ScienceDaily®

Your source for the latest research news

Developmental dynamics of the maize leaf transcriptome

Date: November 4, 2010

Source: Boyce Thompson Institute for Plant Research

Photosynthesis is arguably the most impressive feat of nature, where plants harvest light energy and convert it into the building blocks of life at fantastically high efficiency. Indeed modern civilization became possible only with the cultivation of plants for food, shelter and clothing.

While scientists have been able to discover details of the fascinating process by which plants store solar energy as chemical energy, how developing plants build and regulate their solar reactors is still poorly understood. How many genes are involved, and which are the most important? How are different cell types endowed with specific biochemical capacities? What signals fine-tune how much sugar is produced, and which bioproducts are generated? The answers to these questions have applications in agriculture, bioenergy and climate change.

Complex and multifaceted questions such as these can be addressed using a new approach to measure gene expression using high throughput sequencing. This method, coined RNAseq, is detailed in a new report from scientists at the Boyce Thompson Institute for Plant Research (BTI) and Cornell University published online in the journal *Nature Genetics*. The study, using the agronomically critical maize (corn) plant as a model, tracks through massive sequencing of gene transcripts, the full complement of expressed genes in a corn leaf. The researchers found that as the leaf develops, entire suites of genes are turned on and off. "Previous studies have often focused on understanding one gene or set of genes that underpin a specific pathway or process," notes Tom Brutnell, an associate scientist at the BTI and the senior author of the study, "However, these new tools have let us examine the expression of all genes in the leaf at very specific stages of development. This provides an unprecedented view of the genetic circuitry of the leaf."

While such results are exciting, they also pose big challenges as scientists work to interpret the datasets. In this study, over 25,000 genes were found to be expressed in each leaf, and nearly half of these are transcribed into at least two different forms, called splicing variants. To make sense out of this flood of information, scientists at BTI, Cornell, Yale, Iowa State and the University of Toronto collaborated to develop systems biology tools that combine computational and statistical methods to analyze large datasets. "The interface between developmental biologists, molecular biologists, and computer scientists that made this work possible, is an excellent example of why systems biology is able to unravel complex biological pathways" commented David Stern, President of BTI.

An important aspect of this work is that it provides insight into the regulation of the unusual form of photosynthesis that maize utilizes referred to as C4 that increases water and nitrogen use efficiencies under hot dry environments. "Some of the most productive food, feed and bioenergy crops utilize C4 photosynthesis including maize, sugarcane and the bioenergy grass Miscanthus," notes Brutnell "This study provides the first comprehensive analysis of gene expression in any C4 plant and thus provides the groundwork for a genetic dissection of this process."

Given the economic importance of C4 plant in the United States and around the world, these findings have numerous potential applications to agriculture. Optimizing photosynthetic capacity could not only enhance the performance of maize, but also enable far-reaching transformations of photosynthesis in species which are currently far less efficient than maize, such as rice or wheat.

Co-authors included Pinghua Li, Lin Wang and Tesfamichael Kebrom, BTI postdoctoral researchers; Lalit Ponnala and Edwin Reidel, postdoctoral researchers at Cornell, Qi Sun and Chris Myers at Cornell's Computational Biology Service Unit, and Robert Turgeon in Plant Biology. Other colleagues included Yaqing Si and Peng Liu at Iowa State University, Neeru Gandotra, Lori Tausta and Tim Nelson at Yale University and Rohan Patel and Nick Provart at the University of Toronto.

The research was funded by the National Science Foundation and the Bill and Melinda Gates Foundation.

Story Source:

The above story is based on materials provided by **Boyce Thompson Institute for Plant Research**. *Note: Materials may be edited for content and length.*

Journal Reference:

1. Pinghua Li, Lalit Ponnala, Neeru Gandotra, Lin Wang, Yaqing Si, S Lori Tausta, Tesfamichael H Kebrom, Nicholas Provart, Rohan Patel, Christopher R Myers, Edwin J Reidel, Robert Turgeon, Peng Liu, Qi Sun, Timothy Nelson, Thomas P Brutnell. **The developmental dynamics of the maize leaf transcriptome**. *Nature Genetics*, 2010; DOI: 10.1038/ng.703

Cite This Page:

MLA   APA   Chicago

Boyce Thompson Institute for Plant Research. "Developmental dynamics of the maize leaf transcriptome." ScienceDaily. ScienceDaily, 4 November 2010. <www.sciencedaily.com/releases/2010/11/101103135249.htm>.