Great Lakes Bioenergy Research Center, University of Wisconsin-Madison, 1575 Linden Drive, Madison, WI 53706, USA

2 DOE Great Lakes Bioenergy Research Center, Michigan State University, East Lansing, MI 48824, USA

http://www.glbrc.org/

Project goals: The overall goal of this study is to understand molecular mechanisms underlying senescence and carbohydrate partitioning in maize. Understanding the senescence program can facilitate manipulation of the timing of onset of senescence and can provide approaches to extend the duration of active photosynthesis. Excess sugars accumulated following grain fill can improve the sugar content of maize stover and consequently ethanol production, or can be redirected to more energy dense compounds such as oils. This study supports a role for sugar accumulation in inducing senescence in maize inbred B73, and is consistent with the idea that providing a vegetative sink to utilize excess photosynthate can both extend the period of active photosynthesis as well as increase the energy density of vegetative tissue.

Abstract: Plant senescence is a degradative process characterized by catabolism of proteins, lipids, and chlorophyll followed by remobilization of breakdown products to the sink. Delay of senescence, therefore, can extend photosynthetic productivity thereby leading to increased carbon fixation in form of grain and biomass yield. However, biochemical and molecular mechanisms regulating leaf senescence are not well understood. In the current study, pre-mature leaf senescence was induced by removal of seed sink through prevention of pollination, and differential metabolic and global transcriptional changes were assessed in leaves and internodes during normal grain filling period. One of the earliest metabolic changes associated with early senescence was hyper-accumulation of several carbohydrates including free, storage (starch), and

structural (xylose) sugars in leaves, and to a lesser extent in internodes. This was associated with transcriptional up-regulation of genes involved in synthesis of storage and structural carbohydrates, and those involved in sugar transport. These observations strongly suggest that, in maize, the lack of sink resulting from pollination prevention leads to reprogramming of sugar partitioning, and the resulting hyper-accumulation of sugars induces early senescence. It is quite conceivable that onset of natural senescence, which coincides with abolition of seed sink due to cessation of grain filling, also results from accumulation of free sugars. Conversely, therefore, it is possible that the availability of an alternative sink (e.g. stalks, leave) for storage of excessive sugars after completion of grain filling could potentially delay the onset of natural senescence, and provide a means to increase the energy content of biofuel feedstocks. Overlaying expression data onto metabolic pathways revealed that, in addition to the known processes related to senescence, several novel pathways including those involved in cell wall biosynthesis were also up-regulated. Currently, we are exploring the molecular mechanisms underlying altered sugar status and early senescence by exploring natural genetic variation in maize. Senescence transcriptome and natural variation provides a framework for identification of novel genes involved in senescence and sugar partitioning which can be exploited for development of value-added biofuel feedstocks.

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